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(43)		1995/06/01

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(19) (CA) **APPLICATION FOR CANADIAN PATENT** (12)

(54) Gene Signature

(72) Matsubara, Kenichi - Japan ;
Okubo, Kousaku - Japan ;

(71) Same as inventor

(30) (JP) 5/355504 1993/11/12

(57) 28 Claims

Notice: This application is as filed and may therefore contain an incomplete specification.



SMART & BIGGAR
BARRISTERS & SOLICITORS

P.O. BOX 2899, STATION D
55 METCALFE STREET, SUITE 900
OTTAWA, CANADA K1P 5Y6

PCT

The Commissioner of Patents
Ottawa-Hull, Canada

July 7, 1995

Dear Sir:

We enclose the necessary papers in connection with the undernoted application, together with a remittance to cover the filing fees.

PCT INFORMATION (complete only for PCT cases)

International PCT Application No.: PCT/JP94/01916

Filed: November 11, 1994

Request for Entry form/Petition enclosed:

Yes / No

Voluntary Amendment Enclosed:

Yes / No

Affidavit for Reinstatement Enclosed:

Yes / No

Translation of Specification Enclosed:

Yes / No as amended

Included in our cheque is the payment of the Maintenance Fee:

Yes / No

Examination Requested under Section 35(1) of the Patent Act:

Yes / No

File No.

76235-1

Application by

KENICHI MATSUBARA and KOUSAKU OKUBO

Assignment to (if any)

Filing Fee

\$300.00

Assignment Fee

Examination Fee

Maintenance Fee

Reinstatement Fee

TOTAL Fees

File No.	76235-1
Application by	KENICHI MATSUBARA and KOUSAKU OKUBO
Assignment to (if any)	
Filing Fee	\$300.00
Assignment Fee	
Examination Fee	
Maintenance Fee	
Reinstatement Fee	
TOTAL Fees	\$300.00

199507 958 344 1-0 1995
10623
3000 32161 300.00
\$500.00
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Yours truly,

JUL 7 1995
JUL 7 1995

IN THE PATENT OFFICE OF CANADA 76235-1

Request for Entry into National Phase under Articles 22 or 39 of the Patent Cooperation Treaty

IN THE MATTER OF PCT INTERNATIONAL APPLICATION

PCT/JP94/01916 filed November 11, 1994 in the name of

Give full
name of
applicant

KENICHI MATSUBARA and KOUSAKU OKUBO

Both JP

1. The above-identified applicant, whose full post office address is Room 804, 18-1, Yamadahi-gashi 3-chome, Suita-shi, Osaka 565 Japan and 11-26, Segawa 2-chome, Minoo-shi, Osaka 562 Japan respectively owns the entire right in Canada to an invention entitled

GENE SIGNATURE

made by

Give
inventor's
full names
and
addresses
here or on
separate
page

KENICHI MATSUBARA: Room 804, 18-1, Yamadahi-gashi 3-chome, Suita-shi,
Osaka 565 Japan

KOUSAU OKUBO: 11-26, Segawa 2-chome, Minoo-shi, Osaka 562 Japan

as described and claimed in the said international application and any amendments thereto. JUL 7 1995

Strike out if
convention
priority is
not
claimed

2. The applicant claims the protection afforded by Section 28(1) of the Patent Act in relation to the following prior filed applications:

COUNTRY:

DATE OF FILING:

SERIAL NO.:

Japan

November 12, 1993

5/353504

3. The applicant hereby appoints SMART & BIGGAR, of Suite 900, 55 Metcalfe Street, Ottawa, Ontario, whose full post office address for mailing purposes is Box 2999, Station D, Ottawa K1P 5Y6, Canada as

(a) its representative for service of any proceedings taken under the Patent Act; and

(b) its agent with full power to appoint an associate agent when required to do so by Section 144 of the Patent Rules and to revoke such appointment, to sign this request and drawings, to amend the specification and drawings, to prosecute the application and to receive the patent granted on said application, and the applicant hereby ratifies any act done by the said appointees in respect of the said application.

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4. ~~The applicant believes it is entitled to claim status as a small entity as defined under Section 2 of the Patent Rules.~~

5. The applicant accordingly hereby requests commencement of national phase procedures consequent to the designation of Canada in such international application and requests that Letters Patent of Canada for such invention be granted to it.

SIGNED at Ottawa Canada this 7th day of July, 1995
TOWN/CITY COUNTRY

KENICHI MATSUBARA and KOUSAKU OKUBO

By Smart & Biggar
PATENT AGENTS



Ottawa Hull K1A 0C9

Smart & Biggar
P.O. Box 2999,
Station D,
Ottawa, Ontario
K1P 5Y6

Your File
76235-1

FILING CERTIFICATE

Patent File No:	2,153,480	Filed:	1994/11/11
Laid-Open Date:	1995/06/01		
Priority Date :	Japan (5/355504)	19931112	
Invention :	Gene Signature		
Owner(s) :	Matsubara, Kenichi; Okubo, Kousaku		
Inventor(s) :	Same as owner		

SPECIAL NOTICE

You are reminded that annual fees to maintain your application (or patent) are needed for each one-year period between the 1st and 19th anniversaries of the filing date. Failure to pay will lead to abandonment of your application (or lapsing of a patent).

A. McLaughlin

DIRECTOR
PATENT BRANCH



Industrie Canada Industry Canada

OPIC - CIPO 191

Canada

CHECKLIST

1. International Application No. : PCT / JP94 / 01916
2. Date of Entry into National Phase : (D/M/Y) 7 - July / 95
3. a) Priority Date : 12 - 1 Nov / 93
International Filing Date : 11 - Nov / 94
- b) Demand-before 19 months : Yes
- c) Entry at : (20) 32 mo. (Chapter I)
30 or 42 mo. (Chapter II)
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5. Entry Form submitted & checked : Yes
6. Copy of Application submitted (Chapter I) (English or French):
(One sided) As filed: As amended:
7. Maintenance Fees paid (24 months from the International Filing Date) (KC 51501) : Yes No
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Evidence : Yes No Change of name : Yes No
Name and address of inventor : (Yes) No
Due date for submission of info. : -- / -- / -- 26/36 months
Due date for reinstatement for information not submitted by 1st due date : -- / -- / -- 32/42 months
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PCT

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国際事務局



特許協力条約に基づいて公開された国際出願

<p>(51) 国際特許分類6 C12N 15/11, C12Q 1/68 // G01N 33/566</p>	<p>A1</p>	<p>(11) 国際公開番号 WO 95/14772 (43) 国際公開日 1995年6月1日 (01.06.95)</p>
<p>(21) 国際出願番号 PCT/JP94/01916 (22) 国際出願日 1994年11月11日(11.11.94) (30) 優先権データ 特願平5/355504 1993年11月12日(12.11.93) JP (71) 出願人; および (72) 発明者 松原謙一(MATSUBARA, Kenichi)[JP/J] 〒565 大阪府吹田市山田東3-18-1-804 Osaka, (JP) 大久保公策(OKUBO, Kousaku)[JP/J] 〒562 大阪府箕面市瀬川2-11-26 Osaka, (JP) (74) 代理人 弁理士 吉田研二, 外(YOSHIDA, Kenji et al.) 〒180 東京都武蔵野市吉祥寺本町1丁目34番12号 Tokyo, (JP)</p>	<p>(81) 指定国 AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KG, KR, KZ, LK, LR, LT, LV, MD, MG, MN, NO, NZ, PL, RO, RU, SI, SK, TJ, TT, UA, US, UZ, VN, 欧州特許(AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI特許(BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO特許(KE, MW, SD, SZ). 添付公開書類 国際調査報告書 補正書</p>	

(54) Title : GENE SIGNATURE

(54) 発明の名称 ジーン・シグナチャー

(57) Abstract

A 3'-directed cDNA library which accurately reflects the abundance ratio of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has been conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomaly or discriminating cells. The cloned gene can produce proteins utilizable as a medicine or the like.

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(57) 要約

種々のヒト組織から、mRNAの細胞内の存在割合を忠実に反映する3'指向cDNAライブラリーを作成した。該ライブラリーに含まれるcDNAを配列決定し、組織毎の各cDNAの出現頻度を調べた。各cDNAにはmRNA濃度に対応する組織毎の発現情報が付加されているので、該cDNAは、細胞の異常を検出したり細胞の識別をするためのプローブ・プライマーなどとして用いることができる。またクローニングされた遺伝子は、医薬品などに利用し得る蛋白質を産生可能である。

情報としての用途のみ

PCTに基づいて公開される国際出願をパンフレット第一頁にPCT加盟国を同定するために使用されるコード

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DK	デンマーク	LI	リヒテンシュタイン	RO	ルーマニア		

FOREIGN LANGUAGE DOCUMENT

RECEIVED WITH THIS APPLICATION

(DOCUMENT ON THE 10TH FLOOR ZONE 5 IN THE FILE PREPARATION SECTION)

21 534 80

DOCUMENT REÇU AVEC CETTE DEMANDE

DANS UNE LANGUE ÉTRANGÈRE

(DOCUMENT AU 10 IÈME ÉTAGE AIRE 5 DANS LA SECTION DE LA
PRÉPARATION DES DOSSIERS)

DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME _____ DE _____

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

2153480

JUMBO APPLICATIONS/PATENTS

**THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE
THAN ONE VOLUME**

THIS IS VOLUME 1 OF 8

NOTE: For additional volumes please contact the Canadian Patent Office

Specification

Title of the Invention

Gene Signature

Fields of the Invention

The present invention relates to purified single-stranded DNA molecules, purified single-stranded DNA molecules complementary thereto or purified double-stranded DNA molecules consisting of said single-stranded DNA molecules, which can specifically hybridize to human genomic DNA, human cDNA or human mRNA at particular sites. The DNA molecules of the present invention can be used for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting and diagnosing cellular abnormalities due to disease and viral infection, or distinguishing and identifying the cell type, and efficiently cloning genes expressed in a tissue-specific manner. The present invention further includes cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products or the like.

Related Arts

Recognizing the importance of the most fundamental attribute of mRNA, that is, "the nature of the cell is determined by the expression pattern of genes as reflected in the population of mRNA", the inventors of the present invention have proposed "body

mapping" as a unique approach to their objective. This is an entirely novel attempt to prepare "the information on gene expression" for presumably about 200 different kinds of cells and tissues present in the human body and elucidate when, where and to what extent a certain gene is expressed, and map genes to the respective organ or cell type in which they are expressed.

While a variety of cells in the living body express various proteins depending on their respective biological functions, the intracellular concentrations of these proteins vary according to the cell type, stage of development and differentiation, environment, etc.

In general, genes are classified into "genes encoding proteins essential for the life of the cell" and "genes encoding proteins responsible for functions specific to the cell". Of these two, "genes encoding proteins essential for the life of the cell" are expressed constantly in all types of cells and also called "housekeeping genes", while "genes encoding proteins responsible for functions specific to the cell" are often expressed specifically in a particular type of cells or a particular group of cells, and also may be specifically expressed at a particular stage of cellular development and differentiation. Furthermore, they are often "inducible genes" and the amount of their expression varies depending upon the environment to which cells are exposed. In other words, cells may grow as a result of the expression of "genes encoding proteins essential for the life of the

cell" and display their specific functions as a result of the expression of "genes encoding proteins responsible for functions specific to the cell".

However, under abnormal cellular conditions due to disease or infection, the expression of genes within individual cells is altered as compared with that under the normal conditions. Especially, during viral infection, RNAs encoding virus-specific proteins are synthesized in large amounts within the cell, leading to the production of said protein in large amounts. In other words, the alteration in the expression level of genes within the cell, especially as reflected in the concentration of intracellular mRNA, can lead to such abnormal cellular conditions as seen in diseases.

Thus, the function of each cell in the living body is closely related to the expression status of genes within the cell. Accordingly, in order to elucidate the function of each cell at molecular level or to investigate the pathogenesis of a disease at molecular level, it becomes necessary to comprehend the expression status of cellular genes, especially the intracellular concentration of each mRNA.

A theoretically possible approach to this objective is the extraction and analysis of all cellular proteins for determination of expression status. However, although it may be possible to isolate a specific protein, in most cases it is almost impossible to completely isolate all of these proteins, because a great variety of proteins are expressed within the

cell.

Another approach is to directly estimate the concentrations of cellular mRNAs corresponding to all intracellular proteins. However, although it may be possible to isolate a specific mRNA, it is practically impossible to completely isolate all of these mRNAs and directly estimate their amounts, because a great variety of mRNAs are synthesized simultaneously within the cell and furthermore they may be unstable and susceptible to enzymatic degradation during their extraction.

This invention aims to provide DNA molecules which can be used as probes or primers required for detecting the overall or individual expression status of mRNAs coding for the corresponding cellular proteins, detecting or diagnosing cellular abnormalities due to disease or virus infection, recognizing and identifying various cell types, and efficiently cloning genes expressed in a tissue-specific manner. Moreover, the present invention aims to provide cloned DNA molecules which can be used to produce proteins useful as pharmaceutical products.

Summary of the invention

In general, the genetic information flows in order from DNA to mRNA and to protein (F. H. C. Crick, 1958). That is, "the information for the amino acid sequence of a protein" is first transcribed into mRNA and then translated into protein.

To explain this in further detail, mammalian genes commonly comprise a region encoding a protein and a region regulating the expression of said gene. The regions of a gene encoding protein (called "exons") are often separated by intervening sequences (called "introns"). When a gene is transcribed into RNA, the introns of the precursor RNA (pre-mRNA) are excised and exons are connected in tandem to form a contiguous structure coding for a particular protein (this process is called "splicing"). On the other hand, the region regulating the expression of gene comprises, in addition to the regions directly regulating transcription such as a promoter and operator which are present upstream of the transcription region, untranslated regions are located both upstream (5') and downstream (3') of the coding region. In particular, 3' untranslated region (3' UTR) is important for regulating expression, since it contributes to the transport and stability of mRNA. During the processing of pre-mRNA, a methylated cap is added at its 5' end, the 3' untranslated region is cleaved at a specific site, a poly(A) tail is attached by adding 100 - 200 adenylate residues to the cleaved end, and the coding regions are spliced together to form mRNA. The protein is then synthesized after attachment of ribosomes to the mRNA.

The inventors of the present invention have elucidated that, in general, when the intracellular level of a particular mRNA is high, the expressed amount of the correspond-

ing protein is also elevated, and also that it is possible to estimate the relative concentration of each intracellular protein by estimating relative intracellular concentration of the corresponding mRNA [DNA sequence 2, 137-144 (1991); Nature genetics, 2, 173-179 (1992)].

Basically in the present invention, mRNA is extracted from a particular cell and cDNA is synthesized by conventional methods using reverse transcriptase. However, in the present invention, cDNA is synthesized using a method developed by the inventors of the present invention so as to reflect the relative intracellular concentration of mRNA. A cDNA library is constructed and a group of cDNAs representing the population of total mRNA are cloned and sequenced.

An approach which appears to be similar to the one used by the inventors of the present invention but is entirely different, is the method of cloning of a cDNA library constructed by the random priming by Venter et al.

Venter's group randomly cloned cDNAs from commercially available cDNA libraries derived from brain cells (catalog No. 936206, 936205 or 935, Stratagene, California) and determined their base sequences [Science 252, 1651-1656 (1991); Nature 355, 632-634 (1992)].

While the method used by Venter et al. involves sequencing of cDNAs obtained by

random priming, this method has the following drawbacks:

1) Since random cloning of various regions of a single-stranded mRNA may often lead to the formation of many cDNA fragments without any mutual overlapping portions, it is difficult to determine whether these cDNA fragments are derived from the same mRNA or a different one,

2) The longer a mRNA strand, the higher the chance for said mRNA to be reverse-transcribed into cDNA, and

3) Since the availability of each primer to be used among random primers differs depending on their base sequences, the relative frequency of cDNA synthesis is variable.

From aforementioned reasons, the relative frequency of appearance of cDNA does not reflect the relative concentration of cellular mRNA. Consequently, it is impossible to determine the relative concentration of each mRNA and the actual population of intracellular proteins by using the method of Venter et al.

However, with the method developed by the inventor of the present invention, it is possible to construct a cDNA library which precisely reflects the relative concentration of mRNA without any of the aforementioned complications. Since, in the present invention, cDNA is synthesized using only "poly-T" as the primer, the 3' ends of the cDNA have "a poly A tail". Therefore, the synthesis of cDNA with "poly-T" as the sole primer is

initiated from the 3' end resulting in the formation of 3'-oriented cDNA. Since the 3' untranslated sequence is unique to a particular mRNA species and not present in other mRNA species [Birnstiel, M. L., et al., Cell 41, 349-359 (1985)], almost all the 3' end-oriented cDNAs hybridize with specific mRNAs. Digestion of the resulting cDNA with a restriction enzyme MboI which recognizes the specific four-base sequence GATC results in the formation of cDNA extending from the 3'-terminus to the first MboI restriction site. In the present invention, each cDNA thus cloned and included in "a cDNA library faithfully reflecting the relative intracellular concentration of mRNA" is called a "gene signature" (abbreviated as GS hereinafter). A GS includes not only the double-stranded DNA but also each single-stranded DNA thereof.

The present invention relates to a purified single-stranded DNA, purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under the sequence identification number (SEQ ID NO) 1 - 7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA. The present invention also relates to a purified single-stranded DNA, a purified single-stranded

DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) or any portion thereof at its 3' region and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA. The present invention also relates to probes and primers consisting of said single-stranded DNA.

The present invention is explained further in detail as follows.

The DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1 - 7837 but also includes a single-stranded DNA containing a portion of said single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

Furthermore, the DNA of the present invention not only includes a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any of the base sequences listed under SEQ ID NO 1- 7837 (wherein T is read as U) or any portion thereof at its 3' region but also includes a single-stranded DNA (or a single-stranded DNA complementary thereto) containing a portion of said

single-stranded DNA (or said single-stranded DNA complementary thereto) if it hybridizes to human genomic DNA, human cDNA or human mRNA.

In addition, the DNA of the present invention not only includes a single-stranded DNA or a single-stranded DNA complementary thereto but also includes a double-stranded DNA consisting of said single strands.

Obviously, the term "contain" as used herein does not necessarily mean that the DNA of the present invention contains at a single site without interruption (1) "a single-stranded DNA (or a single-stranded DNA complementary thereto) comprising any of the base sequences listed under SEQ ID NO 1-7837 or a portion thereof" or (2) "a single-stranded DNA (or a single-stranded DNA complementary thereto) which is complementary to a mRNA containing any or any portion of the base sequences listed under SEQ ID NO 1 - 7837 (wherein T is read as U) at its 3' region or a portion of said single-stranded DNA." In other words, the term "contain" is applicable also to the case where one or more exogenous bases are inserted in the base sequence of the DNA (1) or (2).

The hybridization to a particular site of human genomic DNA, human cDNA or human mRNA can be achieved under standard conditions (see e.g., Molecular Cloning: A Laboratory Manual, Sambrook, J., et al., Cold Spring Harbor Laboratory Press, 1989).

In the following preferred embodiment, there will be described methods for constructing a

cDNA library which reflects precisely the relative intracellular concentration of mRNA, cloning cDNA groups which correspond to total mRNA, and determining the base sequence of each cDNA.

First, cells from specific tissues, for example, cells from organs, for example, cells derived from human liver (HepG2) are grown, and the total mRNA is extracted by standard procedures. mRNA thus obtained is attached to a vector to construct a cDNA library.

For example, mRNA is attached to the vector plasmid pUC19, which has the M13 sequences flanking the cloning site, as follows.

pUC19 is cleaved by HincII and PstI and poly-T of 20 bp - 30 bp is added to the PstI-digested end to which the 3'-end poly-A tail of the mRNA is hybridized (Fig. 1a). After the DNA strand is extended with conventional methods using reverse transcriptase, a double stranded DNA is formed with DNA polymerase (Fig. 1b). The double stranded DNA thus obtained is cleaved with the restriction enzyme MboI which recognizes a specific four base sequence (Fig. 1c).

MboI, which recognizes a four base sequence (GATC), cleaves the DNA within a few hundred bases from the poly-A tail. Since MboI is found to digest, without exception, about 300 human cDNAs which were randomly selected from the GenBank data base

by the inventor of the present invention, this enzyme cleaves the cDNA to be cloned at a specific site. In addition, as pUC19 is prepared in dam^+ *E. coli*, e.g., *E. coli* JM109 and since its adenine at the MboI recognition site is methylated (G^mATC), it is not cleaved by MboI.

Subsequently, in order to prepare a vector containing the double-stranded DNA which has previously been attached to pUC19 and has the MboI-cleaved end, the pUC19 DNA is digested with BamHI to make termini cohesive with the MboI-cleaved end. Since the recognition sequence of BamHI (GGATCC) contains that of MboI (GATC), the extended portion of the double-stranded DNA is not cleaved with BamHI.

The resulting double-stranded DNA is then circularized by standard ligation methods, and the recombinant vector plasmid thus prepared is introduced into *E. coli*, e.g., *E. coli* DH5 in order to make a cDNA library.

With this method, only a clone containing the base sequence upstream of the poly-A tail of the mRNA is obtained.

Since the average size of the inserted cDNA fragment is relatively small, 270 bp, it is free from biased cloning resulting from variations in the efficiency of cDNA synthesis and transformation that occur in the case of larger sized DNAs. Furthermore, because instability due to repeated base sequences and the like is eliminated, the cDNA library of

the present invention faithfully represents the relative concentration of mRNA in the cell.

Furthermore, when the cDNA inserted into the vector is relatively short, it is possible to accurately amplify the cDNA fragment using the sequence of the vector flanking it as a primer. It is also possible to determine the base sequence from the 5' end directly by the PCR without interference from the 3' poly-A tail which will reduce the accuracy of sequence determination.

Amplification of the GS, i.e., the cDNA fragment inserted into the vector, is performed as follows.

The *E. coli* cells in which the cDNA library is introduced are grown using standard methods and lysed. Debris contained in the bacterial lysate are removed by centrifugation and the supernatant containing the vector DNA is recovered. The vector DNA thus obtained is used as the DNA template for amplification by the PCR (Fig. 1d, amplification with PCR primers 1 and 2).

Base sequences flanking both ends of the GS is properly selected for use as primers and the PCR is performed under standard conditions. PCR products thus obtained are subjected to the elongation reaction using fluorescence primers complementary to the vector sequence flanking the 5' end of the GS, and the sequence is determined with an

autosequencer (Fig. 1d, sequence determination with dye primer).

Based on the results of the sequence determination of each GS, the species and the frequency of appearance of the GS in each tissue or cell type are analyzed.

As to each cell type not only normal cells but also cells under pathogenic conditions (such as tumor cells, virus infected cells, etc.) can be used without any restriction. For example, liver cells (from fetus, neonate or adult), various hematopoietic cells (granulocytic, monocytic, etc.), lung cells, adipocytes, endothelial cells, osteoblasts, colon mucosa cells, retinal cells and hepatoma cells (HepG2, etc.), and promyelocytic leukemia cells (HL60, etc.) will be used. The appearance frequency for each GS is described for each cell type in Tables 1 through 219. There, patent number represents "SEQ ID NO for each GS", size represents the "length of each GS", and F represents the "sum of appearance frequencies in the cells studied". In addition, hepG2 stands for "hepG2 (a liver cancer cell line)", HL60 stands for "HL60 promyelocytic leukemia cell line", granulo stands for "granulocytoid, HL60 stimulated by DMSO", mono stands for "monocytoids, HL60 stimulated by TPA", 40 w liver stands for "40 w neonatal liver", 19 w liver stands for "liver of a 19 weeks old fetus, adult liver is "adult liver ", lung stands for "adult lung", adipose stands for "subcutaneous adipose tissue", endothel stands for "primary cultured aortic endothelium", osteoblast stands for "primary cultured osteoblast", colon mucosa is

"colon mucosa", small cell carci stands for "small cell carcinoma of lung", retina is "retina", cerebral cortex is "cerebral cortex", adenocarci (lung) stands for "adenocarcinoma of lung", squamous cell ca (lung) stands for "squamous cell carcinoma of lung", keratinocyte stands for "primary cultured keratinocyte", fibroblast stands for "primary cultured fibroblast", Alzheimer stands for "Alzheimer temporal lobe", cerebellum stands for "cerebellum", visceral fat is "visceral fat", corneal epithelium is "corneal epithelium", peripheral granulocyte is "peripheral granulocyte", neuroblastoma is "neuroblastoma" and taste bud of tongue is "taste bud of tongue".

"Accession number of target mRNA" represents the accession number of the entry in GenBank Release 79 whose base sequence has homology with that of each GS, "match %" represents the percent homology of the GS sequence relative to that of said homologous sequence, "match starts at (GS)" represents the base position counted from the 5'-end of the GS at which the region for homology calculation starts, "match starts at (GenBank)" represents the base position counted from the 5'-end of the GenBank sequence at which the region for homology calculation starts, and "GenBank target size" represents the whole length of the GenBank sequence corresponding to the GS. The columns in Tables 1 - 219 represent the same items as in Table 1.

Based on the data in Tables 1 - 219, each GS can be classified into several groups.

A GS, which is expressed at high frequency in a specific cell or groups of cells with similar property, for example, promyelocytic leukemia cell, granulocyte and monocyte and not expressed entirely or expressed very little in other cells (groups), is a likely GS corresponding to the gene encoding "the protein responsible for functions specific to the cell" (e.g., GS0001553, GS0002047, GS0004895, etc.). On the other hand, a GS, which is expressed commonly in every kind of cell, most likely corresponds to the gene encoding "the protein essential for the life of the cell" (e.g., GS0000019, GS0000155, GS000861, etc.). In addition, some GSs are expressed at low frequency (e.g., GS0000013, GS0002399, GS0003155, etc.).

Since the GS with the sequence determined as described above will reflect the population of mRNA expressed in a particular cell, it must be possible to find the relative concentration of mRNA in each cell by determining the appearance frequency for each GS in a cDNA library derived from that cell. Therefore, to confirm the correlation between the appearance frequency for each GS in a cDNA library and the relative concentration of cellular mRNA, the GS thus obtained was labeled with ^{32}P by standard methods and used as the probe in the following hybridization test. mRNA isolated from a specific cell is hybridized to said ^{32}P -labeled probe under standard conditions. The results of this Northern hybridization test were such that, when a GS found with high appearance

frequency in a cDNA library was used as a probe, a dense band was formed, confirming the correlation of the frequency of appearance of the GS with the relative concentration of mRNA in the cell (see Example 5).

Similarly, the colony hybridization test of the cDNA library constructed as described above with a ^{32}P -labeled probe prepared as described above showed a close correlation between the frequency of appearance of the GS and the number of colonies hybridized with said GS (see Example 6), confirming the correspondence of the frequency of appearance of the GS and relative concentration of the GS in a cDNA library.

From the above results, by determining the appearance frequency of each GS in a cDNA library derived from a variety of cells, it has become possible to determine the expression status of the gene (or mRNA) corresponding to each GS. This fact implies conversely that each GS may be useful for industrial purposes as a specific probe or primer encoding information about the expression status of its corresponding gene (or mRNA) for each cell. For example, when it is proven that "a certain GS appears at high frequency only in a cDNA library derived from tissue A, that is, the gene corresponding to said GS is specifically expressed only in tissue A", by conventional cloning of the corresponding full-length cDNA using said GS as a probe or primer, it is possible to clone a full-length gene which is expressed in a tissue-specific manner.

Furthermore, for example, when it is proven that "the frequency of appearance of a certain GS is low in a cDNA library derived from tissue B, that is, the appearance frequency of the gene corresponding to said GS is low in tissue B", by examining the expression frequency of the gene corresponding to said GS in a test sample of tissue B from a patient using said GS as a probe or primer, it may be possible to identify the pathogenic gene, wherein an unusually high expression frequency of said gene being a strong indication that said GS may be the gene involved in the pathogenesis. Furthermore, by conventional methods for cloning said full-length cDNA using said GS as a probe or primer, it is possible to isolate said pathogenic gene and elucidate its characteristics.

In practice, the DNA of the present invention may be used as a probe or primer for detecting and diagnosing disease, cloning a pathogenic gene or related gene, cloning a viral gene, identifying and recognizing cell types, cloning a species-specific promoter and gene mapping.

One GS corresponds to one mRNA. It is therefore obvious that any portion of cDNA complementary to each mRNA carry the same "information for expression" as the GS. Accordingly, the DNA of the present invention is not restricted to "the DNA comprising the GS itself or portion thereof", but also includes the DNA comprising, for example, "a full-length cDNA complementary to each mRNA" and "the non-GS region of the cDNA

complementary to each mRNA or a portion thereof". They can be used as a probe or primer comprising the same "expression information" as that of the GS and can be used as a probe or primer in a similar manner as a GS. For example, by using a GS or a portion thereof as a probe or primer, it is obviously possible for those skilled in the art to readily isolate "a full-length cDNA corresponding to each mRNA" or "the non-GS region of the cDNA complementary to each mRNA or a portion thereof". For example, as described hereinafter, conventional techniques such as "5' RACE", "nesting" and "inverse PCR" can be used.

An example of the method for detecting disease using the GS of the present invention will be described. As shown in Tables 1 - 219, with the method described above it is possible to detect a GS present specifically in a cDNA library constructed from each tissue by detecting and comparing the frequency of appearance of GS in each tissue. It is also possible to identify a GS corresponding to a protein which is expressed commonly in various tissues or which is expressed at low frequency. These GSs are denatured and then fixed on an appropriate filter, for example, nylon filter or nitrocellulose filter. It is convenient to use a single filter with many GSs fixed on it. Usage of a single filter on which many denatured DNAs are fixed is well known. An example may be "the Escherichia coli Gene Mapping Membrane" (Takarashuzo, code No. 9035). It is a single nylon

filter on which the cosmid contigs of genomic DNA of *E. coli* are fixed. It is possible to prepare a filter comprising a group of specific GSs corresponding to proteins expressed in a particular tissue, a filter comprising a group of GSs corresponding to proteins commonly expressed in various tissues, or a filter comprising a group of GSs corresponding to proteins expressed at low frequency. The single-stranded GSs fixed on these filters are then hybridized to labeled complementary DNA fragments synthesized using "random primers" prepared from template mRNA extracted from a test tissue, using four labeled nucleotides and reverse transcriptase (labeled mRNA can also be hybridized to the filters). Similarly, labeled complementary fragments synthesized using mRNA extracted from normal tissue as the template are hybridized (labeled mRNA can also be hybridized to the filters). If the profile of hybridization to a group of GSs has been categorized beforehand by comparing the hybridization profile of various pathogenic tissues to that of corresponding normal tissues, it is possible to diagnose the pathogenic condition of a particular test tissue by comparing the hybridization profile of the test tissue with that of the corresponding normal tissue and assigning that profile to a certain category. Virus infection can be detected in the same manner as in the case of other diseases.

Next, an example of the method for cloning pathogenic genes or their related genes using the GS of the present invention is described. As described above, using the filter on

which denatured GSs are fixed, the GS-hybridization profile of various pathogenic tissues and that of corresponding normal tissues are compared. A considerable difference in the hybridization intensity between normal and pathogenic tissues will be an indication that the particular GS corresponds to a pathogenic gene. If a filter comprising only GSs specific for a particular tissue is applied to a sample from that particular tissue, the probability for detecting the GS with a great difference in hybridization intensity is elevated. Also a filter comprising GSs corresponding to proteins whose expression is low will facilitate the identification of the GS corresponding to the pathogenic gene by detecting an intense signal, because the hybridization signal for these GSs is usually weak. Once a GS corresponding to a pathogenic gene is found, said pathogenic gene can be cloned by established methods such as genomic Southern hybridization using said GS as a probe and/or a primer.

Furthermore, a method for cloning a full-length gene using a GS as a probe or primer is described in detail. Cloned genes isolated in the present invention are also appropriate for use in the production of proteins useful as pharmaceutical products. mRNA is extracted from tissues by conventional methods and cDNA libraries are then prepared (See Molecular Cloning, 2nd ed. Vol. 2, Section 8 New York; Cold Spring Harbor Laboratory). In this case, it is desirable to extract mRNA from tissues in which the target gene is highly expressed. One method to detect a specific gene in libraries thus

prepared is, for example, to select positive clones via hybridization using a whole or partial GS as a probe. In general, since a GS is specific for a particular mRNA, hybridization can be carried out under certain stringent conditions. Probes used are at least more than 25 bases long, preferably more than 50 bases long, and more preferably more than 100 bases long.

Furthermore, if cDNA libraries, in which the cDNA for a specific gene is concentrated, are prepared, they will be preferable for selecting said specific gene. One method useful for this purpose is carried out as follows: 1) preparation of an affinity chromatographic column of resin on which the denatured GS corresponding to the specific gene is fixed; 2) application of mRNA extracted from a tissue to said column and retention of the mRNA species corresponding to the specific gene on said column; 3) elution and concentration of said retained mRNA; and finally 4) preparation of cDNA libraries using said concentrated mRNA species as the template. Another method is the selective amplification of cDNA corresponding to the specific gene by the PCR. Selective amplification of a specific gene is carried out as follows: using a partial sequence of a GS localized toward the 3' end of the specific gene as primer, cDNA is synthesized from mRNA with reverse transcriptase and 4 NTPs. To the 3' end of a single-stranded cDNA thus obtained a homopolymer such as poly-T is attached by the action of "terminal deoxyribonucleotide

transferase (TdT)". In addition, using "a primer complementary to the homopolymer" and "a primer used in said reverse transcriptase reaction, or a primer whose sequence is included in the same GS but is located proximal to the 5' end", cDNA corresponding to the specific gene may be selectively amplified by the PCR [see 5'RACE (5' Rapid Amplification of cDNA ends): PNAS, Vol. 85, pp. 8998 - 9002 (1988); Nucleic Acids Res., Vol. 17, pp. 2919-2932 (1989)]. In addition, instead of the attachment of a homopolymer, there is another method comprising the following steps: 1) a single stranded anchor DNA is linked to the 3' end of a single stranded cDNA using "T4 DNA ligase"; and 2) said cDNA is amplified by the PCR using a primer complementary to said anchor DNA [Nucleic Acids Res., Vol. 19, pp. 5227-5232 (1991)]. Said primer is desirably more than 13 bases long, preferably more than 15 bases long, and more preferably more than 18 bases long. Furthermore, in order to enhance the efficiency of heat denaturation in the cycling reaction, said primer is preferably less than 50 bases long and more preferably less than 30 bases long. By linking said amplified DNA to a vector, a cDNA library concentrated with respect to the target gene is prepared.

In addition, it may be also possible to isolate a cDNA clone corresponding to the specific gene directly from the PCR products. Specifically, the PCR products are first separated by gel electrophoresis, subjected to Southern blotting analysis using the dena-

tured GS as a probe, and examined for the presence of a band which specifically hybridizes to said GS. If a GS-hybridized band is detected, it is highly possible to isolate the cDNA clone corresponding to the specific gene by excising said band from the gel and subjecting it to direct cloning.

As described above, in order to further amplify the specific gene previously amplified by the PCR, it may be possible to perform the second PCR of the primary PCR products by replacing either or both primers previously used with a primer having the base sequence internal to said two primers (nesting) (Journal of Virology, Vol. 64, p. 864 (1990)). Nesting may be performed directly upon the products of the primary PCR.

Alternatively, if a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of the primary PCR products, nesting may be performed for the DNA obtained by excision of the band followed by extraction. In the case where a band which specifically hybridizes to the GS is detected by the Southern blotting analysis of nested products using the denatured GS as a probe, it is highly possible to successfully isolate the cDNA clone corresponding to the target gene by excising said band from the gel and subjecting it to direct cloning.

The isolated cDNA clone corresponding to the target gene may often correspond to the full-length mRNA, but it may be a cDNA with the 5' end deleted. In the case where

the 5' end is deleted, it is possible to isolate the full-length cDNA clone by conventional methods. For example, by screening a cDNA library using a probe comprising the base sequence in the 5' end region of the cloned cDNA, since the target position of said probe is shifted further toward the 5' end of the full-length cDNA than in the case of using a GS as a probe, it is possible to isolate only longer cDNA clones as the positive clone. Also by synthesizing cDNA using "a primer comprising the base sequence in the 5' end region of the cloned cDNA" with mRNA as the template followed by PCR amplification of "a single stranded cDNA having a homopolymer or anchor DNA sequence at the 5' end" and using "the primer used for previous cDNA synthesis or a primer having the sequence internal to that of said primer" and "a homopolymer or a primer complementary to anchor primer" as described above for the 5' RACE method, only the sequence toward the 5' side of the cDNA may be selectively amplified since the position of said primer is shifted further toward the 5' side of the full-length cDNA. Even if the cDNA thus obtained has a deletion at the 5' end, the population of cDNA fragments covering the full-length of the long cDNA may be obtained by repeating this procedure. It may be easy for those skilled in the art to obtain a full-length cDNA by suitably linking said cDNA fragments having overlap segments together.

Alternatively, by performing the inverse PCR (Inverse PCR: Genetics, Vol. 120, p.

621 (1988); Molecular Cloning, 2nd ed., Vol. 2, 14.12-14.13 (New York; Cold Spring Harbor Laboratory)), it may be possible to isolate a cDNA clone extending externally from the GS, that is, in the genomic DNA region. Specifically, the target DNA (genomic DNA or cDNA) is digested with restriction enzymes into fragments of about 2-3 kb and then circularized by ligating the cleaved ends. By performing the PCR for said DNA using "a set of primers which are complementary to the cDNA clone isolated using the GS or the GS as a probe or primer, and thereby making the direction of DNA synthesis mutually opposite (outward), it may be possible to amplify the DNA region extending externally from the GS. There is known a method to isolate a full-length genomic DNA of a specific gene by repeating this procedure (Nucleic Acids Res., Vol. 16, p. 8186 (1988)).

In addition, although "Taq polymerase" is conventionally used in the PCR described above, the cloning procedure may be more efficiently performed using the "LAPCR (long and accurate PCR" technique (Nature Genet., Vol. 7, p. 350-351 (1994), Nature., Vol.369, p.684-685(1994)).

Furthermore, needless to say that by linking said full-length gene thus obtained to a suitable expression vector followed by its expression in an appropriate host, it is possible to obtain the corresponding gene product (Molecular Cloning, 2nd ed.).

Next, there will be described an example of the method for identifying and recognizing cell types using the GS of the present invention. As shown in Tables 1 - 219, based on the appearance frequency of GS in each tissue and its comparison among tissues, it is possible to identify those GSs specifically present in a cDNA library constructed for each tissue. These "tissue-specific GSs" are fixed on a filter. It will be more convenient if GSs specific to each tissue are collected and fixed on a filter as a whole (e.g., a GS block specific for hepatocytes or cerebral cortex cells). As described above, to this filter are hybridized labeled complementary fragments synthesized using "random primers" prepared from mRNA extracted from test tissues or cells, "nucleotide containing 4 labeled nucleotides", and "reverse transcriptase". (Directly labeled mRNA can also be hybridized to the filters.) Depending on the type of tissues or cells, intense hybridization signals will be observed with the GS groups specific to said tissue or cell. Furthermore, a tissue-specific promoter can be cloned by structure analysis of the 5' upstream sequence through the cloning of the corresponding gene using established methods such as genomic Southern hybridization with the "tissue-specific GS" as the probe and/or primer.

These tissue-specific promoters thus obtained are useful for gene therapy in the future.

Gene therapy in a narrow sense aims to supplement the defective protein of patients

using gene technology, and in this case it is necessary to express the exogenous gene in a desired tissue in a desired quantity. For this purpose, a promoter which is known to be expressed in a specific tissue in a desired quantity (in most cases a large quantity is desired) is highly useful. Although, at present, a virus promoter is often used, it can be inactivated by endogenous modification such as methylation. Promoters provided by tissue-specific GSs will be ideal substitutes for viral promoters.

There will be described the method for chromosomal assignment of DNA corresponding to the GS of the present invention using the probe derived from the GS obtained as described above.

First, the Southern blotting method will be described.

According to this method, for example, chromosomes are isolated from a lymphoblast cell line of human normal karyotype (e.g., GM0130b), and then a monochromosomal hybrid cell is prepared by introducing each human chromosome into non-human cells, such as rodent cells, and cultured on a large scale by standard methods. Then the DNAs extracted from said hybrid cells are digested with various restriction enzymes and subjected to agarose gel electrophoresis. Then, the electrophoresed DNAs are hybridized to ³²P-labeled GS prepared as described above and used as the probe. By identifying the hybrid cell the DNA of which is hybridized to said probe, it is possible to identify the

chromosome in which the DNA corresponding to the GS of the present invention is present. Southern hybridization test of the total human genomic DNA using each labeled GS as a probe formed a single band corresponding to the GS, indicating that the DNA of the present invention can be used as a desirable probe for human genomic DNA. It is obvious that a desirable probe for human genomic DNA can be used also as a desirable probe for human cDNA and human mRNA.

A method similarly using the PCR to determine chromosomal localization of the GS of the present invention will be described.

To prepare most appropriate primers, base sequences are selected from the sequence of the GS in question by conventional methods, for example, by using the computer software OLIGO4.0 (National Biosciences) and the oligonucleotides (20-24mer) having the selected sequences are synthesized. The preferred size of the sequence to be amplified by the PCR is from 50mer to 100mer.

Using the primers thus synthesized and the chromosomal DNA extracted from the monochromosomal hybrid cell as such as the template, amplification by the PCR is performed in a conventional manner. Resulting PCR products are subjected to non-denatured acrylamide gel electrophoresis and stained with ethidium bromide for fluorescent detection. The sizes of these PCR products are then determined.

Chromosomal assignment is confirmed when the presence of a PCR product of correct size is confirmed.

It is evident that a chromosome or chromosomes in which the DNA corresponding to a GS is localized can be identified by using these procedures. It has also become evident that the DNA of the present invention can be used as desirable primers for human genomic DNA since a single band has resulted from amplification of the total human genomic DNA by the PCR using primers designed based on each tested GS. Obviously, a desirable primer for human genomic DNA is also a desirable primer for human cDNA and human mRNA.

Brief Description of Figures

Fig. 1 shows the preparation of 3' MboI cDNA library.

Fig. 2 shows the results of tests of primers. A shows the location of primers on the vector; and B shows the electrophoretic patterns of DNA fragments amplified using the primers (A). Primers used are as follows: lane 1, FW (-40)/RV (-14); lane 2, FW (-40)/RV (-36); lane 3, FW (-40)/RV (-71); lane 4: FW (-40)/RV (-29); and lane 5, FW (-47)/RV (-48). Artifacts are indicted by arrows.

Fig. 3 shows the electrophoretic pattern of PCR products using FW(-40) and RV(-14) as primers. The lane at the right end shows the electrophoretic pattern of size

markers and the other lanes show the PCR products using FW (-40)/RV (-14) as primers.

Fig. 4 shows the mRNA concentration reflecting the frequency of appearance of each GS in the cDNA library: especially, Figs 4A - 4D, experimental results; Fig. 4E, photographs of colonies; and Fig. 4F, summary.

Fig. 5 shows the appearance frequencies for various cDNAs in the 3'-directed HepG2 cDNA library.

Fig. 6 shows the genetic mapping of each GS (gs) using PCR.

Fig. 7 shows the genetic mapping of each GS (gs) using PCR.

Fig. 8 shows the genetic mapping of each GS (gs) using PCR.

Fig. 9 shows the genetic mapping of each GS (gs) using PCR.

Fig. 10 shows the genetic mapping of each GS (gs) using PCR.

Fig. 11 shows the chromosomal mapping of GS001418 (gs001418) using PCR.

Fig. 12 shows the chromosomal mapping of GS001457 (gs001457) using PCR.

Fig. 13 shows Southern blotting of human total chromosomes using the GS as a probe.

Fig. 14 shows Southern blotting of human total chromosomes using the GS as a probe.

Fig. 15 summarizes the characteristics of hybrid cells used for Southern hybrid-

dization.

Fig. 16 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000152 (clone s14g02) as a probe.

Fig. 17 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000041 (clone s650) as a probe.

Fig. 18 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000181 (clone hm01e01) as a probe.

Fig. 19 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000055 (clone c13a18) as a probe.

Fig. 20 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000180 (clone s479) as a probe.

Fig. 21 shows Southern blotting of chromosomal DNA from the hybrid cells using GS000094 (clone s173) as a probe.

Fig. 22 shows Southern blotting of chromosomal DNA from the hybrid cells using junk (clone hm01g02) as a probe.

Fig. 23 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double cleavage with EcoRI and BamHI.

Fig. 24 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Fig. 25 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Fig. 26 shows the chromosomal mapping of each GS by Southern blotting. E stands for EcoRI, Ba stands for BamHI, Bg stands for BglII and E/B stands for double digestion with EcoRI and BamHI.

Preferred embodiments of the invention

In the following section, there will be explained preferred embodiments of the present invention. However, the present invention will not be restricted to these preferred embodiments.

[Example 1]

Preparation of mRNA

Cytoplasmic RNA was extracted from a liver cancer cell line HepG2 (Aden., et al., Nature 282, 615-617, 1979) using standard procedures [Sambrook, J., et al., Molecular Cloning, 2nd ed. (New York: Cold Spring Harbor Laboratory), vol. 1, pp. 7.3-7.36, 1989].

Briefly, HepG2 cells grown in Dulbecco's modified Eagle medium supplemented with 10% FCS were lysed in RNA extraction buffer [0.14 M NaCl, 1.5 mM MgCl₂, 10 mM Tris-HCl (pH 8.6), 0.5% NP-40, 1 mM DTT, 1000 units/ml RNase inhibitor (Pharmacia)] by using a Vortex mixer for 30 sec and then left standing on ice for 5 min. Nuclei and other cell debris were precipitated by centrifuging at 12,000 g for 90 sec, and the supernatant was deproteinized with Proteinase K followed by phenol extraction. RNA was precipitated by isopropanol and rinsed with 70% ethanol. Finally, the poly A⁺ fraction was collected by oligo dT column fractionation (Aviv., et al., Proc. Natl. Acad. Sci. USA 69, 1408-1412, 1972).

[Example 2]

Preparation of vector primer DNA and construction of cDNA libraries

To prepare a vector primer, pUC19 DNA amplified in JM109 cells (Yanisch-Perron, C., et al., Gene 33, 103-119, 1985) was digested with PstI to completion and a poly T-tail was added with terminal transferase (Pharmacia) to a mean length of 26. This process was monitored by the incorporation of ³H-deoxythymidine triphosphate [Okayama, H., et al., Methods in Enzymology (San Diego: Academic Press), vol. 154, pp. 3-28, 1987]. The product was digested by HincII, and the resulting short fragments were eliminated by chromatography with Sepharose S-300. Then the T-tailed plasmid was purified by an

oligo dA column and stored in 50% ethanol at a concentration of 1 $\mu\text{g}/\mu\text{l}$.

Fig. 1 shows the outline of the construction of the cDNA library. Two micrograms each of the cytoplasmic Poly A⁺ RNA and the vector primer DNA were co-precipitated in 70% ethanol containing 0.3 M Na-acetate and the pellet was dissolved in 12 μl of distilled water. For the first strand synthesis, after heat denaturation at 76°C for 10 min, 4 μl of 5 x reaction buffer [250 mM Tris-HCl (pH 8.3), 375 mM KCl, 15 mM MgCl₂], 2 μl of 0.1 M DTT and 1 μl of 10 mM each of dATP, dCTP, dGTP and dTTP were added to the sample at 37°C. The reaction was initiated by the addition of 200 units of reverse transcriptase MMLV-H-RT (BRL), and after incubation at 37°C for 30 min, stopped by transferring the reaction tube onto ice. For the second strand synthesis, to the aforementioned reaction mixture the following was added: 92 μl of distilled water, 32 μl of 5 x E. coli reaction buffer [100 mM Tris-HCl (pH 7.5), 20 mM MgCl₂, 50 mM (NH₄)₂SO₄, 500 mM KCl, 250 $\mu\text{g}/\text{ml}$ of BSA, 750 μM βNAD], 3 μl of 10 mM each of dATP, dCTP, dGTP and dTTP, 15 units of E. coli ligase (Pharmacia), 40 units of E. coli polymerase (Pharmacia), and 1.5 units of E. Coli RNase H (Pharmacia). The reaction mixture was then incubated at 16°C for 2 h and heated to 65°C for 15 min. Then 20 units each of BamHI and MboI were added, and the reaction mixture was incubated at 37°C for 1 h and heated again at 65°C for

30 min. Finally, the sample was diluted up to 1 ml with 1 x E. coli reaction buffer, and 100 units of E. coli ligase were added. The resulting mixture was incubated at 16°C overnight. An aliquot of this mixture was used to transform competent E. coli DH5 cells (Toyobo). Transformants were selected by ampicillin resistance. The product was named "3' MboI cDNA library".

[Example 3]

Amplification of cDNA insert by PCR

The plasmid-carrier E. coli colonies were picked into 96-well plates containing 125 μ l of LB medium (Davis, R. W., et al., Advanced Bacterial Genetics. New York: Cold Spring Harbor Laboratory, 1980) in each well and incubated in a moist chamber at 37°C for 24 h. A replica culture was made for every plate using a 96-pinned replica device (Sigma) and the master plates were stored at -80°C for future use. After overnight incubation at 37°C, 50 μ l of the culture from each well of these replicas were transferred to polycarbonate 96-well plates (Techne). Bacteria were collected by centrifugation in an Omnispin H4211 rotor (Sorvall) at 1500 rpm for 5 min, resuspended in 50 μ l of water, covered with a layer of mineral oil and lysed at 95°C for 30 min in a metal bath. Debris were removed by centrifugation at 3600 rpm for 30 min in the same rotor.

Five microliters of the supernatant were added to 20 μ l of distilled water and kept at

95°C for 10 min under a layer of mineral oil. Then the denatured lysate was subjected to PCR by adding 25 μ l of 2 x reaction mixture [40 mM Tris-HCl (pH 8.9 at 23°C), 3 mM MgCl₂, 50 mM KCl, 200 μ g gelatin/ml] containing 5 pmol each of primers, 5 nmol each of dATP, dCTP, dGTP, dTTP and 1.25 units of Taq DNA polymerase (Cetus) at 70°C.

Temperature cycling reactions were carried out immediately after addition of the reaction mixtures using a thermal cycler either for microfuge tubes (PJ1000, Perkin Elmer Cetus) or for a 96-well plate (PHC-3, Techne); 35 repeated cycles of 30 sec at 96°C, 1 min at 55°C, and 2 min at 72°C without a final extension step were performed.

For this method, the correct choice of primers for the PCR reaction is crucial.

Therefore, preliminary tests were performed using the following primers with a predicted T_m of above 60 °C.

The primers tested were a pair of primers, FW(-47) and RV(-48), which are identical to the commercially available 24 mer primers, a second pair of primers, [FW(-40) and RV(-29)], which are a longer version (21 mer) of the well-tested sequencing primers, and the primers RV(-71) and RV(-14), which have a triplet sequence at the 3' terminus identical with that in FW(-40) but is in the opposite orientation (Fig. 2A).

In most of the cases where various combinations of primers were tested, short PCR artifacts appeared, besides the expected major products (Fig. 2B, arrows indicate the PCR

artifacts.). These artifacts could be reduced by raising the annealing temperature, lowering the primer concentration or lowering the substrate concentration but in all cases the yield of the products was not high enough to serve as a template for the sequencing reaction without concentration thereof.

However, since one pair of primers [SW(-40) and RV(-14)] did not yield artifacts (Fig. 3), this pair was selected for further tests, and was found to give reproducible results. Similar results were obtained with randomly selected cDNA clones. Therefore, only this pair of primers SW(-40) and RV(-14) was used as the primers of the present embodiment.

[Example 4]

DNA sequencing

The PCR products were drop-dialyzed against TE [10 mM Tris-HCl (pH 8.0), 1 mM EDTA] on millipore filter (VS 0.025 μ m) for 90 min while stirring. Forty-eight samples are easily applied on a single filter of 150 mm diameter. Without further purification the samples were subjected to the Cycle Sequencing protocol (Applied Biosystems, 1991) using dye labeled primers with minor modifications. For dideoxycytidine sequencing reaction, 2 μ l of the dialyzed PCR reaction product (about 0.2 pmol of template DNA) were added to 3 μ l of a reaction mixture containing 0.4 pmol of

FAM M13 (-21) Primer (Applied Biosystems) in 160 mM Tris-HCl (pH 8.9), 40 mM $(\text{NH}_4)_2\text{SO}_4$, 10 mM MgCl_2 , 50 μM dATP, 12.5 μM dCTP, 75 μM 7-deaza-dGTP (Boehringer Mannheim Biochemicals), and 50 μM dTTP, 25 μM dddCTP, 0.8 unit of Taq Polymerase (Perkin Elmer Cetus), and subjected to 15 plus 15 cycles of the reaction (95°C 30 sec, 60°C 1 sec, 70°C 1 min and 95°C 30 sec, 70°C 1 min) according to the manufacturer's recommendation in a 96-well plate using a thermal cycler (PHC-3, Techne). The three other sequencing reactions for dideoxyguanosine, dideoxyadenosine, and dideoxythymidine were performed in parallel (with TMRA, JOE, and ROX primers respectively, supplied by Applied Biosystems) in an identical fashion, except that twice the volume of all the ingredients was added to the dideoxyguanosine and dideoxythymidine reactions. Each sample, from a set of four was cooled to 4°C, pooled, precipitated with ethanol, resuspended in 6 μl of a solution of formamide/50 mM EDTA (5/1 by v/v), loaded onto sequencing gel and analyzed by a DNA autosequencer (Model 373A Ver 1.0.1, Applied Biosystems).

[Example 5]

The frequency of appearance of each GS of the cDNA library reflects mRNA population.

To confirm that our 3'-directed regional cDNA library was a non-biased representation of the mRNA population in HepG2 cells, the inserts of four cDNA clones (EF-1 α ,

α -1-antitrypsin, hnRNP core protein A1 and inter- α -trypsin inhibitor) from the clones redundantly obtained by random selection of cDNA were radiolabeled and used as probes in a Northern analysis of poly A⁺ mRNA from the HepG2 cells. (The results are shown in Fig. 4A-D, and summarized in Fig. 4F.) The relative band intensity of the four mRNA species demonstrated that their relative ratios were 52, 24, 1 and 1.2, respectively (lane iii in Fig. 4F). Then the same set of probes was used for measuring the number of colonies hybridizing with each probe in the same cDNA library of 8,800 clones (Fig. 4E).

The clonal frequencies were 307, 128, 7 and 9, or in ratio, 44, 17, 1 and 1.3, respectively (lane iv in Fig. 4F). These two estimates agreed, showing that the cDNA library used is a non-biased representation of the mRNA population. The ratio was practically unchanged when different preparations of mRNA from the same cell were tested.

Fig. 4 shows the proportionality of the composition of the 3'-directed cDNA library and of the mRNA. Fig. 4A, 2 μ g of poly A⁺ RNA from HepG2 cells was electrophoresed in lanes 1-4 of a formamide agarose gel containing ethidium bromide (5 μ g/ml) and then exposed to UV. Lane 5 is the RNA ladder (BRL) used as size markers (kb). In Fig. 4B, the filter was northern blotted using the following ³²P-labeled 3'-specific cDNA probes: Elongation factor-1 α (lane 1), α 1-antitrypsin (lane 2), hnRNP core protein A1 (lane 3),

inter- α -trypsin inhibitor (lane 4). In Fig. 4C, one pmol each of the non-labeled cDNA fragments, [EF-1 α (lane 1), α 1-antitrypsin (lane 2), HnRNP core A1 (lane 3), inter- α -trypsin inhibitor (lane 4), were electrophoresed in a 2% agarose gel, then photographed. Fig. 4D is a Southern analysis of the blotted filter from Fig. 4C, using the same set of radioactive probes. Lane 5 shows the migration pattern of the reference 1 kb ladder (BRL). Hard copies of these screen images were taken at 8 h for b, and 1 h for d. The radioactivity in each band was counted directly in a scinti-scanner (β -603; Betagen) and registered in (i) and (ii) in Fig. 4F. The observed band intensities were corrected based on the band intensities in Fig. 4D (ii in Fig. 4F), and normalized relative to the value of probe 3 (HnRNP core A1, lane iii in Fig. 4F) as 1 (iii in Fig. 4F). These values represent the relative content of each mRNA species in the original mRNA preparation. Fig. 4E shows the results of colony hybridization of the membranes carrying 8,800 colonies of the 3'-directed cDNA library using the same set of the four radioactive probes. Positive colonies were counted and registered (iv in Fig. 4F), then normalized with the value of HnRNP core protein A1 as 1. The numbers in B, D and E in Fig. 4 represent the probe No. in Fig. 4F. Fig. 4F shows a remarkable agreement between the values of lanes (iii) and (v).

[Example 6]

Population study of the cDNA library

To analyze further the composition of the cDNA library, 7 and 10 clones were selected from the redundant (group I) and solitary (group II) sequence groups, respectively, and these inserts were used as radiolabeled probes for colony hybridization (Fig. 6). The frequencies of the colonies that hybridized with group I probes were roughly identical to those that were randomly picked and sequenced. These frequencies were about 3.5%–0.1%. Nearly 52% of the cDNA library population consisted of the redundant sequence group containing 173 species. When 8 probes from group II were tested, 18 positive colonies were identified among 26,400 colonies screened, giving an average frequency of 0.007%. Two probes did not hybridize with any of the 26,400 colonies, resulting in the average frequency of <0.004%. Thus, the average frequency of the 10 probes in group II was several orders of magnitude less than the lowest of group I.

The results are summarized in Fig. 5, showing the appearance frequencies of various DNA species in the 3'-directed HepG2 cDNA library. In Fig. 5, seven cDNA probes (a15 through tb042) were selected from the 162 identified genes in the redundant group (group I), and ten (s155 through s632) were randomly chosen from the solitary group (group II). In columns A, B and C, each one of the insert DNAs was radiolabeled and used as a probe for colony hybridization tests of 982 (A), 8,800 (B) or 26,400 colonies (C). NT indicates

"not tested". The DDBJ entry names of the 17 clones listed in this table are HUM000A15, HUM000C321, HUM00TB038, HUMHM01B02, HUM0C13A04, HUMHM02D02, HUM00TB042, HUM000S155, HUM000S159, HUM000S639, HUM000S635, HUM000S170, HUM000S154, HUM000S167, HUM000S645, HUM000S647, and HUM000S632.

[Example 7]

Analyses of sequencing errors

All the sequence data presented in this specification were obtained by repeated cycles of enzymatic amplification of the plasmid inserts, followed by cycle sequencing with Taq polymerase. Sequences of 60 clones that showed data bank matches were examined for discrepancies from the data bank entries. It was found that the accuracy in the region 1-100 bp distant from the cloning site was 98.7%, indicating that the primers or probes designed with the sequence in this region could be obtained practically without any erroneous sequences or even if they contain any errors, they are functionally without problems.

[Example 8]

Mapping of GS by PCR.

<cDNA sequence>

cDNA library was constructed from mRNA of DMSO treated HL60 cells. The methods for construction of the 3'-directed cDNA library and for sequence analysis of the library components are the same as described in Examples 1-4.

<PCR primer>

Primer design was performed by using the computer software OLIGO 4.0 (National Biosciences) which eliminates possible formation of inter- or intra-molecular secondary structures. In addition to the primer design, transfer of oligonucleotide sequences to the local database and synthesizer were semiautomated using a Macintosh computer linked with a network. DNA oligomers were synthesized on an automated DNA synthesizer (Model 394, Applied Biosystems) on a 40 nmol scale. The synthesized oligomers were used as PCR primers without further purification.

<Preparation of Genomic DNA>

The human genomic DNA was extracted from the normal karyotype lymphoblastoid cell line GM0130b.

Mouse and Chinese hamster genomic DNAs were purchased from Clontech. Monochromosomal hybrid cells utilized for mapping panel were commonly used ones which have been described previously. Briefly, chromosomes 3, 4, 9, 11, 12, 13, 15, 22 and Y were carried in human-Chinese hamster monochromosomal hybrid cells, and

chromosomes 1, 2, 5, 6, 7, 8, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20, 21 and X were carried in the human-mouse monochromosomal hybrid cells A9 series. The integrity of the hybrid cells were monitored by *in situ* hybridization.

<Amplification by Polymerase Chain Reaction>

PCR was performed according to standard protocols (Saiki, R. K., et al., Science 230, 1350-1354, 1985), using 10 pmol of each primer on a whole 20 μ l scale reaction, with 35 thermal cycles of 30 sec at 94°C, 60 sec at an annealing temperature, and 90 sec at 72°C, using a Perkin-Elmer 9600 thermal cycler. Annealing temperature was determined according to the "optional annealing temperature" estimated by the Program OLIGO.

<Analysis of the PCR Products>

The PCR products were run on an 8% polyacrylamide non-denatured gel (Acrylamide:Bis-acrylamide = 19:1, 1 mm thick) at 300 V for 1 h, followed by staining in 90 mM Tris-borate, 2 mM EDTA buffer solution containing 0.25 μ g/ml ethidium bromide for 15 min. The size of the amplification products were determined relative to the 10 bp DNA ladder (BRL). Detection of fluorescence was performed by using a laser fluorescent image analyzer (FM-BIO, Hitachi Software Engineering). The image data were transferred to a computer for analysis.

<Results of Analysis of the PCR Products>

Among various species of 3'-directed cDNA GSs obtained from granulocytoid cells, 195 novel GSs which did not match the sequences deposited in Genbank Release 76 were selected and used for designing primers for the PCR. The PCR was performed with these primers using the total human genomic DNA as the template.

Among the 195 primer pairs, 191 (98%) yielded products whose size matched those expected within 5 nt. The results are summarized in Figs. 6 - 10 whose figure legends are as follows: GS, gene signature; CN, clone name; Chromosomal position, chromosome numbers to which GSs were mapped; Sequence of primers, DNA sequences of primers (Sense, sense strand; anti-sense, anti-sense strand); AT, annealing temperature; HO, Observed size of PCR products with total human genomic DNA (nt); HE, Expected size of PCR products with total human genomic DNA (nt); MO, Observed size of PCR products with mouse genomic DNA (nt); CO, Observed size of PCR products with Chinese hamster genomic DNA (nt); G, Number of "hits" of GS in the granulocytoid (DMSO treated HL60) cDNA library after analyzing altogether 1000 clones; T, Total number of "hits" of the GS after analyzing altogether 3000 clones from the three cDNA libraries of HL60 with and without induction by DMSO or TPA. Question marks ("?.") indicate that the PCR products did not yield a clear band.

"M" indicates that the PCR products yielded a band which was indistinguishable

from the band observed after the reaction using mouse DNA as the template. Similarly, "C" indicates that the PCR products yielded a band which was indistinguishable from the band after the reaction using Chinese hamster DNA as the template.

The overall rate of success of the PCR was 191/195 (98%), although GSs were randomly selected from the cDNA sequences, indicating that the quality of the cDNA library used in this work was reliable, and that the sequence analyses and primer designs were performed appropriately. Thus, the possible chances of failure of the PCR caused by presence of an intron(s) in the relevant cDNA sequences is negligible in working with the GS, as introns virtually do not lie in the poly A proximal 3'-region of vertebrate genes (Wilcox et al., *Nucleic Acids Res.* 19, 1837-1843, 1991). This is a big advantage compared to the use of partial fragmented cDNA sequences obtained from randomly primed cDNA libraries (Adams et al., *Science* 252, 1651-1656, 1991) or from 5'-directed cDNA libraries.

<Chromosomal assignments of GS>

The 191 primer pairs that yielded PCR products from total human DNA were used for chromosomal assignments of the GSs with the monochromosomal hybrid cell panel. At least 119 GSs were assigned to a single chromosome. As an example, GS001418, shown in Fig. 11, was assigned to chromosome number 3. With some clones, extra

products were obtained, some of which were assigned to the same chromosome, whereas others to different chromosomes. An example, GS001457, is shown in Fig. 12. Sixty-two (33%) clones yielded the expected PCR products with two or more different chromosomes. Thirty-five cases (18%) yielded PCR products whose size were indistinguishable from background rodent genomic DNA. Among these, 21 GSs produced products indistinguishable from mouse and Chinese hamster DNA. Ten GSs yielded no expected PCR products with the monochromosomal cell panel DNA, although the expected PCR products from total human genomic DNA were observed. The 10 cases probably arose from a small deletion in the hybrid cells. Five clones obtained from HepG2 cDNA library have been analyzed also by Southern blot analysis. Four out of the 5 GSs (GS000053, GS000120, GS000271 and GS000279) gave consistent results with those obtained by the PCR. One GS (GS000228), which was uncertainly assigned to chromosome Y because of the weak signal detected by the Southern blot method, was assigned to chromosome 11 by PCR.

[Example 9]

Mapping of GS by Southern blot method

<Cell lines>

Total human genomic DNA was isolated from the human normal karyotype lymphoblastoid cell line GM0130b. Monochromosomal hybrid cells used as the mapping

panel are shown in Fig. 15. Hybrid A9(neo-x)-y cells as described by Koi, et al. (Jpn. J. Cancer Res. 80, 413-418, 1989) were donated by Dr. M. Oshimura, Faculty of Medicine, Tottori University, passaged 3 times and frozen for storage. The loss or rearrangements of chromosomes could have occurred during this period. The GM series was obtained from the Mutant Cell Repository, National Institute of General Medical Science (NIGMS) (Camden, NJ). To confirm that human chromosomes remained intact in the hybrid cells after storage in liquid nitrogen, metaphase spreads of the hybrid cells were monitored by chromosome staining based on *in situ* hybridization using biotinylated total human DNA as the probe (Durnam, D. M., et al., Somatic cell Mol. Genet. 11, 571-577, 1985). Intact, as well as translocated or fragmented human chromosomes were easily detected by this means. In a hybrid cell mapping panel, chromosomes 11, 12 and 15 were represented by the hybrid cell lines A9(neo-11)-1, A9(neo-12)-4 and A9(neo-15)-2, respectively, and in another panel, they were represented by the hybrid cell lines GM10927A, GM10868 and GM11418, respectively.

<Isolation of genomic DNA and Southern blotting>

High molecular weight DNA was extracted from cells using sodium dodecyl sulfate (SDS) and Proteinase K, followed by phenol-chloroform extraction and ethanol precipitation. DNAs were digested overnight with a combination of two restriction enzymes

including EcoRI, BamHI and BglII. About 5 μ g of each digest was electrophoresed in an 0.8% agarose gel, then transferred to Hybond N⁺ membrane (Amersham) with 0.4 N NaOH. The membrane was rinsed in 2 x SSC and stored at 4°C for subsequent use.

Clones containing a novel sequence and having more than 150 bp were selected as probes. The cDNA inserts of the clones were amplified by the PCR. The PCR products were isolated by electrophoresis through a 2% low-melting temperature agarose gel (Nusieve : SeaPlaque, 3 : 1), followed by excision. The gel was removed by melting at 65°C and digesting with β -Agarose I (Bio Labs) at 40°C for 1 h. The probes were labeled with [α -³²P]dCTP by random priming using a commercial kit (Amersham). Hybridization proceeded at 65°C in a high salt buffer containing 6xSSC, 1x Denhardt's solution and 0.5% SDS, in the presence of 0.1 mg/ml of sonicated, denatured salmon sperm DNA. The membranes were washed in 2xSSC, 0.1% SDS at 65°C for 30 min, then twice for 30 min in 0.1xSSC, 0.1% SDS at 65°C, and analyzed using a Fuji BAS-2000 imaging analyzer.

<Analyses with Genomic DNA>

Among the HepG2 3'-directed cDNA libraries described in Examples 1 and 2, 160 novel clones were selected and used as probes for Southern blots.

Total human genomic DNA was isolated from a cell line GM0130b that has a normal karyotype, and digested with the restriction enzymes, EcoRI, BamHI and BglII alone or in

combination. The GS clones used as probes were the 3'-directed cDNAs. Each of these cDNAs covers a region between the poly(A) site and the nearest MboI site (GATC) (Okubo, K., et al., *Nature Genetics* 2, 173-179, 1992) and thus do not have restriction sites for BamHI or BglII. In addition, because the average size of GS is 270 bp, the chances of having an EcoRI site in the cDNA moiety were not high. In fact, only 7 clones out of the 160 analyzed had an EcoRI restriction site.

Membranes blotted with digested human genomic DNA were hybridized with radio-labeled GS probes and washed at high stringency. Since the 3'-terminal region of cDNA has, in general, a unique sequence which differs from that of protein encoding regions which tend to have conserved motifs, cross hybridization with unrelated cDNA sequences will not occur under such stringency. Examples of the results of hybridization are shown in Figs. 13 and 14. Clones s503 and s632 (Figs. 13a and 13b; junk) respectively represent unique single band producers. As shown below, 67 clones belonged to this class. The positions of the GS sequence relative to the restriction sites were inferred from the band patterns. Clone s311 (Fig. 13c; GS000092) showed a single band with EcoRI -as well as (EcoRI+BamHI)-digested DNA, but two bands of different sizes in other double digests. The double digestion thus helped resolve multiple GSs. Similar results were obtained with clone c13a08 (Fig. 13d; GS000055), in which there were 2 bands with

EcoRI- or (EcoRI+BamHI)-digested DNAs, and 4 when digested with (EcoRI+BglII) or (BamHI+BglII). On the other hand, 4 hybridization bands appeared with clone s479 with EcoRI alone, but the number of bands decreased with (EcoRI+BglII) and (BamHI+BglII) (Fig. 14e; GS000180). These results indicate that genomic DNAs should be digested in various ways to reveal the maximum number of hybridizing fragments. The results of the analysis showed that 41, 10, 7 and 19 clones contained 2, 3, 4 and 5 or more bands, respectively. Clones s14f01 and tw1-46 (Figs. 14f and 14g; GS000407 and junk, respectively) contained at least 10 bands in each lane. Since the EcoRI restriction site is not present in the two GS sequences, the multiplicity of bands is likely to represent the multiple copy number of these genes. Clone kmb07 moved as a smear (Fig. 14h; junk), even after intensive high stringency washes, suggesting that this probe has a repetitious sequence which has not been hitherto identified.

<Chromosomal assignments>

A set of monochromosomal hybrid cells carrying a single human chromosome in a background of rodent chromosome was collected (Fig. 15). Thirteen cell lines were microcell hybrids established by Koi et al. (Koi, M., et al., Jpn. J. Cancer Res. 80, 413-418, 1989) and the others were obtained from NIGMS. The results of monitoring the human chromosomes in these cell lines by *in situ* hybridization using biotinylated total

human DNA are also presented in Fig. 15.

The GSs were assigned to chromosomes using hybrid cell mapping panels. Three types of membranes were prepared, each having DNAs prepared from hybrid cells, and digested with EcoRI, (EcoRI+BamHI), or (BamHI+BglII). Among these three types of membranes, the one which should have yielded the maximum number of bands was used for each GS probe, according to the results of total genomic Southern blots. Examples of hybridization results are shown in Figs. 16 – 22. The numeral on each lane represents the human chromosome numbers which is contained in the hybrid cell, and H stands for the total human chromosomes. Clone s14g02 (GS000152; Fig. 16) that showed a single hybridization band with the total human DNA digested with EcoRI (lane H), showed the corresponding band only with the hybrid cell line containing human chromosome 4. Thus, this GS lies in chromosome 4.

The clone s650 (GS000041; Fig. 17) was assigned to chromosome 12 which showed a characteristic 7.5kb band in the presence of an (EcoRI+BamHI)-digested membrane. However, with an EcoRI digested DNA, the clone could not be assigned, as the human-specific and the cross-reacting rodent DNA fragments overlapped. The single, but shorter fragment band (1.3kb) which appeared in lanes 3, 4, 9, 13 and 22 represents the homologous DNA sequence in Chinese hamster, and the 3.3kb band in other lanes

represents the homologous DNA in the mouse.

Clone hm01e01 (GS000181; Fig. 18) exhibited two fragments when hybridized to total human DNA treated with EcoRI alone, and these corresponding bands appeared in lanes 1 and 2. Thus, the two members of this gene family are located on two chromosomes.

Fig. 19 shows that clone c13a08 (GS000055) exhibited 4 bands when hybridized to (BamHI+BglII)- or (EcoRI+BglII)-digested total human DNA, although only 2 bands appeared with EcoRI- or (EcoRI+BamHI)-digested human DNA. Therefore, the (BamHI+BglII)-digested DNA panel was used for this clone. Two bands (12.3kb and 7.5kb) appeared in lane 7, a 5.2kb band in lane 2, and a 3.2kb band in lane 17. Two bands (6.0kb and 3.8kb) that cross-reacted with Chinese hamster DNA appeared in lanes 3, 4, 9, 13 and 22, and a single band (3.5kb) that cross-reacted with mouse DNA appeared in other lanes.

Clone s479 (GS000180; Fig. 20) showed 4 EcoRI fragments with total human DNA. The hybridization to an EcoRI-digested DNA panel yielded in bands of 10.5kb in lanes 7 and 19, 8.5kb in lane 8, 7.8kb in lanes 11 and 12, and 3.5kb in lane 11. Thus, the human specific genes are dispersed among chromosomes 7, 8, 11, 12 and 19, among which the 10.5 and 7.8kb bands in the total DNA both consist of two overlapping fragments. As

shown in lane H, the intensity of these overlapping fragments was higher than normal.

The 3.5kb band in lane H, as well as in lane 11 was also intense, suggesting that it also represents overlapping fragments.

Clone s173 (GS000094) exhibited 5 bands in EcoRI-cleaved total DNA (Fig. 21).

Four corresponding fragments included a 4.5kb fragment in lane 1. Another 4.5kb band was observed in lane 4, indicating that the corresponding band in lane H overlapped. In addition, an intense 3.1kb band was observed in lane 17.

Clone hm01g02 (junk; Fig. 22) exhibited many bands with total DNA, and with those from monochromosomal hybrids. This clone must represent a multiple and closely related family of genes. It also contains a sequence conserved in homologous rodent genes which also give rise to multiple bands. Since most of the human specific and rodent bands overlapped, the chromosomes could not be assigned. Other combinations of restriction enzymes did not resolve the overlap.

The results of the total genomic DNA analyses and the chromosome assignments of 160 GSs are summarized in Figs. 23 - 26. Through total genomic DNA analyses using 4 differently digested human DNAs, 67 clones were categorized into a single band group, 41 in a two band group, 10 in a three band group, 7 in a four band group and 19 in a group that yielded five or more bands. Nine clones did not show any hybridization band under

fixed conditions.

Assignment of two band clones showed that the two genes lie in different chromosomes in 15 of them, whereas the gene represented by clone s317 originated from the same chromosome. The three band clones s308 (GS000412) and s401 (GS000224) showed that two of the fragments lie on the same chromosome, and clone hm05g02 (GS000209) and s17a10 (GS000294) showed bands in different chromosomes. Clones displaying four or more bands showed a relatively dispersed distribution among chromosomes. "junk" in Example 9 is the DNA segment cloned by the same method used for GS but is not numbered.

[Example 10 Cloning of gene using GS]

[10A. Cloning of a full length cDNA encoding a human ribosomal protein, homologue of yeast S28. Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(1)]

Using a primer (5'-TGAAAATTTATTACTACAGTGTTTTTCACCA-3' (SEQ ID NO:7839)) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00500 and a primer (5'-TAATACGACTCACTATAGGG-3' (SEQ ID NO: 7840)) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, HcpG2 cDNA

library was amplified by the PCR and a full length cDNA clone encoding a human ribosomal protein, a homologue of yeast ribosomal protein S28 was isolated. (Hori et al., Nucl. Acids Res. 21: 4394, 1993).

[10B. A human ribosomal protein homologous to rat L9 ribosomal protein—Cloning of the full length cDNA by PCR using a primer comprising a partial sequence of a GS(2)]

Using a primer 5'-CTTCTTTCTGTAGCCAGGTAAGTCT-3' (SEQ ID NO: 7841) that is a partial sequence of a DNA which is substantially the same as the complementary strand of HUMGS00418 and a primer (SEQ ID NO: 7840) complementary to the vector (pSPORT) sequence that is located external to the 5' end of the cDNA, a full length cDNA clone encoding a human ribosomal protein homologous to rat L9 was isolated (Hori et al., Nucl. Acids Res. 21:4395, 1993).

[10C. A human protein homologous to bovine phosphatidylethanolamine-binding protein. Cloning of the full length cDNA by hybridization using a probe comprising a partial sequence of a GS]

By hybridization with the probe,

5'-GATCGTTCTTCATGGGGGTAAGAAAAGCTGGTCTGGAGTTGCTGAATG

TTGCATTAATTGTCCTGTTTGCTTGTAGTTGAATAAAAATAGAAACCTGAAT

GAAGGAAA-3' (SEQ ID NO:7838), that comprises a partial sequence of HUMGS00421,

a full length cDNA clone encoding a human protein homologous to bovine phosphatidylethanolamine-binding protein was isolated (Hori et al., Gene 140:293, 1994).

[10D. Human mpl-ligand. Cloning of a cDNA coding for the human mpl-ligand using a GS]

This embodiment employs the 5' SLIC (single ligation to single stranded cDNA) method which is an improved version of the 5'RACE (rapid amplification of cDNA ends) method, and is described in Nucleic Acids Res., 19, 5227-5232 (1991).

①Reverse transcription of cDNA and attachment of anchor

The template was prepared using the reagents of the 5'-AmpliFinder™ Kit (Toyobo, Inc.) in accordance with the protocol included therewith. Specifically, 2 μ g of human fetal liver poly A⁺RNA (Clontech Laboratories, Inc.) and 10 pmol of the primer PA-6, a primer corresponding to the 3' end of the gene signature (GS) sequence HUMGS02342 and consisting of the sequence 5'-TTTTCGGCGCTCCCATTTATTCCTT-3' (SEQ ID NO: 7842), were mixed together and then denatured by heating the mixture at 65°C for 5 min. The cDNA was synthesized by combining the denatured sample with AMW reverse transcriptase, RNase inhibitor, dNTPs, and a reaction buffer, and then heating the resultant mixture at 52°C for 30 min. EDTA was then added to the mixture to stop the reaction.

Thereafter, the RNA was hydrolyzed by adding NaOH to the reaction mixture and heating the resultant mixture at 65°C for 30 min. The mixture was then neutralized with acetic acid. A suspension of glass beads (GENO-BIND™) and NaI were added to the neutralized solution and the cDNA was adsorbed onto the beads. The cDNA, adsorbed onto the beads, was washed with an aqueous solution of 80% EtOH, and then eluted in 50 µl of distilled water. Glycogen was added to the solution of purified cDNA, and the cDNA was precipitated with EtOH and resuspended in 6 µl of distilled water. The resultant suspension (2.5 µl) was added to a solution containing 4 pmol of AmpliFINDER Anchor (5'-CACGAATTCACTATCGATTCTGGAACCTTCAGAGG NH₂-3') (SEQ ID NO: 7843) provided with the Kit, T4 RNA ligase, and a ligation (reaction) buffer. The reaction mixture was incubated at room temperature overnight, and the AmpliFINDER Anchor primer in the reaction mixture was thereby ligated to the 3' end of the cDNA. The ligated product was then used as a template for the subsequent PCR.

② Amplification by PCR

The primary PCR was carried out using the template produced in the procedure described above (①), the Anchor primer,

5'-CTGGTTCGGCCACCTCTGAAGGTTCCAGAATCGATAG-3' (SEQ ID NO: 7846)

and the PA-5 primer consisting of the sequence

5'-CTCGCTCGCCCATCCTTATACAGGCTCAGTTTTGTCT-3' (SEQ ID NO: 7844).

Specifically, 1 μ l of the template was mixed with Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-5 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 μ l and the PCR was performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.). The reaction mixture was subjected to 40 cycles of the PCR, wherein each cycle consisted of incubating the sample in sequence at 94°C for 1 min, 63°C for 1 min, and 72°C for 3 min and, in the last PCR cycle, at 72°C for an additional 8 min. The products of the PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered using a Sephaglas Bandprep Kit™ (Pharmacia Corp.) in accordance with the protocol included therewith. Specifically, the gel was dissolved in a solution of NaI and the resultant mixture was heated at 60 °C for 10 min. Sephaglas™ BP was added to the gel mixture and the DNA was adsorbed onto the glass beads contained therein. The glass beads, containing the adsorbed DNA, were then washed three times with a Wash Buffer provided with the Kit and eluted in 30 μ l of TE buffer (10 mM Tris-HCl pH 8.0, 1mM

EDTA).

One μ l of the eluted DNA was used as a template in a secondary PCR. In order to enhance the specificity of the secondary PCR, the reaction was performed with PA-4 primer which consisted of the sequence

5'-CTCGCTCGCCCATGTATAGGGACAGCATTTCTGAGAG-3' (SEQ ID NO: 7845)

and was positioned within the template sequence internal to the PA-5 primer and the Anchor primer. Specifically, 1 μ l of the template was mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-4 primer and Anchor primer. The resultant reaction mixture was diluted with distilled water to a final volume of 50 μ l, preheated at 94°C for 6 min, and the secondary PCR was then performed under the same conditions described above (①) for the primary PCR. The products of the secondary PCR were resolved by electrophoresis in a 1% agarose gel and a broad band of approximately 800 bp in length, representing a product of the PCR, was detected. The detected band was excised from the agarose gel and the DNA contained therein was recovered and purified under the same conditions as described above (①) for the primary PCR.

③ Subcloning into plasmid vector

The purified DNA product of the secondary PCR was subcloned into the plasmid vector pUC18 (pharmacia Corp.), using a SureClone™ Ligation Kit (Pharmacia Corp.) in accordance with the protocol included therewith. Specifically, the purified DNA was added to a solution containing Klenow polymerase, polynucleotide kinase and a reaction buffer, mixed and heated at 37°C for 30 min in order to create blunt-ended termini and to phosphorylate the 5' terminus of the DNA molecules contained in the reaction mixture. The blunt-ended and phosphorylated DNA was combined with a solution containing 50 ng of a dephosphorylated and Sma I-cleaved pUC18 vector provided with the Ligation Kit, T4 DNA ligase, DTT and a ligation reaction buffer, and the resultant mixture was warmed at 16°C for 3 hr. One sixth volume of the reaction solution was employed to transform E. coli competent cells using standard methods. Specifically frozen E. coli competent cells (Wako Pure Chemical Industries, Ltd.) were thawed and mixed with the ligated DNA. The resultant mixture was incubated on ice for 20 min, heat-treated at 42°C for 45 sec, and then incubated on ice for 2 min. A medium [Hi-Competence Broth (Wako Pure Chemical Industries, Ltd.)] was added to the mixture containing the transformed E. coli cells. The mixture was incubated for 37°C for 1 hr and then spread onto agar plates containing 100 µg/ml Ampicillin, 40 µg/ml X-Gal (6-bromo-4-chloro-3-indolyl-β-D-galactoside), 0.1 mM IPTG

(isopropyl- β -D-thiogalactopyranoside) and cultured overnight at 37 °C. White colonies were selected from the colonies which consequently appeared on the agar plates and analyzed by the PCR to determine the presence or absence of the DNA insert. Specifically, a sample of a selected colony was picked with a sterilized toothpick and used to inoculate a 50 μ l reaction solution containing 1 unit of Taq DNA polymerase, dNTPs, PCR buffer, 200 μ M each of the M13 P4-22 primer consisting of the sequence 5'-CCAGGGTTTTCCCAGTCACGAC-3' (SEQ ID No: 7847) and M13 P5-22 primer consisting of the sequence 5'-TCACACAGGAAACAGCTATGAC-3' (SEQ ID No: 7848), wherein both primers are comprised of sequences complementary to the pUC18 vector. The resultant mixture was heated at 94°C for 6 min and then subjected to 30 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence, at 94°C for 1 min, 55°C for 1 min, and 72°C for 2 min. The amplified insert was detected by electrophoresis of the PCR products on an agarose gel and thereby the clone pR02342-2, containing an insert, was selected.

④ Sequencing of cDNA

The plasmid DNA was prepared using the QIAprep-Spin Kit (Funakoshi, Ltd.) in accordance with the standard alkali-SDS protocol included therewith. Specifically, *E. coli*

cells transformed with the DNA of clone pR02342-2 were cultured overnight in Luria Broth medium containing 100 $\mu\text{g/ml}$ Ampicillin. The cultured cells were then pelleted by centrifugation and resuspended in P1 solution provided in the Kit. The resultant cell suspension was mixed with the P2 alkali solution of the Kit, incubated at room temperature for 5 min, neutralized with N3 solution of the Kit, incubated on ice for an additional 5 min and then centrifuged. The supernatant obtained from the centrifuged solution was applied to a QIAprep-Spin column. The Spin column was then washed in sequence with PB and then PE solution of the Kit and the DNA was eluted from the column with TE buffer. Sequencing of the eluted DNA was then carried out using the sequencing kit PRISMTM Terminator Mix (Applied Biosystem Corp). Approximately 1 μg of the purified DNA was mixed with a solution containing 3.3 pmol of either the M13 P4-22 primer or M13 P5-22 primer and 9.5 μl of PRISMTM Terminator Mix. The M13 P4-22 and M13 P5-22 primer were used to sequence both strands of the DNA insert of clone pR02342-2. The resultant mixture was diluted to a final volume of 20 μl with distilled water and subjected to 25 cycles of the PCR wherein each cycle consisted of incubating the sample in sequence at 96°C for 30 sec, 50 °C for 15 sec, and 60 °C for 4 min. The excess primers and fluorescent dye present in the reaction mixture were removed by gel filtration using a MicroSpinTM S-200 HR column (Pharmacia Corp.) and the DNA products of the sequencing reaction were

precipitated with EtOH. The precipitated DNA was resuspended, sequenced using an automated sequencer, "Model 373A" (Applied Biosystem Corp.), and thereafter analyzed to determine the nucleotide sequence.

The analysis of the nucleotide sequence revealed that the insert of clone pR02342-2, including the PA-4 primer, was 608 bp in length. The sequence of this insert was subjected to a search for homologous sequences entered in the Gen Bank data base, and a 100% match was found to a sequence in the cDNA which encodes the human mpl-ligand (Accession No. L 33410, Nature 369, 533-538, 1994). Further comparison of the insert of clone pR02342-2 with the cDNA sequence of the human mpl-ligand, revealed that the cloned insert contained 81 bp of the 3' coding region of open reading frame. In addition, the insert of clone pR02342-2 contained an additional sequence extending beyond the 3' end of the human mpl-ligand cDNA sequence registered under Gen Bank Accession No. L 33410. These findings suggest that, using the GS HUMGS02342, the inventors of the present invention succeeded in cloning a cDNA clone pR02342-2, which could possibly have a different and more desirable property for expression than the human mpl-ligand cDNA represented by the sequence registered under Gen Bank Accession No. L 33410.

⑤ Cloning of the full-length cDNA encoding the human mpl-ligand

In order to find an optimal PCR primer, an appropriate computer program is used to search the sequence downstream of the coding region of the human mpl-ligand (clone pR02342-2) and thereby a primer PA-7 is designed and synthesized. A PCR similar to that described above in ② is performed using the template produced by the procedure described above in ①, the Anchor primer, and the PA-7 primer. Specifically, 1 μ l of the template is mixed with 2.5 units of Taq DNA polymerase (Takara Shuzo Inc., Code No. R001A), dNTPs, a PCR buffer, and 10 pmol each of the PA-7 primer and Anchor primer. The resultant reaction mixture is diluted with distilled water to a final volume of 50 μ l and the PCR is performed in a DNA Thermal Cycler 480 (Perkin Elmer Cetus Corp.) under conditions similar to that described above in ②. The products of the PCR are then resolved by electrophoresis on a 1% agarose gel and a band greater than 1300 bp in length, representing a product of the PCR, is recovered and cloned into a suitable vector in a manner similar to that described in ③. The cloned DNA is sequenced in a manner similar to that described in ④. The sequence is then compared to that of the human mpl-ligand cDNA registered under Gen Bank Accession No. L 33410 to confirm the presence of the full-length open reading frame.

Alternatively, using the Takara La PCR Kit (Takara Shuzo Inc., Code No. RR011) in accordance with the protocol included therewith, performing the 5'RACE procedure using

primers similar to those described above in ②, a cDNA of approximately 2 Kb in length, corresponding to the human mpl-ligand, was isolated.

The tables of appearance frequencies for all GSs related to the present invention are followed by "Sequence Listing" for these GSs, wherein HUMGS numbers after the heading 'clone' represent GS numbers. In the sequence table, N in the base sequence stands for "A or C or G or T or U". However, since nucleic acids in the Sequence Listing are DNAs, "T or U" stands for T in this case.

By the present invention, it has become possible to provide DNA molecules which carry "the information for expression" in various cells and can be used for detecting and diagnosing the cellular abnormalities, recognizing and identifying cells and further efficiently cloning genes which are expressed in a tissue-specific manner, and furthermore cloned DNA molecules which can be used for the production of proteins useful as pharmaceutical products.

A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
00021	00020	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	651
00019	00018	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00018	00017	128	17	8	2	26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00017	00016	25	3	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00016	00015	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00015	00014	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00014	00013	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00013	00012	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00012	00011	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00011	00010	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00010	00009	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00009	00008	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00008	00007	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00007	00006	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00006	00005	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00005	00004	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00004	00003	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00003	00002	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00002	00001	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	551
00001	GS																															551

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
22	00023	00021	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
23	00026	00022	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
24	00028	00023	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
25	00029	00024	5	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.8	534	1	520	1431	
26	00030	00025	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
27	00031	00026	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
28	00033	00027	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
29	00034	00028	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
30	00036	00029	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
31	00037	00030	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
32	00038	00031	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
33	00039	00032	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
34	00040	00033	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
35	00041	00034	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
36	00042	00035	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
37	00043	00036	9	2	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
38	00044	00037	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
39	00045	00038	5	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
40	00046	00039	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
41	00047	00040	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
42	00048	00041	10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
43	00049	00042	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X67951	94.4	322	1	483	937
44	00050	00043	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X57847	93.6	392	1	348	1182
45	00051	00044	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M24070	96	421	1	1039	1452
46	00053	00045	4	1	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
47	00055	00046	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
48	00056	00047	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
49	00057	00048	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
50	00060	00049	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
51	00061	00050	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
52	00062	00051	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
53	00064	00052	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
54	00065	00053	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
55	00066	00054	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
56	00067	00055	2	1	0	0	0	0	0	0	0	0	0	0	0																		

Table 2

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK			
58	00069	00057	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M34664	92.4	344	1	1484	2202			
59	00070	00058	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
60	00071	00059	7	1	0	3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
61	00072	00060	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
62	00073	00061	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
63	00074	00062	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
64	00075	00063	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
65	00076	00064	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
66	00077	00065	34	1	3	2	5	1	0	0	2	2	0	1	1	1	1	0	1	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0		
67	00078	00066	12	1	0	1	1	0	0	0	1	0	0	0	0	0	0	1	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0		
68	00079	00067	2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
69	00080	00068	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
70	00081	00069	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
71	00082	00070	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
72	00083	00071	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
73	00084	00072	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
74	00085	00073	26	5	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
75	00086	00074	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
76	00087	00075	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
77	00088	00076	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
78	00089	00077	33	1	3	2	2	0	1	0	1	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
79	00090	00078	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
80	00091	00079	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
81	00092	00080	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
82	00093	00081	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
83	00094	00082	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
84	00095	00083	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
85	00096	00084	62	6	5	4	2	0	0	0	1	2	5	1	3	1	1	5	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
86	00097	00085	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
87	00098	00086	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
88	00099	00087	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
89	00100	00088	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
90	00101	00089	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
91	00102	00090	44	2	4	0	0	0	0	0	1	1	6	2	1	2	8	0	1	1	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
92	00103	00091	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
93	00104	00092	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 3

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
94	00105	00093	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
95	00106	00094	8	2	1	1	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0								
96	00107	00095	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
97	00108	00096	31	2	3	0	0	1	0	2	0	1	0	3	0	0	0	0	3	6	2	1	1	0	1	2	0	0	3	X63237	94.8	384	1	532	
98	00109	00097	5	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0								
99	00110	00098	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
100	00111	00099	38	7	0	0	1	9	13	6	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0				
101	00113	00100	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
102	00114	00101	38	1	1	5	0	1	0	0	3	0	1	3	1	1	0	4	3	1	0	9	0	1	0	0	2	0	0	0	0	0	0		
103	00115	00102	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
104	00116	00103	17	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	6	1	M14630	95.6	362	1	840	1200	
105	00117	00104	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
106	00118	00105	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
107	00119	00106	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0								
108	00120	00107	5	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
109	00121	00108	4	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
110	00122	00109	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
111	00123	00110	14	2	0	0	2	0	0	0	0	0	0	0	0	1	1	0	1	2	0	0	0	0	0	0	1	0	X55954	98.8	336	1	144	479	
112	00124	00111	6	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
113	00125	00112	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
114	00127	00113	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
115	00128	00114	6	2	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0								
116	00129	00115	11	1	0	0	1	0	0	0	1	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	X54326	98	348	1	4238	4586	
117	00130	00116	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X65923	96.6	348	1	168	518	
118	00131	00117	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
119	00132	00118	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
120	00133	00119	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
121	00134	00120	24	1	0	0	1	0	1	1	1	0	1	2	0	4	1	1	0	0	3	1	1	1	3	0	0	0	M16600	99.1	339	1	2205	2543	
122	00135	00121	81	5	4	0	14	2	4	2	0	2	0	4	1	1	0	3	5	14	1	12	1	2	4	0	0	0	M10119	99.7	307	1	416	723	
123	00136	00122	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
124	00137	00123	10	2	1	0	0	0	0	1	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
125	00138	00124	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
126	00139	00125	8	1	1	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
127	00140	00126	13	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
128	00141	00127	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
129	00142	00128	9	1	0	0	0	0	0	0	0	0	0	1	1	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0			

Table 4

[illegible]

Table 5

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BGBH	BI	BK
166	00179	00165	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
167	00180	00166	7	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
168	00181	00167	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
169	00182	00168	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
170	00183	00169	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
171	00184	00170	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
172	00185	00171	13	2	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
173	00186	00172	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
174	00187	00173	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
175	00188	00174	11	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
176	00189	00175	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
177	00190	00176	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
178	00191	00177	3	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
179	00192	00178	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
180	00193	00179	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
181	00194	00180	34	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
182	00195	00181	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
183	00196	00182	67	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
184	00197	00183	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
185	00198	00184	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
186	00199	00185	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
187	00200	00186	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
188	00201	00187	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
189	00202	00188	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
190	00203	00189	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
191	00204	00190	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
192	00205	00191	5	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
193	00206	00192	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
194	00207	00193	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
195	00209	00194	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
196	00210	00195	14	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
197	00211	00196	128	8	24	2	10	0	0	4	2	5	16	9	1	5	0	3	0	1	1	1	0	0	0	0	0	0	0	0	0	0
198	00212	00197	16	1	1	0	0	0	0	1	0	0	0	1	0	1	0	2	1	0	4	0	0	0	0	0	0	0	0	0	0	0
199	00213	00198	8	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
200	00215	00199	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
201	00216	00200	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 6

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BGBH	BI	BK	
202	00217	00201	5	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
203	00218	00202	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
204	00219	00203	13	2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	99.5	220	1	1216	1435
205	00220	00204	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
206	00221	00205	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
207	00222	00206	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
208	00223	00207	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
209	00224	00208	8	1	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
210	00225	00209	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
211	00226	00210	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
212	00227	00211	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
213	00228	00212	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
214	00230	00213	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
215	00231	00214	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.5	202	31	733	934
216	00232	00215	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
217	00233	00216	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
218	00234	00217	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
219	00235	00218	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
220	00236	00219	11	1	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
221	00237	00220	11	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
222	00238	00221	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
223	00239	00222	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
224	00240	00223	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
225	00241	00224	12	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
226	00242	00225	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
227	00243	00226	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
228	00244	00227	65	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
229	00245	00228	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
230	00246	00229	26	3	5	0	0	0	0	0	0	3	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
231	00247	00230	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
232	00248	00231	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
233	00249	00232	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
234	00250	00233	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
235	00251	00234	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
236	00252	00235	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
237	00253	00236	16	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 7

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
238	00254	00237	38	1	0	0	2	0	0	1	2	1	0	1	0	2	0	1	3	0	0	0	0	1	3	20	0	0	M24096	98.1	214	1	1152	1365	
239	00255	00238	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
240	00256	00239	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
241	00257	00240	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
242	00258	00241	6	1	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	1	0	1	0	0	X04588	95.4	217	3	1857	2077	
243	00259	00242	2	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0								
244	00260	00243	4	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	1	0	0							
245	00261	00244	17	2	1	0	1	0	1	0	0	0	0	1	0	1	0	1	1	0	0	0	3	2	2	2	0	0	X65460	99	204	1	1607	1809	
246	00262	00245	50	2	7	2	0	1	1	2	0	3	6	0	1	3	0	0	3	0	1	2	0	4	4	0	6	2	M17885	98.6	211	1	888	1097	
247	00263	00246	2	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
248	00264	00247	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
249	00265	00248	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
250	00266	00249	3	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0							
251	00267	00250	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	3	0	X55330	99.1	107	83	1	2150	
252	00268	00251	5	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
253	00269	00252	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X63679	98.3	116	1	1152	1267	
254	00270	00253	9	1	0	1	0	0	0	0	0	0	1	0	1	0	3	0	1	0	0	0	0	0	0	0	0	0	X04526	95.2	209	1	2887	3088	
255	00271	00254	24	2	0	1	2	0	1	0	0	2	0	0	0	5	0	1	2	0	1	0	0	2	0	4	0	X75683	99	210	1	92	301		
256	00272	00255	9	1	0	0	0	0	0	1	2	0	0	0	1	0	0	0	1	0	1	0	0	0	1	0	1	0	J05262	100	197	1	931	1148	
257	00273	00256	119	9	6	4	13	2	11	2	1	12	14	0	6	0	6	0	3	1	3	0	0	2	3	3	15	3	X64899	94.8	192	1	626	819	
258	00274	00257	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
259	00275	00258	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
260	00276	00259	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
261	00277	00260	36	3	0	0	0	0	8	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M29882	100	191	1	234	424	
262	00278	00261	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
263	00279	00262	10	2	0	1	1	0	0	0	0	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
264	00280	00263	3	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
265	00281	00264	8	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X64228	99.5	196	1	6389	6597	
266	00282	00265	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L07395	97.9	190	1	2036	2226	
267	00283	00266	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
268	00284	00267	4	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
269	00285	00268	89	6	14	1	8	0	3	4	1	4	4	3	5	3	5	0	2	5	1	1	4	1	3	2	0	8	1						
270	00286	00269	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	L11284	96.3	189	1	1999	2222	
271	00287	00270	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
272	00288	00271	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
273	00289	00272	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 8

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK			
274	00290	00273	85	5	9	3	8	4	2	1	1	1	1	7	4	1	4	5	0	2	6	5	3	6	1	0	2	0	5	0	X66699	99.5	184	1	163	349
275	00291	00274	8	1	0	0	0	0	0	0	0	1	1	2	0	0	0	0	0	1	0	1	0	0	0	0	1	1	0	0	X66699	99.5	184	1	163	349
276	00292	00275	49	4	12	1	0	2	1	1	4	6	4	4	0	2	0	0	5	4	0	1	0	1	0	1	0	0	0	0	M60854	100	181	1	358	538
277	00293	00276	74	6	13	1	6	2	4	3	3	2	5	0	1	0	4	0	0	2	2	0	0	0	1	5	0	11	3	0	M60854	100	181	1	358	538
278	00294	00277	5	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
279	00295	00278	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	
280	00296	00279	8	1	4	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	M86737	100	183	1	2641	2839
281	00297	00280	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
282	00298	00281	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
283	00299	00282	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
284	00300	00283	24	2	1	0	0	0	1	0	0	1	1	2	0	3	1	4	2	0	1	1	0	0	1	1	0	0	0	0	M37104	98.3	179	1	294	471
285	00301	00284	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
286	00302	00285	4	1	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
287	00303	00286	17	2	2	0	0	0	0	1	0	0	0	0	0	0	0	1	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
288	00304	00287	48	2	1	2	2	0	0	1	0	1	3	2	0	3	1	0	4	2	6	0	1	0	0	0	0	2	2	2	L09260	96	176	1	1141	1322
289	00305	00288	46	1	6	0	2	2	3	1	2	1	4	4	2	2	0	3	0	1	4	1	0	2	2	1	2	0	0	0	M26880	99.4	175	1	2088	2309
290	00306	00289	4	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
291	00307	00290	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
292	00308	00291	10	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	3	1	0	2	0	0	0	0	0	0	Y00052	96.7	183	1	542	723
293	00309	00292	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
294	00310	00293	6	1	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	M72709	98.8	85	1	1634	1717	
295	00311	00294	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
296	00312	00295	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
297	00313	00296	17	1	0	1	0	1	0	0	1	0	0	0	0	0	1	0	2	1	0	3	2	0	0	0	2	0	0	0	Y00472	96.8	63	1	767	829
298	00314	00297	45	1	3	1	3	0	1	1	5	1	1	1	0	7	2	0	3	2	0	3	0	0	4	3	2	0	0	2	X06617	96.4	168	1	378	543
299	00315	00298	21	3	4	1	0	0	1	0	1	3	2	0	0	0	1	0	0	3	0	0	0	0	0	0	2	0	0	0	L06498	99.4	161	1	345	505
300	00316	00299	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
301	00317	00300	10	1	0	0	0	3	0	2	0	0	0	0	1	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	S63912	96.8	63	1	1126	3043
302	00320	00301	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
303	00322	00302	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
304	00323	00303	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
305	00325	00304	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
306	00327	00305	20	1	3	1	0	0	1	2	0	0	0	0	0	2	1	0	0	0	0	2	3	0	0	0	0	0	0	0	X03342	96.4	169	1	328	505
307	00328	00306	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
308	00329	00307	5	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
309	00330	00308	8	1	0	2	3	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 9

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
310	00331	00309	6	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
311	00332	00310	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X12517	98.8	165	1	554	733	
312	00333	00311	16	1	0	0	0	0	0	0	0	1	4	0	0	0	0	0	0	2	2	0	0	0	0	0	0	M34539	98.1	157	1	1375	1532	
313	00334	00312	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
314	00335	00313	86	1	16	4	3	1	1	0	3	7	3	1	6	6	1	3	2	1	1	1	1	4	2	5	10	3M36072	100	165	1	727	891	
315	00336	00314	47	1	2	2	2	0	0	1	0	5	6	0	1	2	0	3	4	3	1	1	1	0	1	8	3	Z12962	96.3	162	1	308	478	
316	00337	00315	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	1	0	0	0							
317	00338	00316	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
318	00339	00317	13	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	6	0	0	J03934	96.8	155	1	857	2447	
319	00340	00318	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
320	00341	00319	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
321	00342	00320	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
322	00343	00321	12	2	0	0	0	0	0	0	2	1	0	0	0	3	0	0	1	0	0	2	0	0	0	0	0	0	L07633	97.4	153	1	833	985
323	00344	00322	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
324	00346	00323	9	1	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	2	0	0	0	1	0	0	0	0	S42658	99.6	250	1	569	826
325	00347	00324	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
326	00348	00325	10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	1	0	0							
327	00349	00326	29	2	0	0	0	0	0	0	2	1	2	0	1	0	0	0	1	1	3	1	1	0	1	5	0	0	X74070	93.7	159	1	699	857
328	00350	00327	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
329	00351	00328	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
330	00352	00329	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
331	00353	00330	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
332	00354	00331	6	1	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0							
333	00355	00332	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
334	00356	00333	43	1	17	0	2	2	1	3	0	0	5	0	0	1	0	0	0	1	1	1	0	0	1	0	1	4	2X53777	96	151	1	582	770
335	00357	00334	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
336	00358	00335	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
337	00359	00336	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
338	00360	00337	19	2	2	1	0	0	0	0	0	1	1	1	0	1	0	0	2	1	0	2	0	0	0	1	2	0	X60036	97.2	145	1	1171	1330
339	00361	00338	11	1	0	0	0	0	0	0	0	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0							
340	00362	00339	19	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
341	00363	00340	29	1	0	0	0	0	0	0	0	1	0	2	1	0	0	0	1	0	0	0	0	0	0	0	0							
342	00364	00341	632	17	0	0	0	0	0	0	109	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	D14696	98.6	141	1	1262	1402
343	00365	00342	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L00132	98.6	290	1	1961	2251	
344	00366	00343	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
345	00367	00344	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 10

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
346	00368	00345	11	1	0	0	0	2	0	0	2	0	0	0	0	0	0	0	3	0	0	1	0	0	0	0	1	M31627	98.6	141	1	1657	1818
347	00369	00346	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	L10379	98.6	142	1	1581	1725	
348	00370	00347	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0						
349	00372	00348	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
350	00373	00349	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
351	00374	00350	10	1	1	0	0	0	1	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
352	00375	00351	36	2	3	0	0	0	0	0	0	3	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
353	00376	00352	21	2	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
354	00377	00353	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
355	00378	00354	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
356	00379	00355	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
357	00380	00356	47	1	12	0	0	0	0	0	0	0	2	5	0	0	0	0	0	0	0	0	0	0	0	0	0						
358	00381	00357	22	1	0	2	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
359	00382	00358	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
360	00383	00359	28	3	1	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
361	00384	00360	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
362	00385	00361	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
363	00386	00362	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
364	00387	00363	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
365	00388	00364	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
366	00389	00365	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
367	00390	00366	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
368	00391	00367	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
369	00392	00368	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
370	00393	00369	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
371	00394	00370	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
372	00395	00371	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
373	00396	00372	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
374	00397	00373	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
375	00398	00374	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
376	00399	00375	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
377	00400	00376	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
378	00401	00377	16	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
379	00402	00378	39	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
380	00403	00379	21	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
381	00404	00380	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 11

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AV	AY	B	BC	BE	BF	BG	BH	BI	BK
382	00405	00381	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
383	00406	00382	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
384	00407	00383	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
385	00408	00384	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
386	00409	00385	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
387	00410	00386	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
388	00411	00387	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
389	00412	00388	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
390	00413	00389	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
391	00414	00390	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
392	00415	00391	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
393	00416	00392	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
394	00417	00393	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
395	00418	00394	116	5	22	1	13	1	5	1	0	10	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
396	00419	00395	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
397	00420	00396	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
398	00421	00397	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
399	00422	00398	16	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
400	00423	00399	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
401	00424	00400	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
402	00425	00401	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
403	00426	00402	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
404	00427	00403	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
405	00428	00404	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
406	00429	00405	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
407	00430	00406	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
408	00431	00407	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
409	00433	00408	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
410	00434	00409	13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
411	00435	00410	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
412	00436	00411	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
413	00437	00412	34	5	4	2	2	0	0	2	1	0	2	1	0	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
414	00438	00413	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
415	00439	00414	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
416	00440	00415	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
417	00441	00416	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 12

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
418	00442	00417	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
419	00443	00418	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
420	00444	00419	71	6	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
421	00445	00420	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
422	00446	00421	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
423	00447	00422	38	2	6	1	1	0	3	2	0	2	6	2	0	1	0	0	3	1	1	0	1	1	0	0	0	0	0	0	0	0	0
424	00448	00423	17	1	0	1	1	0	0	0	0	1	2	0	1	0	1	0	1	0	2	0	1	0	1	0	0	0	0	0	0	0	0
425	00450	00424	30	3	2	2	2	0	0	0	0	0	0	0	0	2	1	0	2	0	3	1	10	2	0	0	0	0	0	0	0	0	0
426	00451	00425	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
427	00453	00426	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
428	00454	00427	7	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
429	00455	00428	10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
430	00456	00429	18	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
431	00457	00430	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
432	00458	00431	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
433	00459	00432	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
434	00460	00433	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
435	00461	00434	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
436	00462	00435	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
437	00463	00436	26	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
438	00464	00437	18	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
439	00465	00438	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
440	00466	00439	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
441	00467	00440	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
442	00468	00441	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
443	00469	00442	6	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
444	00470	00443	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
445	00471	00444	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
446	00473	00445	10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
447	00474	00446	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
448	00475	00447	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
449	00477	00448	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
450	00478	00449	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
451	00479	00450	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
452	00480	00451	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
453	00481	00452	24	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 13

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
454	00482	00453	7	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	
455	00483	00454	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	
456	00484	00455	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
457	00485	00456	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
458	00486	00457	6	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
459	00487	00458	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
460	00488	00459	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
461	00489	00460	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
462	00491	00461	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
463	00493	00462	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
464	00494	00463	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
465	00495	00464	12	1	2	1	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
466	00496	00465	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
467	00497	00466	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
468	00498	00467	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
469	00500	00468	54	6	4	1	1	0	2	2	3	3	3	2	3	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
470	00503	00469	8	1	2	0	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
471	00504	00470	56	1	5	1	0	0	1	1	0	2	2	2	2	3	4	2	1	6	2	3	2	0	13	0	1	0	0	0	0	0	0	
472	00505	00471	7	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
473	00506	00472	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
474	00507	00473	9	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
475	00510	00474	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
476	00511	00475	7	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
477	00532	00476	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
478	00533	00477	44	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
479	00534	00478	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
480	00535	00479	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
481	00536	00480	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
482	00537	00481	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
483	00538	00482	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
484	00539	00483	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
485	00540	00484	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
486	00541	00485	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
487	00542	00486	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
488	00543	00487	65	9	4	1	0	0	2	2	0	2	11	0	0	2	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
489	00544	00488	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 14

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
490	00545	00489	36		3	0	2	0	0	2	1	2	3	0	1	3	1	1	0	2	1	1	0	1	3	0	7	1M94314	93.4	439	1	75	556	
491	00546	00490	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
492	00547	00491	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
493	00548	00492	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M64716	94.4	478	2	24	497	
494	00549	00493	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
495	00551	00494	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
496	00552	00495	4		1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
497	00553	00496	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
498	00554	00497	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
499	00555	00498	4		1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	D14662	97.5	481	1	395	1653
500	00556	00499	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
501	00557	00500	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
502	00558	00501	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
503	00560	00502	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
504	00561	00503	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
505	00562	00504	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
506	00564	00505	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
507	00565	00506	70		4	2	5	0	1	1	1	1	1	4	5	1	1	0	4	6	2	1	2	0	25	0	2M30684	96.4	415	1	519	929		
508	00567	00507	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L06432	95.9	98	162	332	549	
509	00568	00508	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
510	00569	00509	10		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
511	00571	00510	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
512	00572	00511	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
513	00573	00512	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
514	00574	00513	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
515	00575	00514	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J04564	93.5	370	4	736	1099	
516	00576	00515	3		1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
517	00577	00516	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
518	00578	00517	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
519	00579	00518	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X52317	96.5	342	1	40	869	
520	00580	00519	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
521	00581	00520	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
522	00582	00521	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
523	00583	00522	34		2	5	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X73460	95.8	378	1	900	1272	
524	00584	00523	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
525	00585	00524	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 15

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
526	00586	00525	6		1	0	0	0	1	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	X07674	95.5	396	1	2559	2970
527	00589	00526	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
528	00590	00527	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
529	00591	00528	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M96954	97.2	351	1	1045	1401
530	00592	00529	15		1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M84643	96.7	331	1	174	506
531	00593	00530	6		1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
532	00594	00531	17		3	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M14199	99.7	341	1	136	475
533	00595	00532	4		1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Y00282	98.5	344	1	1968	2509
534	00596	00533	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
535	00597	00534	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
536	00598	00535	3		1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
537	00599	00536	4		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
538	00600	00537	12		2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
539	00601	00538	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
540	00602	00539	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
541	00603	00540	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
542	00604	00541	4		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
543	00606	00542	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
544	00607	00543	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
545	00608	00544	22		5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	U02619	93.3	193	1	6800	6996
546	00609	00545	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Z11566	99.1	321	1	878	1640
547	00610	00546	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
548	00611	00547	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
549	00612	00548	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
550	00614	00549	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
551	00615	00550	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
552	00616	00551	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X67688	96.5	318	1	1735	2106
553	00617	00552	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
554	00618	00553	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
555	00619	00554	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
556	00620	00555	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
557	00621	00556	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
558	00622	00557	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
559	00623	00558	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	S43127	98.298		1	1145	1441
560	00624	00559	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
561	00625	00560	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 16

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
562	00626	00561	4		2	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
563	00627	00562	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
564	00628	00563	4		1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
565	00629	00564	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
566	00630	00565	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
567	00631	00566	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
568	00632	00567	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
569	00633	00568	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
570	00634	00569	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M19961	93.6	283	1	171	494
571	00635	00570	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
572	00636	00571	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
573	00637	00572	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
574	00638	00573	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
575	00639	00574	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
576	00640	00575	10		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
577	00641	00576	8		2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M55621	98.3	289	1	2311	2602
578	00642	00577	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
579	00643	00578	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
580	00644	00579	24		5	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X13482	96	277	1	760	1054
581	00645	00580	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
582	00646	00581	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
583	00647	00582	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
584	00648	00583	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
585	00649	00584	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
586	00650	00585	52		14	2	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
587	00651	00586	9		4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
588	00652	00587	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
589	00653	00588	13		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
590	00654	00589	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
591	00656	00590	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
592	00657	00591	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
593	00658	00592	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
594	00659	00593	6		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
595	00661	00594	9		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
596	00662	00595	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
597	00663	00596	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 17

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
598	00664	00597	3		1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0							
599	00665	00598	2		1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
600	00666	00599	5		1	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	X65867	98.4	248	1	1335	1692	
601	00667	00600	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
602	00668	00601	8		2	0	1	0	0	0	1	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
603	00669	00602	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
604	00670	00603	12		1	0	0	0	0	0	2	0	2	1	0	0	0	0	1	1	0	0	0	0	0	0	1	0	X60857	98.4	249	1	600	851
605	00671	00604	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
606	00672	00605	7		3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	X66975	97.9	241	1	2915	3319
607	00673	00606	3		1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	X57500	96.2	240	1	2728	2969
608	00674	00607	5		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
609	00675	00608	31		4	1	4	0	1	0	2	1	1	0	0	2	5	0	0	1	0	2	0	0	0	0	6	0	X01124	100	237	1	291	530
610	00676	00609	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
611	00677	00610	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
612	00678	00611	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
613	00679	00612	15		1	1	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
614	00680	00613	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
615	00681	00614	7		1	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	X01457	100	238	1	2484	2739
616	00682	00615	3		1	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	X563912	99.2	254	1	1304	3043
617	00683	00616	20		1	2	0	1	0	0	0	1	1	0	1	0	2	2	1	3	0	0	0	0	0	2	0	X13238	96.1	230	1	194	422	
618	00684	00617	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	X021065	95.8	237	1	1728	3755
619	00685	00618	18		2	5	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
620	00686	00619	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
621	00687	00620	16		1	3	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
622	00688	00621	40		1	1	2	0	1	3	0	0	4	0	3	2	2	2	1	2	1	5	1	1	1	0	2	1	X80927	98.4	246	1	1494	1741
623	00690	00622	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
624	00691	00623	3		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
625	00692	00624	6		2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
626	00693	00625	4		1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
627	00694	00626	3		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
628	00695	00627	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
629	00696	00628	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
630	00697	00629	7		2	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
631	00698	00630	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X18082	96.9	226	1	1640	1880
632	00699	00631	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
633	00700	00632	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 18

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
634	00701	00633	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
635	00702	00634	2		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
636	00703	00635	17		4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	172			466	635
637	00704	00636	45		4	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	217			506	722
638	00705	00637	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
639	00706	00638	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
640	00707	00639	10		1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.3	209			887	1093
641	00708	00640	32		1	0	0	0	0	0	3	3	3	2	0	1	0	2	0	2	3	0	0	0	0	0						
642	00710	00641	2		1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
643	00711	00642	3		1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	127	84		3	135
644	00712	00643	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
645	00713	00644	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
646	00714	00645	13		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
647	00715	00646	1		1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99	202			531	732
648	00716	00647	48		5	3	3	0	0	0	2	1	3	0	1	3	1	0	2	9	2	2	2	3	1	0	94	200			291	495
649	00717	00648	6		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.5	198			2231	2444
650	00718	00649	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
651	00719	00650	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
652	00720	00651	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
653	00721	00652	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
654	00722	00653	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
655	00723	00654	11		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
656	00725	00655	10		1	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	0	0	0	0	0	0	97	202			509	753
657	00726	00656	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
658	00727	00657	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
659	00728	00658	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
660	00729	00659	7		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
661	00730	00660	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
662	00731	00661	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
663	00732	00662	47		6	3	4	0	0	0	1	1	1	0	1	6	2	0	2	7	0	4	3	0	0	0						
664	00733	00663	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
665	00734	00664	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
666	00735	00665	11		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
667	00736	00666	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
668	00737	00667	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
669	00738	00668	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 19

Table 20

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AC	AS	AL	AW	AY	B	BE	BF	BG	BH	BI	BK
706	00779	00705	3		3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X55668	92.6	149	1	824	965
707	00780	00706	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X70944	100	152	1	2916	3071
708	00781	00707	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
709	00782	00708	8		1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
710	00783	00709	5		1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
711	00784	00710	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
712	00785	00711	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M37716	100	145	1	329	491
713	00786	00712	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
714	00787	00713	8		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
715	00788	00714	4		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
716	00789	00715	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
717	00790	00716	5		1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M15502	96.5	141	1	1310	1447
718	00791	00717	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X59417	96.6	149	1	824	979
719	00792	00718	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
720	00793	00719	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
721	00794	00720	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
722	00795	00721	42		1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
723	00796	00722	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L14754	98.5	133	1	3761	3892
724	00797	00723	36		4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J02984	100	137	1	362	498
725	00798	00724	4		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
726	00799	00725	13		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X63423	94.3	141	1	545	691
727	00800	00726	6		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
728	00801	00727	9		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J04823	99.2	132	1	342	472
729	00802	00728	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
730	00803	00729	7		1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
731	00804	00730	5		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
732	00805	00731	6		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
733	00806	00732	7		1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
734	00807	00733	23		2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X69392	98.5	134	1	357	773
735	00808	00734	8		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
736	00809	00735	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
737	00810	00736	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
738	00811	00737	4		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	V00568	95.4	130	1	1953	2121
739	00813	00738	7		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
740	00814	00739	8		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
741	00815	00740	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 21

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK		
742	00816	00741	14		1	5	1	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	5	0	0	M33552	100	125	1	1507	1631		
743	00817	00742	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0								
744	00818	00743	20		4	1	1	0	2	1	0	0	0	0	4	0	2	0	0	0	0	0	0	0	1	3	0								
745	00819	00744	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
746	00820	00745	18		1	0	0	0	2	0	1	0	0	1	0	2	0	1	2	1	0	0	2	1	2	1	0								
747	00821	00746	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
748	00822	00747	3		1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
749	00823	00748	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
750	00824	00749	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0							
751	00825	00750	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
752	00826	00751	6		1	0	1	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	1	0							
753	00827	00752	10		1	1	0	0	2	0	0	0	0	0	0	1	2	0	0	2	0	0	0	0	0	1	0	M89913	99.2	123	1	716	837		
754	00828	00753	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
755	00829	00754	3		2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
756	00830	00755	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
757	00831	00756	5		1	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
758	00832	00757	6		1	0	0	1	0	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
759	00833	00758	5		1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
760	00834	00759	13		1	0	0	0	0	0	2	0	1	0	0	1	0	0	1	4	0	0	0	0	1	0	0	0	0						
761	00835	00760	5		1	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
762	00836	00761	8		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
763	00837	00762	3		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
764	00839	00763	7		1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
765	00840	00764	8		1	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
766	00841	00765	10		5	1	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0						
767	00842	00766	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
768	00843	00767	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
769	00844	00768	5		1	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
770	00845	00769	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
771	00846	00770	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
772	00847	00771	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
773	00848	00772	12		1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
774	00849	00773	2		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
775	00850	00774	12		1	1	0	0	0	0	0	2	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
776	00851	00775	14		5	1	0	1	0	0	0	0	0	0	0	1	2	0	0	3	0	0	0	0	0	0	0	0	0	0					
777	00852	00776	1		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 22

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK		
778	00853	00777	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M34082	90.5	105	1	591	702	
779	00854	00778	8	1	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0						
780	00855	00779	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
781	00856	00780	4	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
782	00857	00781	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
783	00858	00782	6	1	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
784	00859	00783	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
785	00860	00784	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
786	00861	00785	34	6	0	2	0	0	1	0	0	1	4	1	0	2	3	0	1	1	0	1	1	0	3	0	6	M31520	93.5	92	5	529	620
787	00862	00786	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2314	
788	00863	00787	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
789	00864	00788	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
790	00865	00789	56	9	2	1	0	0	0	0	2	2	8	2	1	4	1	0	3	5	4	0	0	0	9	2	0	1	0	0	1	1067	1155
791	00866	00790	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
792	00867	00791	8	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
793	00868	00792	5	1	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
794	00869	00793	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
795	00870	00794	4	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
796	00871	00795	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
797	00872	00796	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
798	00873	00797	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
799	00874	00798	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
800	00875	00799	21	2	3	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
801	00876	00800	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
802	00877	00801	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
803	00878	00802	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
804	00879	00803	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
805	00880	00804	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
806	00882	00805	20	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
807	00883	00806	5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
808	00884	00807	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
809	00885	00808	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
810	00886	00809	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
811	00887	00810	14	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
812	00889	00811	17	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
813	00890	00812	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 23

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK			
814	00891	00813	5	1	0	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0	0	0	0	1	0	0	0								
815	00892	00814	4	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0									
816	00894	00815	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
817	00895	00816	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
818	00896	00817	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
819	00897	00818	10	2	1	0	0	0	0	0	0	1	1	0	0	1	0	0	0	1	0	0	0	0	0	0									
820	00898	00819	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0									
821	00900	00820	27	1	0	2	0	0	0	0	1	1	0	0	0	6	1	1	3	0	2	4	2	0	0	0	0	00558	100	69	1	1528	1596		
822	00903	00821	3	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0								
823	00904	00822	8	1	0	0	0	0	0	0	1	1	2	0	1	0	0	0	0	0	0	1	1	0	0	0	0								
824	00905	00823	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0								
825	00906	00824	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.6	73	1	989	1250		
826	00908	00825	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
827	00910	00826	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									
828	00911	00827	9	1	0	0	0	0	0	0	1	0	0	0	0	1	0	2	2	0	0	0	0	0	0	0	0								
829	00912	00828	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
830	00913	00829	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
831	00914	00830	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0								
832	00915	00831	2	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0								
833	00917	00832	43	3	1	3	0	0	3	3	0	2	1	1	5	6	3	0	0	0	3	3	1	1	1	0	2								
834	00918	00833	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
835	00919	00834	7	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	97.2	109	1	1711	2488	
836	00920	00835	4	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
837	00922	00836	9	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0								
838	00924	00837	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
839	00925	00838	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
840	00926	00839	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
841	00929	00840	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
842	00930	00841	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
843	00931	00842	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
844	00932	00843	16	1	1	0	0	0	0	0	1	0	0	0	0	0	1	4	1	1	0	0	0	0	0	0	0	0							
845	00934	00844	34	3	1	1	0	0	1	5	0	2	3	0	0	3	2	3	0	0	0	0	2	0	6	0	1	0	0	100	48	1	392	439	
846	00935	00845	6	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	94.2	52	1	9332	9390		
847	00936	00846	8	2	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
848	00937	00847	62	1	5	0	0	0	0	0	12	0	6	4	0	2	0	0	2	2	1	0	3	2	5	0	15	0							
849	00938	00848	8	1	0	2	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0							

Table 24

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AN	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
850	00955	00849	6	3	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
851	00972	00850	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
852	00973	00851	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
853	00974	00852	59	0	2	0	1	0	0	0	0	0	0	0	0	1	0	5	6	0	5	16	9	5	1	6	2	0	0	0	0	0	
854	00976	00853	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
855	00977	00854	5	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0						
856	00978	00855	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
857	00979	00856	3	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
858	00980	00857	12	0	2	0	0	0	0	0	0	0	0	1	0	3	1	0	1	0	0	0	0	0	0	0	0	2	0				
859	00981	00858	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
860	00982	00859	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
861	00983	00860	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
862	00984	00861	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
863	00985	00862	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
864	00986	00863	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
865	00987	00864	2	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
866	00988	00865	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
867	00989	00866	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
868	00990	00867	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
869	00991	00868	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
870	00992	00869	3	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
871	00993	00870	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
872	00994	00871	19	0	2	1	0	0	0	0	0	1	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0						
873	00995	00872	23	0	3	1	1	0	1	1	1	0	0	0	0	2	0	1	3	0	2	0	0	1	3	0	1	1	0				
874	00996	00873	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
875	00997	00874	2	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
876	00998	00875	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
877	00999	00876	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
878	01000	00877	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
879	01001	00878	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
880	01002	00879	2	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
881	01003	00880	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
882	01004	00881	4	0	1	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0						
883	01005	00882	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
884	01006	00883	3	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0						
885	01007	00884	33	0	3	0	0	0	0	0	1	1	0	2	2	1	0	5	1	1	2	2	1	3	0	0	2						

Table 25

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
886	01009	00885	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
887	01010	00886	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
888	01011	00887	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
889	01012	00888	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
890	01013	00889	5		0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
891	01015	00890	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
892	01016	00891	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
893	01017	00892	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
894	01018	00893	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
895	01019	00894	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
896	01020	00895	8		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
897	01021	00896	9		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
898	01023	00897	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
899	01024	00898	6		0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
900	01025	00899	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
901	01026	00900	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
902	01027	00901	4		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
903	01028	00902	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
904	01029	00903	13		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
905	01030	00904	9		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
906	01032	00905	14		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
907	01033	00906	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
908	01034	00907	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
909	01035	00908	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
910	01036	00909	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
911	01037	00910	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
912	01038	00911	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
913	01039	00912	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
914	01040	00913	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
915	01041	00914	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
916	01042	00915	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
917	01043	00916	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
918	01044	00917	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
919	01045	00918	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
920	01046	00919	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
921	01047	00920	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 26

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
922	01048	00921	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	1089
923	01049	00922	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
924	01051	00923	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
925	01052	00924	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
926	01053	00925	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4221
927	01054	00926	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
928	01055	00927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
929	01057	00928	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
930	01061	00929	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
931	01062	00930	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1460
932	01063	00931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
933	01064	00932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
934	01065	00933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
935	01066	00934	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
936	01067	00935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
937	01068	00936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
938	01069	00937	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
939	01070	00938	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
940	01071	00939	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
941	01072	00940	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
942	01073	00941	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
943	01074	00942	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4972
944	01075	00943	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
945	01076	00944	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
946	01077	00945	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
947	01078	00946	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	917
948	01079	00947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
949	01080	00948	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
950	01081	00949	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
951	01082	00950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
952	01083	00951	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
953	01084	00952	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
954	01085	00953	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
955	01086	00954	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
956	01087	00955	18		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
957	01088	00956	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 27

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
958	01089	00957	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0M16592	91.8	367	1	1410	1926	
959	01090	00958	2		0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
960	01091	00959	5		0	3	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
961	01092	00960	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0D12902	93	343	16	1	1391	
962	01093	00961	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
963	01094	00962	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
964	01095	00963	3		0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0						
965	01096	00964	9		0	1	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	1	0X66899	96.9	193	1	1981	2371	
966	01097	00965	2		0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
967	01098	00966	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
968	01099	00967	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0X52195	98.4	64	1	477	540	
969	01100	00968	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0Z23064	96.9	354	3	1513	1894	
970	01101	00969	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
971	01102	00970	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
972	01103	00971	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
973	01104	00972	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
974	01105	00973	8		0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0M60091	98.6	351	1	945	1295	
975	01106	00974	16		0	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
976	01107	00975	11		0	2	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	2	0	2J03801	98.3	348	1	1142	1487	
977	01108	00976	5		0	1	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0M75883	97.7	347	1	2227	2572	
978	01109	00977	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
979	01110	00978	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
980	01111	00979	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
981	01112	00980	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
982	01115	00981	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0L20010	99.4	308	1	7851	8240
983	01116	00982	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
984	01117	00983	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
985	01118	00984	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
986	01119	00985	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
987	01120	00986	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
988	01122	00987	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
989	01123	00988	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
990	01126	00989	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
991	01127	00990	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
992	01128	00991	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0X70218	92.2	332	1	837	1382
993	01129	00992	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 28

Table 29

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1030	01168	01029	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
1031	01169	01030	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
1032	01170	01031	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1033	01171	01032	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1034	01172	01033	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1035	01173	01034	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1036	01174	01035	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1037	01175	01036	14		0	1	2	1	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1038	01176	01037	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X76717	98.9	275	1	21	415
1039	01177	01038	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1040	01178	01039	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1041	01179	01040	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1042	01180	01041	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1043	01181	01042	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1044	01182	01043	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1045	01183	01044	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1046	01184	01045	7		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1047	01186	01046	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1048	01187	01047	8		0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1049	01188	01048	5		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1050	01189	01049	13		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M83246	97.9	285	1	1055	1349
1051	01191	01050	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1052	01192	01051	8		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1053	01193	01052	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1054	01194	01053	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1055	01195	01054	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M94083	96	278	1	1374	1685
1056	01196	01055	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1057	01197	01056	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1058	01198	01057	10		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1059	01199	01058	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Y00281	92.8	290	1	1934	2397
1060	01200	01059	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1061	01201	01060	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1062	01202	01061	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1063	01203	01062	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M32011	94.6	276	1	1931	2206
1064	01204	01063	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1065	01205	01064	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 30

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
1066	01207	01065	5		0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
1067	01208	01066	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1068	01209	01067	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1069	01210	01068	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1070	01211	01069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1071	01212	01070	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1072	01213	01071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1073	01214	01072	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1074	01215	01073	15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1075	01216	01074	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1076	01217	01075	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1077	01218	01076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1078	01219	01077	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1079	01220	01078	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1080	01221	01079	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1081	01222	01080	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1082	01223	01081	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1083	01224	01082	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1084	01225	01083	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1085	01226	01084	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1086	01227	01085	15		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1087	01228	01086	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1088	01229	01087	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1089	01230	01088	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1090	01231	01089	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1091	01232	01090	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1092	01233	01091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1093	01235	01092	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1094	01236	01093	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1095	01237	01094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1096	01238	01095	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1097	01239	01096	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1098	01240	01097	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1099	01241	01098	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1100	01242	01099	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1101	01243	01100	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 31

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1138	01283	01137	9		0	2	1	1	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	2527
1139	01284	01138	2		0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	669
1140	01285	01139	6		0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1141	01286	01140	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1142	01287	01141	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1143	01288	01142	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1144	01289	01143	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1145	01290	01144	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1146	01291	01145	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1147	01292	01146	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1148	01293	01147	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1149	01294	01148	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1150	01295	01149	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1151	01296	01150	6		0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1152	01297	01151	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1153	01298	01152	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1154	01299	01153	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1155	01300	01154	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1156	01301	01155	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1157	01302	01156	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1158	01303	01157	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1159	01304	01158	10		0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1160	01305	01159	28		0	2	1	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1161	01306	01160	3		0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1162	01307	01161	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1163	01308	01162	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1164	01309	01163	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1165	01310	01164	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1166	01311	01165	6		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1167	01312	01166	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1168	01313	01167	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1169	01314	01168	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1170	01315	01169	8		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1171	01316	01170	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1172	01317	01171	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1173	01318	01172	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 33

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1174	01319	01173	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1175	01320	01174	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1176	01321	01175	19		0	3	2	1	2	0	1	1	0	0	1	0	2	0	0	0	0	0	1	0	2	2	1	0					
1177	01322	01176	3		0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
1178	01323	01177	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1179	01324	01178	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1180	01325	01179	17		0	1	0	0	0	0	0	0	2	0	1	0	1	0	0	2	1	0	0	0	0	0	0						
1181	01326	01180	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1182	01327	01181	4		0	2	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1183	01328	01182	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1184	01329	01183	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1185	01330	01184	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1186	01331	01185	3		0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1187	01332	01186	3		0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1188	01333	01187	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1189	01334	01188	7		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1190	01335	01189	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1191	01336	01190	4		0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1192	01337	01191	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1193	01338	01192	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1194	01339	01193	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1195	01340	01194	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1196	01341	01195	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1197	01342	01196	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1198	01343	01197	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1199	01344	01198	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1200	01345	01199	4		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1201	01346	01200	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1202	01347	01201	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1203	01348	01202	13		0	2	0	0	0	1	1	0	0	1	0	0	4	0	0	0	0	0	0	0	0	0	0						
1204	01349	01203	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1205	01350	01204	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1206	01351	01205	7		0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1207	01352	01206	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1208	01353	01207	2		0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
1209	01354	01208	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 34

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BGBH	BI	BK	
1210	01355	01209	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1211	01356	01210	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1212	01357	01211	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1213	01358	01212	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1214	01359	01213	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.3	127	1	453	579
1215	01360	01214	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1216	01361	01215	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1217	01362	01216	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1218	01363	01217	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1219	01364	01218	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1220	01365	01219	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1221	01366	01220	1		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1222	01367	01221	21		0	3	1	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1223	01368	01222	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1224	01369	01223	5		0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1225	01370	01224	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1226	01371	01225	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1227	01372	01226	7		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1228	01373	01227	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1229	01374	01228	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1230	01375	01229	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1231	01377	01230	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1232	01378	01231	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1233	01379	01232	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1234	01380	01233	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1235	01381	01234	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1236	01382	01235	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1237	01383	01236	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1238	01384	01237	16		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1239	01385	01238	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1240	01386	01239	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1241	01387	01240	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1242	01388	01241	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1243	01389	01242	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1244	01390	01243	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1245	01391	01244	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 35

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1246	01392	01245	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1247	01393	01246	5		0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1248	01394	01247	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1249	01395	01248	7		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1250	01396	01249	4		0	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1251	01397	01250	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1252	01398	01251	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1253	01400	01252	1		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1254	01401	01253	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1255	01402	01254	7		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1256	01403	01255	6		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1257	01404	01256	16		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1258	01405	01257	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1259	01406	01258	7		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1260	01407	01259	3		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1261	01408	01260	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1262	01409	01261	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1263	01410	01262	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1264	01411	01263	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1265	01412	01264	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1266	01413	01265	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1267	01414	01266	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1268	01415	01267	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1269	01416	01268	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1270	01417	01269	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1271	01418	01270	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1272	01419	01271	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1273	01420	01272	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1274	01421	01273	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1275	01422	01274	3		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1276	01423	01275	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1277	01424	01276	12		0	2	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1278	01426	01277	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1279	01427	01278	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1280	01428	01279	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1281	01429	01280	4		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 36

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
1282	01430	01281	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1283	01431	01282	6		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X51346	99.3	144	1	1470	1612
1284	01432	01283	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1285	01433	01284	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1286	01434	01285	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1287	01435	01286	7		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1288	01436	01287	1		0	1	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0						
1289	01437	01288	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1290	01438	01289	3		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1291	01439	01290	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1292	01440	01291	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M11948	90.5	84	59	342	425
1293	01441	01292	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1294	01442	01293	4		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1295	01443	01294	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1296	01444	01295	3		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1297	01445	01296	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1298	01446	01297	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1299	01447	01298	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1300	01448	01299	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1301	01449	01300	10		0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1302	01450	01301	4		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1303	01451	01302	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1304	01452	01303	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1305	01453	01304	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1306	01454	01305	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1307	01455	01306	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1308	01456	01307	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1309	01457	01308	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1310	01458	01309	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1311	01459	01310	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1312	01460	01311	2		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1313	01461	01312	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1314	01462	01313	6		0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1315	01463	01314	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1316	01464	01315	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1317	01466	01316	1		0	1	0	0	0	0	0	0	0	0	0	0	0															

Table 37

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AV	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
1318	01467	01317	4		0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
1319	01468	01318	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1320	01469	01319	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0							
1321	01470	01320	3		0	1	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0							
1322	01471	01321	2		0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1323	01472	01322	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1324	01473	01323	9		0	2	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0						
1325	01474	01324	2		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1326	01475	01325	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1327	01476	01326	19		0	4	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	10	0	0							
1328	01477	01327	4		0	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0	0	0	0	0							
1329	01478	01328	5		0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1330	01479	01329	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1331	01481	01330	3		0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1332	01482	01331	2		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1333	01483	01332	9		0	2	2	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0							
1334	01484	01333	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1335	01485	01334	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1336	01486	01335	3		0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1337	01487	01336	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1338	01488	01337	4		0	1	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0							
1339	01489	01338	5		0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	2	0						
1340	01490	01339	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1341	01491	01340	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1342	01492	01341	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1343	01493	01342	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1344	01494	01343	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1345	01495	01344	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1346	01496	01345	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	X54637	100	116	1	4058	4176	
1347	01497	01346	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1348	01498	01347	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1349	01499	01348	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1350	01500	01349	3		0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1351	01501	01350	3		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1352	01502	01351	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1353	01503	01352	9		0	1	2	0	0	0	1	0	0	2	0	0	0	0	0	1	0	0	0	0	1	0	0							

Table 38

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AU	AV	AW	BABC	BE	BF	BG	BH	BI	BK	
1354	01505	01353	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1355	01506	01354	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1356	01507	01355	5	0	0	1	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	1	0	X55187	98.3	406	1	1923	2327	
1357	01508	01356	13	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	M29064	99.1	112	1	1617	1760	
1358	01509	01357	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1359	01510	01358	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1360	01511	01359	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1361	01512	01360	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1362	01513	01361	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1363	01514	01362	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1364	01515	01363	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M73554	93.6	110	1	3448	4221	
1365	01516	01364	7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1366	01517	01365	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1367	01518	01366	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1368	01519	01367	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1369	01520	01368	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1370	01521	01369	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1371	01522	01370	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1372	01523	01371	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1373	01524	01372	7	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	SS4711	96.5	231	62	1	229	
1374	01525	01373	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1375	01526	01374	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1376	01527	01375	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1377	01528	01376	16	0	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1378	01529	01377	7	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1379	01530	01378	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1380	01531	01379	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1381	01532	01380	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1382	01533	01381	19	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1383	01534	01382	8	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1384	01535	01383	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1385	01537	01384	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1386	01538	01385	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1387	01539	01386	12	0	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1388	01540	01387	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1389	01541	01388	6	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 39

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1390	01542	01389	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X06814	90.1	101	1	552	702
1391	01543	01390	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1392	01544	01391	4		0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1393	01545	01392	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1394	01546	01393	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1395	01547	01394	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1396	01548	01395	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1397	01549	01396	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1398	01550	01397	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1399	01551	01398	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	025538	100	95	1	6102	6196
1400	01552	01399	10		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1401	01553	01400	5		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1402	01554	01401	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1403	01555	01402	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1404	01556	01403	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M95767	97.8	89	1	1208	1618
1405	01557	01404	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1406	01558	01405	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1407	01560	01406	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1408	01561	01407	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1409	01562	01408	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1410	01563	01409	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1411	01564	01410	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1412	01565	01411	6		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1413	01566	01412	9		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M79463	100	84	1	3492	3587
1414	01567	01413	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X71428	94.2	86	1	1734	1822
1415	01568	01414	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1416	01569	01415	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1417	01570	01416	7		0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1418	01571	01417	10		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X65019	98.8	82	1	1263	1358
1419	01572	01418	4		0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J03805	96.3	81	1	1449	1529
1420	01573	01419	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1421	01574	01420	11		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1422	01575	01421	6		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1423	01576	01422	6		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1424	01577	01423	5		0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1425	01578	01424	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 40

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1426	01579	01425	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1427	01580	01426	4		0	1	0	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
1428	01581	01427	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1429	01582	01428	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1430	01583	01429	5		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1431	01584	01430	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1432	01585	01431	8		0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1433	01586	01432	2		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1434	01587	01433	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1435	01588	01434	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1436	01589	01435	10		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1437	01590	01436	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1438	01591	01437	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1439	01592	01438	4		0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1440	01593	01439	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1441	01594	01440	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1442	01595	01441	7		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1443	01596	01442	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1444	01597	01443	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1445	01598	01444	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1446	01599	01445	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1447	01600	01446	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1448	01601	01447	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1449	01602	01448	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1450	01603	01449	5		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1451	01604	01450	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1452	01605	01451	2		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1453	01606	01452	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1454	01607	01453	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1455	01608	01454	23		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1456	01609	01455	16		0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1457	01610	01456	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1458	01611	01457	3		0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1459	01612	01458	5		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1460	01614	01459	4		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1461	01615	01460	1		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 41

Table 42

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
1498	01703	01497	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1499	01704	01498	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1500	01705	01499	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1501	01706	01500	12		0	0	4	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.1 421	1	120	580
1502	01707	01501	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.3 471	1	1652	2113
1503	01708	01502	5		0	0	1	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	0	0			
1504	01709	01503	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1505	01710	01504	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1506	01711	01505	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1507	01713	01506	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1508	01714	01507	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.4 448	1	1052	1497
1509	01715	01508	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1510	01718	01509	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1511	01719	01510	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1512	01720	01511	43		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1513	01721	01512	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3 345	1	1239	1672
1514	01722	01513	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.8 461	1	913	1362
1515	01724	01514	9		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1516	01726	01515	5		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1517	01727	01516	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1518	01728	01517	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1519	01729	01518	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1520	01730	01519	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1521	01731	01520	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1522	01732	01521	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.2 426	1	2322	2745
1523	01733	01522	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.9 364	1	888	1167
1524	01734	01523	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1525	01735	01524	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1526	01736	01525	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1527	01737	01526	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1528	01738	01527	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1529	01739	01528	8		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1530	01740	01529	8		0	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1531	01741	01530	5		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1532	01742	01531	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1533	01745	01532	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				

Table 43

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AL	AW	AY	BABC	BE	BF	BGBH	BI	BK	
1534	01746	01533	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1535	01747	01534	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1536	01748	01535	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1537	01749	01536	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.7	358	1	850	2177	
1538	01750	01537	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.2	358	1	278	637	
1539	01751	01538	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1540	01752	01539	4		0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
1541	01753	01540	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1542	01754	01541	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1543	01755	01542	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1544	01756	01543	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1545	01758	01544	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1546	01759	01545	7		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1547	01760	01546	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1548	01761	01547	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1549	01763	01548	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1550	01764	01549	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1551	01765	01550	7		0	0	1	1	0	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	94.7	337	1	1615	1958
1552	01766	01551	63		0	0	6	15	2	4	2	0	4	0	5	1	1	0	6	1	10	3	0	0	1	0	0	0	93.4	318	1	61	372
1553	01767	01552	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0						
1554	01768	01553	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
1555	01769	01554	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1556	01770	01555	5		0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.9	385	1	3963	4354
1557	01771	01556	1		0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1558	01772	01557	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.6	322	1	2348	2709	
1559	01773	01558	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.4	309	1	2120	2428	
1560	01774	01559	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.9	185	138	906	1098	
1561	01775	01560	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.3	374	1	1105	1478	
1562	01776	01561	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1563	01777	01562	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1564	01778	01563	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1565	01779	01564	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1566	01780	01565	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1567	01781	01566	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1568	01782	01567	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1569	01783	01568	3		0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 44

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1570	01784	01569	2		0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1571	01785	01570	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1572	01786	01571	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1573	01787	01572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1574	01788	01573	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1575	01789	01574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1576	01790	01575	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1577	01791	01576	34		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1578	01792	01577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1579	01793	01578	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1580	01794	01579	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1581	01795	01580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1582	01796	01581	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1583	01797	01582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1584	01798	01583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1585	01799	01584	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1586	01800	01585	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1587	01801	01586	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1588	01802	01587	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1589	01803	01588	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1590	01804	01589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1591	01805	01590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1592	01806	01591	26		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1593	01807	01592	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1594	01808	01593	47		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1595	01809	01594	19		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1596	01810	01595	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1597	01811	01596	39		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1598	01812	01597	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1599	01813	01598	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1600	01814	01599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1601	01815	01600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1602	01816	01601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1603	01817	01602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1604	01818	01603	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1605	01819	01604	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 45

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BGBH	BI	BK
1606	01820	01605	9		0	0	1	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	0				
1607	01821	01606	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1608	01822	01607	7		0	0	2	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1609	01823	01608	24		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0				
1610	01824	01609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1611	01825	01610	3		0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0				
1612	01826	01611	6		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0				
1613	01827	01612	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1614	01828	01613	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1615	01829	01614	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1616	01830	01615	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1617	01831	01616	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1618	01832	01617	8		0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
1619	01833	01618	1		0	0	1	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0				
1620	01834	01619	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1621	01835	01620	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1622	01836	01621	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1623	01837	01622	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1624	01838	01623	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1625	01839	01624	2		0	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
1626	01840	01625	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1627	01841	01626	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1628	01842	01627	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1629	01843	01628	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1630	01844	01629	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1631	01845	01630	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1632	01846	01631	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1633	01847	01632	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1634	01848	01633	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1635	01849	01634	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1636	01850	01635	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1637	01851	01636	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1638	01852	01637	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1639	01853	01638	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1640	01854	01639	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1641	01855	01640	7		0	0	1	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					

Table 46

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	ABC	BE	BF	BGBH	BI	BK	
1642	01856	01641	5		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	M33146	100	186	6	1612	1797
1643	01857	01642	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1644	01858	01643	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1645	01859	01644	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1646	01860	01645	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1647	01861	01646	18		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1648	01862	01647	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1649	01863	01648	18		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1650	01864	01649	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1651	01865	01650	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1652	01866	01651	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1653	01867	01652	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1654	01868	01653	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1655	01869	01654	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1656	01870	01655	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1657	01871	01656	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1658	01872	01657	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1659	01873	01658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1660	01874	01659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1661	01875	01660	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1662	01876	01661	11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1663	01877	01662	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1664	01878	01663	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1665	01880	01664	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1666	01881	01665	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1667	01882	01666	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1668	01883	01667	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1669	01884	01668	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1670	01885	01669	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1671	01886	01670	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1672	01887	01671	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1673	01888	01672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1674	01889	01673	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1675	01890	01674	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1676	01891	01675	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
1677	01892	01676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 47

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
1678	01893	01677	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1679	01895	01678	7		0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1680	01896	01679	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1681	01897	01680	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1682	01898	01681	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1683	01899	01682	14		0	0	2	0	0	0	0	0	2	0	0	3	1	0	0	1	1	3	0	0	0	0	0	0	0	0	0	0	0	
1684	01900	01683	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1685	01901	01684	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1686	01902	01685	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1687	01903	01686	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1688	01904	01687	3		0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1689	01905	01688	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1690	01906	01689	3		0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1691	01907	01690	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1692	01908	01691	21		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1693	01909	01692	4		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1694	01910	01693	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1695	01911	01694	10		0	0	1	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1696	01912	01695	5		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1697	01913	01696	2		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1698	01914	01697	3		0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1699	01915	01698	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1700	01916	01699	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1701	01917	01700	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1702	01918	01701	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1703	01919	01702	111		0	0	5	0	1	0	3	5	6	12	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1704	01920	01703	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1705	01921	01704	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1706	01922	01705	3		0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1707	01923	01706	2		0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1708	01924	01707	3		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1709	01925	01708	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1710	01926	01709	24		0	0	2	0	0	0	2	0	0	3	0	0	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1711	01927	01710	3		0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1712	01928	01711	10		0	0	4	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1713	01929	01712	19		0	0	1	0	1	0	4	0	0	0	0	0	2	1	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 48

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
1714	01930	01713	2		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
1715	01931	01714	4		0	0	2	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
1716	01932	01715	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1717	01933	01716	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1718	01934	01717	5		0	0	0	1	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.5	276	1	756	1120
1719	01935	01718	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1720	01936	01719	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1721	01937	01720	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.9	114	1	2834	2986	
1722	01938	01721	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1723	01939	01722	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1724	01940	01723	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1725	01941	01724	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1726	01943	01725	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1727	01944	01726	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1728	01945	01727	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1729	01946	01728	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1730	01947	01729	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.2	328	1	236	852	
1731	01948	01730	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1732	01949	01731	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1733	01950	01732	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1734	01951	01733	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1735	01952	01734	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1736	01953	01735	17		0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1737	01954	01736	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1738	01955	01737	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1739	01956	01738	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1740	01957	01739	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1741	01958	01740	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1742	01959	01741	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1743	01960	01742	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1744	01961	01743	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98	100	1	3640	3740	
1745	01962	01744	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1746	01963	01745	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1747	01964	01746	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1748	01965	01747	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1749	01966	01748	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 49

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
1750	01967	01749	13		0	0	1	1	0	0	1	0	0	0	1	2	1	0	0	0	2	1	0	0	1	0	0	X14986	100	57	36	1	57	
1751	01968	01750	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1752	01969	01751	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1753	01970	01752	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1754	01972	01753	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1755	01973	01754	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1756	01974	01755	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1757	01975	01756	6		0	0	0	0	0	0	0	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
1758	01976	01757	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1759	01977	01758	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1760	01978	01759	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1761	01979	01760	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1762	01981	01761	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1763	01982	01762	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1764	01983	01763	16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1765	01984	01764	3		0	0	0	0	0	0	0	3	2	3	0	1	0	1	0	2	1	0	0	0	0	0	0	0						
1766	01985	01765	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1767	01986	01766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1768	01987	01767	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1769	01988	01768	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1770	01989	01769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1771	01990	01770	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1772	01991	01771	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M57502	98.6	71	1	449	520	
1773	01992	01772	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L06132	98.5	66	1	1742	1806	
1774	01994	01773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1775	01995	01774	18		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1776	01996	01775	1		0	0	0	0	0	0	0	2	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	X13710	93.8	65	1	1039	1100	
1777	01997	01776	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1778	01998	01777	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X13973	95.2	62	1	1860	1921	
1779	01999	01778	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1780	02000	01779	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1781	02001	01780	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1782	02002	01781	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1783	02003	01782	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1784	02005	01783	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
1785	02006	01784	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M16750	96.6	58	1	2239	2297	

Table 50

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
1786	02007	01785	15		0	0	1	0	0	0	0	0	1	0	2	0	0	2	0	1	4	0	0	0	1	2	0	0	0	100	56	1	1064	1119
1787	02010	01786	7		0	0	1	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1788	02011	01787	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1789	02012	01788	16		0	0	0	0	0	0	2	2	0	1	0	1	0	0	0	1	0	0	1	3	0	0	1	0						
1790	02013	01789	12		0	0	2	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0						
1791	02025	01790	8		0	0	1	0	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1792	02039	01791	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1793	02040	01792	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1794	02041	01793	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1795	02042	01794	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1796	02043	01795	8		0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1797	02044	01796	5		0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1798	02045	01797	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1799	02046	01798	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1800	02047	01799	13		0	0	0	0	2	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1801	02048	01800	5		0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1802	02049	01801	20		0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1803	02050	01802	5		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1804	02051	01803	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1805	02052	01804	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1806	02053	01805	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1807	02054	01806	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1808	02055	01807	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1809	02056	01808	2		0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1810	02057	01809	5		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1811	02058	01810	5		0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1812	02059	01811	6		0	0	0	0	1	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1813	02060	01812	8		0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1814	02062	01813	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1815	02063	01814	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1816	02064	01815	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1817	02065	01816	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1818	02066	01817	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1819	02067	01818	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1820	02068	01819	3		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1821	02069	01820	7		0	0	0	0	1	1	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 51

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AI	AK	AM	AQ	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1822	02070	01821	2		0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
1823	02071	01822	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1824	02072	01823	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1825	02073	01824	16		0	0	0	1	0	0	1	2	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1						
1826	02074	01825	7		0	0	0	1	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0						
1827	02075	01826	7		0	0	0	1	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1828	02076	01827	4		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0						
1829	02077	01828	3		0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
1830	02078	01829	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1831	02079	01830	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1832	02080	01831	11		0	0	0	1	1	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
1833	02081	01832	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1834	02082	01833	7		0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1835	02084	01834	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1836	02085	01835	83		0	0	0	16	26	40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1837	02086	01836	4		0	0	0	2	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
1838	02087	01837	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1839	02088	01838	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1840	02089	01839	2		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1841	02090	01840	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1842	02091	01841	9		0	0	0	2	1	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
1843	02092	01842	11		0	0	0	2	1	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1844	02093	01843	11		0	0	0	2	3	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1845	02094	01844	6		0	0	0	1	2	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0						
1846	02095	01845	2		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1847	02096	01846	2		0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1848	02097	01847	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1849	02098	01848	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1850	02099	01849	3		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1851	02100	01850	5		0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0						
1852	02101	01851	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1853	02102	01852	5		0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1854	02103	01853	5		0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1855	02104	01854	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1856	02105	01855	109		0	0	0	6	4	3	10	0	36	22	0	0	0	0	0	0	0	0	0	0	0	0	0						
1857	02106	01856	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 52

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
1858	02107	01857	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1859	02108	01858	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1860	02110	01859	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1861	02111	01860	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1862	02112	01861	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1863	02113	01862	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1864	02115	01863	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1865	02116	01864	12		0	0	0	3	2	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1866	02117	01865	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1867	02118	01866	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1868	02119	01867	8		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1869	02120	01868	19		0	0	0	3	12	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1870	02121	01869	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1871	02122	01870	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1872	02123	01871	28		0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1873	02124	01872	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1874	02126	01873	7		0	0	0	6	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1875	02127	01874	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1876	02128	01875	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1877	02129	01876	4		0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1878	02130	01877	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1879	02131	01878	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1880	02132	01879	2		0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1881	02133	01880	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1882	02134	01881	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1883	02135	01882	6		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1884	02136	01883	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1885	02137	01884	4		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1886	02138	01885	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1887	02139	01886	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1888	02140	01887	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1889	02141	01888	8		0	0	0	5	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1890	02142	01889	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1891	02143	01890	3		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1892	02144	01891	8		0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1893	02145	01892	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 53

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BGBH	BI	BK	
1894	02146	01893	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1895	02147	01894	4		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1896	02148	01895	21		0	0	0	3	6	6	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1897	02149	01896	4		0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1898	02150	01897	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1899	02151	01898	14		0	0	0	9	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1900	02152	01899	7		0	0	0	1	0	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1901	02153	01900	6		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1902	02154	01901	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1903	02155	01902	28		0	0	0	7	3	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1904	02156	01903	8		0	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1905	02157	01904	35		0	0	0	1	0	2	0	0	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1906	02158	01905	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1907	02159	01906	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1908	02160	01907	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1909	02161	01908	9		0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1910	02162	01909	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1911	02163	01910	4		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1912	02164	01911	5		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1913	02165	01912	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1914	02166	01913	4		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1915	02167	01914	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1916	02168	01915	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1917	02169	01916	9		0	0	0	2	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1918	02170	01917	3		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1919	02171	01918	6		0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1920	02172	01919	4		0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1921	02173	01920	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1922	02174	01921	25		0	0	0	4	1	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1923	02175	01922	4		0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1924	02176	01923	13		0	0	0	3	1	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1925	02177	01924	7		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1926	02178	01925	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1927	02179	01926	2		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1928	02180	01927	1		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
1929	02181	01928	14		0	0	0	1	0	0	0	0	1	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 54

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AW	AY	B	ABC	BE	BF	BG	BH	BI	BK
1966	02240	01965	5		0	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0						
1967	02241	01966	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1968	02242	01967	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1969	02243	01968	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1970	02244	01969	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1971	02245	01970	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1972	02246	01971	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1973	02247	01972	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1974	02248	01973	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1975	02249	01974	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1976	02250	01975	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1977	02251	01976	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1978	02252	01977	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1979	02253	01978	3		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1980	02254	01979	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1981	02255	01980	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1982	02256	01981	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1983	02257	01982	10		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1984	02258	01983	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1985	02259	01984	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1986	02260	01985	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1987	02261	01986	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1988	02262	01987	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1989	02263	01988	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1990	02264	01989	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1991	02265	01990	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1992	02266	01991	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1993	02267	01992	12		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1994	02268	01993	9		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1995	02269	01994	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1996	02270	01995	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1997	02271	01996	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1998	02272	01997	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
1999	02273	01998	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2000	02274	01999	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2001	02275	02000	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 56

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BGBH	BI	BK
2002	02281	02001	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2003	02282	02002	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2004	02283	02003	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2005	02285	02004	10		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2006	02287	02005	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2007	02288	02006	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2008	02289	02007	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2009	02290	02008	16		0	0	0	0	0	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2010	02291	02009	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2011	02292	02010	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2012	02293	02011	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2013	02294	02012	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2014	02295	02013	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2015	02296	02014	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2016	02297	02015	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2017	02298	02016	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2018	02299	02017	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2019	02300	02018	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2020	02301	02019	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2021	02302	02020	5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2022	02303	02021	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2023	02304	02022	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2024	02305	02023	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2025	02306	02024	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2026	02307	02025	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2027	02308	02026	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2028	02309	02027	18		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2029	02310	02028	3		0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2030	02311	02029	6		0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2031	02312	02030	5		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2032	02313	02031	6		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2033	02314	02032	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2034	02315	02033	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2035	02316	02034	12		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2036	02317	02035	5		0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2037	02318	02036	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 57

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2038	02319	02037	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2039	02321	02038	7		0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1	99.3	137	1	1095	1231
2040	02322	02039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.1	129	10	1673	1801	
2041	02323	02040	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2042	02324	02041	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2043	02325	02042	5		0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2044	02326	02043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2045	02327	02044	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2046	02328	02045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2047	02329	02046	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2048	02330	02047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2049	02331	02048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2050	02332	02049	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2051	02333	02050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2052	02334	02051	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2053	02336	02052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2054	02337	02053	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2055	02338	02054	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2056	02339	02055	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2057	02340	02056	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2058	02341	02057	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2059	02342	02058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2060	02343	02059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2061	02345	02060	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2062	02346	02061	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2063	02347	02062	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2064	02348	02063	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2065	02349	02064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2066	02350	02065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2067	02351	02066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2068	02352	02067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2069	02353	02068	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2070	02354	02069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2071	02355	02070	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2072	02356	02071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2073	02357	02072	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 58

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
2074	02358	02073	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X69078	97.9	95	1	3127	3228
2075	02359	02074	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
2076	02360	02075	3		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
2077	02361	02076	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2078	02362	02077	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2079	02363	02078	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2080	02364	02079	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2081	02365	02080	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2082	02366	02081	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2083	02367	02082	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2084	02368	02083	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2085	02369	02084	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2086	02370	02085	2		0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	Y00317	98.5	67	1	2027	2093
2087	02371	02086	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2088	02372	02087	6		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2089	02373	02088	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2090	02374	02089	38		0	0	0	0	1	1	1	5	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2091	02375	02090	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2092	02376	02091	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2093	02377	02092	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2094	02378	02093	4		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X64594	100	56	1	1839	1927
2095	02379	02094	1		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2096	02380	02095	2		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2097	02382	02096	13		0	0	0	0	1	0	0	0	2	1	1	2	0	0	0	0	0	0	0	0	0	0						
2098	02399	02097	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2099	02400	02098	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2100	02401	02099	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2101	02402	02100	6		0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2102	02403	02101	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2103	02404	02102	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2104	02406	02103	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2105	02408	02104	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2106	02409	02105	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2107	02411	02106	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2108	02412	02107	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2109	02413	02108	3		0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 59

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AO	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
2110	02414	02109	2		0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M65131	97.9	340	1	1994	2798	
2111	02415	02110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2112	02416	02111	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2113	02417	02112	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	K01396	96.5	347	1	559	1352	
2114	02418	02113	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	K01763	97.6	211	152	1022	1234	
2115	02419	02114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2116	02420	02115	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2117	02421	02116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2118	02422	02117	7		0	0	0	0	0	1	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2119	02423	02118	3		0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2120	02424	02119	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2121	02425	02120	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2122	02426	02121	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2123	02427	02122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2124	02428	02123	4		0	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2125	02429	02124	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2126	02430	02125	3		0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2127	02431	02126	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2128	02432	02127	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2129	02433	02128	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2130	02434	02129	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2131	02435	02130	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	K01500	96.4	309	1	1214	1520
2132	02436	02131	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	K00485	93	214	12	107	323
2133	02437	02132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2134	02438	02133	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2135	02439	02134	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2136	02441	02135	5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2137	02442	02136	3		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2138	02443	02137	8		0	0	0	0	0	1	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J04794	96.7	301	1	834	1132
2139	02444	02138	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2140	02445	02139	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L19297	100	294	1	790	1083
2141	02446	02140	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2142	02447	02141	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2143	02448	02142	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2144	02449	02143	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2145	02450	02144	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 60

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
2146	02452	02145	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0				
2147	02453	02146	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2148	02454	02147	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2149	02455	02148	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2150	02456	02149	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2151	02457	02150	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2152	02458	02151	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2153	02459	02152	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2154	02461	02153	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2155	02462	02154	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2156	02463	02155	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2157	02464	02156	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2158	02465	02157	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2159	02466	02158	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2160	02467	02159	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2161	02468	02160	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2162	02469	02161	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2163	02471	02162	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2164	02472	02163	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2165	02473	02164	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2166	02474	02165	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2167	02475	02166	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2168	02476	02167	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2169	02477	02168	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2170	02478	02169	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2171	02479	02170	6		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2172	02480	02171	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2173	02481	02172	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2174	02482	02173	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2175	02483	02174	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2176	02484	02175	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2177	02486	02176	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2178	02487	02177	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2179	02488	02178	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2180	02489	02179	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
2181	02490	02180	16		0	0	0	0	0	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				

Table 61

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
2182	02491	02181	4		0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
2183	02493	02182	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2184	02494	02183	2		0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2185	02495	02184	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2186	02496	02185	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2187	02497	02186	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2188	02498	02187	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2189	02499	02188	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2190	02500	02189	3		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2191	02501	02190	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2192	02502	02191	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2193	02503	02192	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2194	02504	02193	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2195	02505	02194	5		0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2196	02506	02195	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2197	02507	02196	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2198	02508	02197	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2199	02509	02198	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2200	02510	02199	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2201	02511	02200	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2202	02512	02201	13		0	0	0	0	0	1	0	1	8	1	0	0	0	0	0	0	0	0	0	0	0	0					
2203	02513	02202	3		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2204	02514	02203	8		0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2205	02515	02204	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2206	02516	02205	5		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2207	02517	02206	6		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2208	02518	02207	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2209	02519	02208	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2210	02520	02209	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2211	02521	02210	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2212	02522	02211	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2213	02523	02212	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2214	02524	02213	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2215	02525	02214	5		0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2216	02526	02215	3		0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2217	02527	02216	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 62

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2218	02528	02217	2		0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2219	02529	02218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2220	02531	02219	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0						
2221	02532	02220	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
2222	02534	02221	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2223	02535	02222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2224	02537	02223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2225	02538	02224	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2226	02540	02225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2227	02542	02226	33		0	0	0	0	0	0	0	0	0	0	12	1	0	0	14	1	0	0	0	0	0	0	0	0	M87790	97.9	96	1	782 877
2228	02543	02227	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2229	02544	02228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2230	02545	02229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2231	02546	02230	19		0	0	0	0	0	0	0	0	0	0	18	0	0	0	0	0	0	0	0	0	0	0	0						
2232	02547	02231	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2233	02548	02232	8		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2234	02549	02233	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2235	02551	02234	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J03826	97.7	86	1	1745 1830	
2236	02552	02235	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2237	02553	02236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2238	02554	02237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2239	02555	02238	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	X51442	100	86	1	182 269
2240	02556	02239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2241	02557	02240	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2242	02559	02241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X02750	97.6	85	1	1696 1843
2243	02560	02242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2244	02562	02243	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2245	02563	02244	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2246	02564	02245	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2247	02565	02246	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2248	02567	02247	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2249	02568	02248	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2250	02569	02249	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2251	02570	02250	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2252	02571	02251	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2253	02572	02252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2657
																													97.1	70	1	2291	

Table 63

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AI	AK	AM	AC	AS	AL	AW	AY	B	ABC	BE	BF	BG	BH	BI	BK
2254	02573	02253	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2255	02574	02254	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2256	02575	02255	3		0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2257	02576	02256	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2258	02577	02257	3		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2259	02578	02258	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2260	02580	02259	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2261	02581	02260	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2262	02582	02261	5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2263	02583	02262	2		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2264	02585	02263	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2265	02586	02264	5		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2266	02588	02265	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2267	02589	02266	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2268	02590	02267	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2269	02591	02268	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2270	02592	02269	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2271	02593	02270	2		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2272	02612	02271	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2273	02627	02272	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2274	02628	02273	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2275	02629	02274	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2276	02630	02275	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2277	02631	02276	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2278	02632	02277	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2279	02633	02278	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2280	02634	02279	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2281	02635	02280	5		0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2282	02637	02281	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2283	02638	02282	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2284	02639	02283	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2285	02640	02284	9		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2286	02641	02285	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2287	02642	02286	3		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2288	02643	02287	4		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2289	02644	02288	1		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 64

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BGBH	BI	BK
2290	02645	02289	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2291	02646	02290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2292	02648	02291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2293	02650	02292	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2294	02651	02293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2295	02652	02294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2296	02653	02295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2297	02654	02296	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2298	02656	02297	20		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2299	02657	02298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2300	02658	02299	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2301	02659	02300	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2302	02660	02301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2303	02661	02302	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2304	02662	02303	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2305	02663	02304	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2306	02664	02305	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2307	02665	02306	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2308	02666	02307	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2309	02667	02308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2310	02668	02309	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2311	02669	02310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2312	02670	02311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2313	02672	02312	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2314	02673	02313	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2315	02675	02314	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2316	02676	02315	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2317	02677	02316	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2318	02678	02317	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2319	02679	02318	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2320	02680	02319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2321	02681	02320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2322	02682	02321	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2323	02684	02322	13		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2324	02685	02323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2325	02686	02324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 65

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2326	02687	02325		2	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
2327	02688	02326	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2328	02689	02327	4		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2329	02690	02328	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2330	02691	02329	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.6	289	1	2370	2881
2331	02692	02330	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2332	02693	02331	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2333	02694	02332	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2334	02695	02333	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2335	02696	02334	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2336	02697	02335	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2337	02698	02336	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2338	02699	02337	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2339	02700	02338	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2340	02701	02339	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2341	02702	02340	5		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2342	02703	02341	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2343	02704	02342	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2344	02705	02343	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2345	02706	02344	13		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2346	02707	02345	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2347	02708	02346	8		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2348	02709	02347	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2349	02710	02348	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2350	02711	02349	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2351	02712	02350	8		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2352	02713	02351	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2353	02714	02352	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2354	02715	02353	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2355	02716	02354	18		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2356	02717	02355	1		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2357	02718	02356	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2358	02719	02357	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2359	02721	02358	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2360	02722	02359	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
2361	02723	02360	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 66

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2362	02724	02361	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2363	02725	02362	2		0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2364	02727	02363	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2365	02728	02364	6		0	0	0	0	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2366	02729	02365	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2367	02730	02366	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2368	02731	02367	7		0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2369	02732	02368	3		0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2370	02733	02369	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2371	02734	02370	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2372	02735	02371	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2373	02736	02372	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2374	02737	02373	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2375	02738	02374	5		0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2376	02739	02375	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2377	02740	02376	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2378	02741	02377	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2379	02742	02378	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2380	02743	02379	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2381	02744	02380	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2382	02745	02381	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2383	02746	02382	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2384	02747	02383	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2385	02749	02384	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2386	02750	02385	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2387	02751	02386	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2388	02752	02387	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2389	02753	02388	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2390	02754	02389	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2391	02755	02390	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2392	02756	02391	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2393	02758	02392	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2394	02760	02393	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2395	02761	02394	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2396	02762	02395	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2397	02764	02396	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 67

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2398	02765	02397	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2399	02767	02398	9		0	0	0	0	0	0	1	0	1	0	0	1	1	0	1	1	0	0	0	1	2	0	0						
2400	02768	02399	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0						
2401	02769	02400	7		0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0						
2402	02770	02401	3		0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0						
2403	02771	02402	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2404	02772	02403	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
2405	02773	02404	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
2406	02774	02405	3		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2407	02775	02406	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2408	02776	02407	2		0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
2409	02777	02408	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		99.5	200	1	2077	2493
2410	02778	02409	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2411	02779	02410	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2412	02780	02411	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2413	02781	02412	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2414	02782	02413	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2415	02783	02414	5		0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2416	02785	02415	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		96.9	163	1	1230	1391
2417	02786	02416	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2418	02787	02417	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2419	02788	02418	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2420	02789	02419	3		0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2421	02790	02420	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		99	192	1	1219	1560
2422	02791	02421	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0		97.9	192	1	3744	3956
2423	02792	02422	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2424	02793	02423	9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2425	02794	02424	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2426	02795	02425	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2427	02796	02426	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2428	02797	02427	3		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2429	02798	02428	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2430	02799	02429	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2431	02800	02430	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2432	02801	02431	9		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2433	02802	02432	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		98.2	171	1	1230	1410

Table 68

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BGBH	BI	BK
2434	02803	02433	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2435	02804	02434	5		0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2436	02805	02435	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2437	02806	02436	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2438	02807	02437	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2439	02808	02438	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2440	02809	02439	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2441	02810	02440	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2442	02811	02441	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2443	02812	02442	12		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2444	02813	02443	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2445	02814	02444	15		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2446	02815	02445	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2447	02816	02446	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2448	02817	02447	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2449	02818	02448	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2450	02819	02449	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2451	02820	02450	29		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2452	02821	02451	22		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2453	02822	02452	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2454	02823	02453	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2455	02824	02454	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2456	02825	02455	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2457	02826	02456	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2458	02827	02457	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2459	02828	02458	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2460	02829	02459	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2461	02830	02460	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2462	02831	02461	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2463	02832	02462	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2464	02833	02463	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2465	02834	02464	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2466	02835	02465	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2467	02836	02466	3		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2468	02837	02467	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2469	02838	02468	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 69

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
2470	02839	02469	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
2471	02840	02470	3		0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
2472	02843	02471	2		0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
2473	02844	02472	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.6	148	1	495	649	
2474	02845	02473	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2475	02846	02474	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2476	02847	02475	11		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2477	02848	02476	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	145	1	1871	2015	
2478	02849	02477	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2479	02850	02478	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2480	02851	02479	9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2481	02852	02480	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2482	02853	02481	8		0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3	287	1	1158	1444	
2483	02854	02482	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2484	02855	02483	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93	9	264	5	1362	1703
2485	02856	02484	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2486	02857	02485	3		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2487	02858	02486	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2488	02859	02487	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2489	02860	02488	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2490	02861	02489	10		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2491	02862	02490	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2492	02863	02491	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2493	02864	02492	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2494	02865	02493	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2495	02866	02494	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.8	134	1	509	1874	
2496	02867	02495	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2497	02868	02496	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2498	02869	02497	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2499	02870	02498	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2500	02872	02499	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2501	02873	02500	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2502	02874	02501	6		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2503	02875	02502	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2504	02876	02503	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2505	02877	02504	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 70

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
2506	02878	02505	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2507	02879	02506	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2508	02880	02507	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2509	02881	02508	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2510	02882	02509	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2511	02883	02510	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2512	02884	02511	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2513	02885	02512	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2514	02886	02513	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2515	02887	02514	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2516	02888	02515	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2517	02889	02516	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2518	02890	02517	6		0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M95724	97.5	119	1	2991	3132
2519	02891	02518	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2520	02893	02519	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2521	02894	02520	89		0	0	0	0	0	0	87	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2522	02895	02521	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2523	02896	02522	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2524	02897	02523	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2525	02898	02524	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2526	02899	02525	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2527	02900	02526	4		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2528	02901	02527	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X02751	98.3	117	1	333	2436
2529	02902	02528	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2530	02903	02529	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2531	02904	02530	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2532	02905	02531	8		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2533	02906	02532	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2534	02907	02533	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2535	02908	02534	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2536	02909	02535	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2537	02910	02536	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2538	02911	02537	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2539	02912	02538	3		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2540	02913	02539	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2541	02914	02540	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 71

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
2578	02959	02577	9		0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	1	0	0	1	2	0	1	0	0	X02751	93.8	80	6	1	2436
2579	02960	02578	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2580	02962	02579	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2581	02963	02580	2		0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2582	02964	02581	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2583	02965	02582	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2584	02966	02583	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2585	02967	02584	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X62744	100	72	1	1011	1100
2586	02968	02585	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X64002	98.6	71	1	1581	2343
2587	02969	02586	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2588	02970	02587	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2589	02971	02588	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2590	02972	02589	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2591	02973	02590	7		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2592	02974	02591	8		0	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L13799	95.5	67	1	436	500
2593	02975	02592	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	U05291	100	65	1	1828	1892
2594	02976	02593	5		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2595	02978	02594	1		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2596	02980	02595	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2597	02981	02596	13		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M84526	93.8	64	1	894	1071
2598	02982	02597	5		0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2599	02983	02598	5		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2600	02984	02599	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2601	02985	02600	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M31210	100	58	1	2699	2757
2602	02986	02601	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2603	02987	02602	3		0	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2604	02988	02603	6		0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	S57501	96.6	58	1	1336	1400
2605	02989	02604	3		0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X16901	96.2	53	1	1357	1408
2606	02990	02605	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2607	02991	02606	9		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2608	02992	02607	9		0	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2609	02993	02608	3		0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X62585	100	54	1	2506	2563
2610	02994	02609	2		0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X03747	96.2	52	1	2154	2208
2611	02995	02610	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2612	02996	02611	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2613	02997	02612	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J04621	98.1	52	1	2626	3414

Table 73

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
2614	02999	02613	1		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2615	03002	02614	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2616	03005	02615	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2617	03028	02616	2		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2618	03030	02617	3		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2619	03031	02618	3		0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2620	03053	02619	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2621	03055	02620	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2622	03056	02621	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2623	03058	02622	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2624	03059	02623	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2625	03060	02624	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2626	03061	02625	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2627	03062	02626	6		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2628	03063	02627	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2629	03064	02628	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2630	03065	02629	4		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2631	03066	02630	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2632	03067	02631	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2633	03068	02632	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2634	03069	02633	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2635	03070	02634	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2636	03071	02635	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2637	03072	02636	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2638	03073	02637	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2639	03074	02638	44		0	0	0	0	0	0	0	3	0	18	0	0	0	0	0	0	0	0	0	0	0	0						
2640	03075	02639	5		0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0						
2641	03077	02640	5		0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2642	03078	02641	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2643	03079	02642	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2644	03080	02643	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2645	03081	02644	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2646	03082	02645	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2647	03083	02646	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2648	03084	02647	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0								

Table 74

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
2650	03086	02649	5		0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
2651	03087	02650	8		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	545630	99.3	298	1	394	691
2652	03088	02651	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2653	03089	02652	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2654	03090	02653	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
2655	03091	02654	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2656	03092	02655	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2657	03094	02656	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2658	03095	02657	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2659	03096	02658	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2660	03097	02659	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2661	03098	02660	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2662	03099	02661	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2663	03100	02662	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2664	03101	02663	2		0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2665	03102	02664	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2666	03103	02665	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2667	03104	02666	3		0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2668	03105	02667	15		0	0	0	0	0	0	0	2	3	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2669	03106	02668	9		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2670	03108	02669	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2671	03109	02670	13		0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2672	03110	02671	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2673	03111	02672	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2674	03112	02673	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2675	03115	02674	3		0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
2676	03116	02675	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2677	03117	02676	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2678	03118	02677	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2679	03119	02678	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2680	03120	02679	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2681	03121	02680	6		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2682	03122	02681	5		0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2683	03123	02682	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2684	03124	02683	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2685	03125	02684	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 75

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2686	03126	02685	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
2687	03127	02686	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2688	03128	02687	19		0	0	0	0	0	0	0	2	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	X15480	96	224	1	500	725
2689	03129	02688	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2690	03131	02689	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2691	03132	02690	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2692	03133	02691	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2693	03134	02692	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2694	03135	02693	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2695	03136	02694	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2696	03138	02695	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X74295	98.5	205	1	507	719
2697	03139	02696	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2698	03140	02697	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2699	03141	02698	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2700	03142	02699	9		0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	X13839	99.5	210	1	1121	1330
2701	03145	02700	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2702	03146	02701	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2703	03147	02702	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2704	03148	02703	12		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2705	03149	02704	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X51405	99.5	205	1	2216	2443
2706	03150	02705	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2707	03151	02706	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2708	03152	02707	8		0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	Z11793	93.9	197	1	154	2038
2709	03153	02708	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2710	03154	02709	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2711	03155	02710	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2712	03156	02711	15		0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2713	03157	02712	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2714	03159	02713	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2715	03160	02714	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2716	03162	02715	4		0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2717	03163	02716	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2718	03164	02717	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2719	03166	02718	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2720	03167	02719	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2721	03168	02720	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 76

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AC	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2722	03169	02721	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
2723	03170	02722	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
2724	03171	02723	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
2725	03172	02724	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	92.5	174	1	2728	2900
2726	03173	02725	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
2727	03175	02726	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2728	03176	02727	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2729	03177	02728	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2730	03178	02729	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2731	03179	02730	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2732	03180	02731	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2733	03181	02732	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2734	03182	02733	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2735	03183	02734	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2736	03185	02735	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2737	03186	02736	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2738	03187	02737	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2739	03188	02738	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2740	03189	02739	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2741	03190	02740	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2742	03192	02741	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2743	03193	02742	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2744	03194	02743	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2745	03195	02744	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2746	03196	02745	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2747	03197	02746	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2748	03198	02747	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2749	03200	02748	52		0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2750	03201	02749	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2751	03202	02750	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2752	03204	02751	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2753	03205	02752	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2754	03206	02753	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2755	03207	02754	9		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2756	03208	02755	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2757	03212	02756	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 77

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
2758	03213	02757	3		0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0					
2759	03214	02758	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2760	03215	02759	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2761	03216	02760	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.3	406	1	3055	3634
2762	03217	02761	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2763	03218	02762	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2764	03219	02763	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2765	03220	02764	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2766	03221	02765	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2767	03222	02766	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2768	03223	02767	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2769	03224	02768	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2770	03225	02769	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2771	03227	02770	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2772	03229	02771	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2773	03230	02772	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2774	03231	02773	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2775	03233	02774	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2776	03234	02775	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2777	03235	02776	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2778	03236	02777	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2779	03237	02778	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2780	03239	02779	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2781	03240	02780	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2782	03241	02781	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2783	03242	02782	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2784	03243	02783	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2785	03244	02784	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2786	03245	02785	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2787	03247	02786	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2788	03248	02787	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2789	03249	02788	6		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2790	03251	02789	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2791	03252	02790	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2792	03253	02791	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2793	03255	02792	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 78

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BE	BF	BG	BH	BI	BK
2794	03257	02793	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2795	03258	02794	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2796	03259	02795	10		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.9	98	1	1010	1115	
2797	03261	02796	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2798	03263	02797	5		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.8	94	1	3055	3549	
2799	03264	02798	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.9	96	1	1840	1942	
2800	03267	02799	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2801	03268	02800	5		0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2802	03271	02801	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2803	03274	02802	7		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2804	03279	02803	8		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2805	03281	02804	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	93	1	720	1071	
2806	03282	02805	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2807	03283	02806	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2808	03284	02807	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2809	03286	02808	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2810	03289	02809	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2811	03294	02810	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	71	1	432	502	
2812	03296	02811	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2813	03297	02812	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2814	03299	02813	1		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2815	03300	02814	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.7	60	1	549	608	
2816	03304	02815	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2817	03305	02816	15		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.7	57	1	1224	1279	
2818	03306	02817	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2819	03307	02818	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2820	03308	02819	2		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2821	03310	02820	7		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2822	03311	02821	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2823	03312	02822	4		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2824	03313	02823	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2825	03315	02824	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2826	03318	02825	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2827	03319	02826	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2828	03324	02827	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2829	03325	02828	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 79

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
2830	03326	02829	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2831	03331	02830	24		0	0	0	0	0	0	0	1	1	10	1	0	0	0	0	0	0	0	0	0	0	0	0						
2832	03332	02831	6		0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2833	03356	02832	2		0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	100.128	1	3228	3355	
2834	03374	02833	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.5	429	1	889	
2835	03375	02834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2836	03376	02835	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2837	03377	02836	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2838	03378	02837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2839	03379	02838	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2840	03380	02839	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.394	1	1021	1537	
2841	03381	02840	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.1	386	1	1063	
2842	03382	02841	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2843	03383	02842	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2844	03384	02843	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2845	03385	02844	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2846	03386	02845	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2847	03387	02846	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2848	03388	02847	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2849	03389	02848	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2850	03390	02849	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2851	03391	02850	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2	325	1	1295	
2852	03392	02851	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2853	03393	02852	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2854	03394	02853	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.2	339	1	704	
2855	03395	02854	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2856	03396	02855	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2857	03397	02856	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2858	03398	02857	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2859	03399	02858	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2860	03400	02859	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2861	03401	02860	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2862	03402	02861	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.2	394	1	1556	
2863	03403	02862	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2864	03404	02863	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2865	03405	02864	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.4	328	1	1237	
																																1560	

Table 80

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AI	AK	AM	AC	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2866	03406	02865	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2867	03407	02866	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2868	03408	02867	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2869	03409	02868	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2870	03410	02869	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2871	03411	02870	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2872	03412	02871	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2873	03413	02872	3		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X66397	97.2	323	1	7170	7496
2874	03414	02873	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2875	03415	02874	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2876	03416	02875	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2877	03417	02876	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2878	03418	02877	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2879	03419	02878	7		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	D13666	96.1	306	1	2485	3213
2880	03420	02879	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2881	03421	02880	4		0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2882	03422	02881	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2883	03423	02882	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2884	03424	02883	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M29536	97.1	373	1	970	1416
2885	03426	02884	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2886	03427	02885	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2887	03428	02886	3		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2888	03429	02887	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2889	03430	02888	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2890	03431	02889	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2891	03432	02890	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2892	03433	02891	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2893	03434	02892	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2894	03435	02893	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2895	03436	02894	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2896	03437	02895	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2897	03438	02896	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2898	03439	02897	6		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X14958	95	282	1	1596	1875
2899	03440	02898	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2900	03441	02899	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M86667	97.6	83	1	1085	1560
2901	03442	02900	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 81

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
2902	03443	02901	14		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	3	4	1	0	0	0	0	0					
2903	03444	02902	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2904	03445	02903	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2905	03446	02904	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2906	03447	02905	5		0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	1	0	0	0	054769	96.2	264	1	161	429
2907	03448	02906	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2908	03449	02907	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2909	03450	02908	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2910	03451	02909	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2911	03452	02910	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2912	03453	02911	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2913	03454	02912	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2914	03455	02913	5		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2915	03456	02914	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2916	03457	02915	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2917	03458	02916	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2918	03459	02917	7		0	0	0	0	0	0	0	0	2	4	0	0	0	0	0	0	0	0	0	0	0	0	098479	95.1	247	1	1311	1557
2919	03460	02918	8		0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2920	03461	02919	5		0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2921	03462	02920	1		0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2922	03463	02921	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2923	03464	02922	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2924	03465	02923	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2925	03466	02924	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2926	03467	02925	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2927	03468	02926	5		0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2928	03469	02927	4		0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
2929	03470	02928	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2930	03471	02929	6		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2931	03472	02930	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2932	03473	02931	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2933	03474	02932	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2934	03476	02933	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2935	03477	02934	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2936	03478	02935	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
2937	03479	02936	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 82

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
2938	03480	02937	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
2939	03481	02938	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
2940	03482	02939	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
2941	03483	02940	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2942	03484	02941	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2943	03485	02942	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	M29063	98.6	212	1	1175	1398	
2944	03486	02943	7		0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2945	03487	02944	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2946	03488	02945	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2947	03489	02946	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2948	03490	02947	3		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2949	03491	02948	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2950	03492	02949	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2951	03493	02950	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2952	03494	02951	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2953	03495	02952	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2954	03496	02953	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2955	03497	02954	3		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	M34671	100	191	1	917	1671	
2956	03498	02955	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2957	03499	02956	5		0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
2958	03500	02957	4		0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2959	03501	02958	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2960	03502	02959	6		0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
2961	03503	02960	4		0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	L25081	96.6	175	1	887	1058	
2962	03504	02961	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2963	03505	02962	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2964	03506	02963	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2965	03507	02964	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2966	03508	02965	3		0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2967	03509	02966	3		0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
2968	03510	02967	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2969	03511	02968	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2970	03512	02969	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2971	03513	02970	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2972	03514	02971	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
2973	03515	02972	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 83

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
2974	03516	02973	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0					
2975	03517	02974	10	0	0	0	0	0	0	0	0	0	4	4	0	0	0	0	0	0	0	0	0	0	0	0					
2976	03518	02975	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	100	96	1	1335	
2977	03519	02976	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	M95929			1433	
2978	03520	02977	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2979	03521	02978	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2980	03522	02979	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	97.6	166	1	2428	
2981	03523	02980	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	S60099			3727	
2982	03524	02981	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2983	03525	02982	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2984	03526	02983	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2985	03527	02984	4	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2986	03528	02985	4	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2987	03529	02986	6	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2988	03530	02987	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2989	03531	02988	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2990	03532	02989	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2991	03533	02990	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2992	03534	02991	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2993	03535	02992	9	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0					
2994	03536	02993	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2995	03537	02994	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2996	03538	02995	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2997	03539	02996	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2998	03540	02997	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
2999	03541	02998	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3000	03542	02999	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3001	03543	03000	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3002	03544	03001	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3003	03545	03002	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3004	03546	03003	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3005	03547	03004	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3006	03548	03005	4	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3007	03549	03006	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3008	03550	03007	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3009	03551	03008	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 84

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3010	03552	03009	4		0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	0							
3011	03553	03010	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0							
3012	03554	03011	5		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	4	0							
3013	03555	03012	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3014	03556	03013	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3015	03557	03014	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3016	03558	03015	5		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1							
3017	03559	03016	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3018	03560	03017	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3019	03561	03018	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3020	03562	03019	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3021	03563	03020	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3022	03564	03021	11		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3023	03565	03022	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3024	03566	03023	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3025	03567	03024	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3026	03568	03025	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3027	03569	03026	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3028	03570	03027	4		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3029	03571	03028	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3030	03572	03029	3		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0							
3031	03573	03030	9		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3032	03574	03031	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3033	03575	03032	17		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3034	03576	03033	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3035	03577	03034	5		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3036	03578	03035	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3037	03579	03036	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3038	03580	03037	3		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0							
3039	03581	03038	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3040	03582	03039	6		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3041	03583	03040	4		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0							
3042	03584	03041	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3043	03585	03042	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3044	03586	03043	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3045	03587	03044	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 85

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BGBH	BI	BK		
3046	03588	03045	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3047	03589	03046	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3048	03590	03047	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3049	03591	03048	9		0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	2	0	0	0	0	0	1	0	L06328	97.8 179	1	1061	1404		
3050	03592	03049	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X59543	97.1 238	1	2559	3075		
3051	03593	03050	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3052	03594	03051	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3053	03595	03052	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3054	03596	03053	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M77693	100 159	1	639	1060	
3055	03597	03054	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3056	03598	03055	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3057	03599	03056	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3058	03600	03057	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	K03199	98.3 58	52	8	1760	
3059	03602	03058	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3060	03603	03059	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3061	03604	03060	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3062	03605	03061	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3063	03606	03062	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3064	03607	03063	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3065	03608	03064	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3066	03609	03065	4		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3067	03610	03066	3		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M12783	93.4 182	1	3284	3798	
3068	03611	03067	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3069	03612	03068	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3070	03613	03069	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3071	03614	03070	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3072	03615	03071	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3073	03616	03072	4		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3074	03617	03073	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3075	03618	03074	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3076	03619	03075	3		0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3077	03620	03076	1		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3078	03621	03077	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3079	03622	03078	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3080	03623	03079	5		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M11718	95 238	1	920	1317
3081	03624	03080	2		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				

Table 86

Table 87

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3118	03683	03117	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3119	03684	03118	2		0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0							
3120	03685	03119	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3121	03686	03120	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3122	03688	03121	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3123	03689	03122	5		0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0							
3124	03690	03123	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0							
3125	03691	03124	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0							
3126	03693	03125	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3127	03694	03126	10		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3128	03695	03127	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3129	03696	03128	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3130	03697	03129	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3131	03698	03130	13		0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0							
3132	03699	03131	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3133	03701	03132	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3134	03702	03133	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3135	03703	03134	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3136	03704	03135	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0							
3137	03705	03136	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3138	03707	03137	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3139	03708	03138	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0							
3140	03709	03139	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3141	03710	03140	4		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0							
3142	03711	03141	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3143	03712	03142	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3144	03713	03143	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3145	03714	03144	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0							
3146	03715	03145	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3147	03716	03146	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3148	03717	03147	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0							
3149	03718	03148	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3150	03719	03149	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3151	03720	03150	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3152	03721	03151	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							
3153	03722	03152	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0							

Table 88

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3154	03723	03153	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0						
3155	03724	03154	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3156	03725	03155	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3157	03726	03156	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1						
3158	03727	03157	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3159	03728	03158	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3160	03729	03159	3		0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0						
3161	03730	03160	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3162	03731	03161	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3163	03732	03162	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3164	03733	03163	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3165	03734	03164	7		0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0						
3166	03736	03165	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3167	03737	03166	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3168	03738	03167	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3169	03739	03168	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3170	03740	03169	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3171	03741	03170	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3172	03742	03171	3		0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0						
3173	03743	03172	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3174	03744	03173	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3175	03745	03174	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3176	03746	03175	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3177	03747	03176	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3178	03748	03177	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3179	03749	03178	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3180	03750	03179	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3181	03751	03180	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3182	03752	03181	8		0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0						
3183	03753	03182	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3184	03754	03183	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3185	03755	03184	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3186	03756	03185	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3187	03757	03186	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3188	03758	03187	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3189	03759	03188	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 89

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
3190	03760	03189	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3191	03761	03190	4		0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0						
3192	03762	03191	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3193	03763	03192	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3194	03764	03193	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3195	03765	03194	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	070904	92.4	276	1	1063	1405
3196	03766	03195	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3197	03767	03196	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3198	03768	03197	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3199	03769	03198	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3200	03770	03199	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3201	03771	03200	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3202	03772	03201	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3203	03773	03202	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3204	03774	03203	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3205	03775	03204	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3206	03776	03205	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3207	03777	03206	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3208	03778	03207	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3209	03779	03208	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3210	03780	03209	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3211	03781	03210	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3212	03782	03211	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3213	03783	03212	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3214	03784	03213	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3215	03785	03214	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3216	03786	03215	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3217	03787	03216	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3218	03788	03217	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3219	03789	03218	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3220	03790	03219	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3221	03791	03220	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3222	03792	03221	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3223	03793	03222	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3224	03794	03223	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3225	03795	03224	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						

Table 90

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3226	03796	03225	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3227	03797	03226	2		0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0						
3228	03798	03227	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3229	03799	03228	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3230	03800	03229	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3231	03801	03230	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0						
3232	03802	03231	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	013639	100 224	1	6255	6478	
3233	03803	03232	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3234	03804	03233	7		0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0						
3235	03805	03234	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3236	03806	03235	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3237	03807	03236	1		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3238	03808	03237	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3239	03809	03238	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3240	03810	03239	1		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3241	03811	03240	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3242	03812	03241	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3243	03813	03242	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	L16896	96.2 213	1	2003	2288	
3244	03814	03243	6		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	M63959	96.2 209	1	1286	1493	
3245	03815	03244	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	M17219	99 208	1	1105	1344	
3246	03816	03245	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3247	03817	03246	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3248	03818	03247	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3249	03819	03248	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	L08240	99.5 201	1	1992	2198	
3250	03820	03249	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	M25785	98.1 209	1	70	874	
3251	03821	03250	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3252	03822	03251	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3253	03823	03252	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3254	03824	03253	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3255	03825	03254	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3256	03826	03255	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3257	03827	03256	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3258	03828	03257	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3259	03829	03258	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3260	03830	03259	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3261	03831	03260	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 91

Table 92

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3298	03870	03297	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3299	03871	03298	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0						
3300	03872	03299	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3301	03873	03300	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3302	03874	03301	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3303	03875	03302	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3304	03876	03303	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3305	03877	03304	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0						
3306	03878	03305	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3307	03879	03306	7		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3308	03880	03307	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3309	03881	03308	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3310	03882	03309	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3311	03883	03310	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3312	03884	03311	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3313	03885	03312	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3314	03886	03313	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3315	03887	03314	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3316	03888	03315	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3317	03889	03316	4		0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0						
3318	03890	03317	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3319	03891	03318	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3320	03892	03319	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3321	03893	03320	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3322	03894	03321	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3323	03895	03322	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3324	03896	03323	7		0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0						
3325	03897	03324	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3326	03898	03325	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3327	03899	03326	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3328	03900	03327	2		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						
3329	03901	03328	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3330	03902	03329	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3331	03903	03330	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3332	03904	03331	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0						
3333	03905	03332	5		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 93

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
3334	03906	03333	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	100	116	1	9804	9940
3335	03907	03334	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	100	116	1	9804	9940
3336	03908	03335	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	100	116	1	9804	9940
3337	03909	03336	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3338	03910	03337	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3339	03911	03338	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3340	03912	03339	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3341	03913	03340	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3342	03914	03341	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3343	03915	03342	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3344	03916	03343	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3345	03917	03344	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3346	03918	03345	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3347	03919	03346	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3348	03920	03347	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3349	03921	03348	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3350	03922	03349	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3351	03923	03350	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3352	03924	03351	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3353	03925	03352	4		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3354	03926	03353	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3355	03927	03354	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3356	03928	03355	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3357	03929	03356	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3358	03930	03357	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3359	03931	03358	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3360	03932	03359	5		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3361	03933	03360	3		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3362	03934	03361	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3363	03935	03362	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3364	03936	03363	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3365	03937	03364	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3366	03938	03365	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3367	03939	03366	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3368	03940	03367	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435
3369	03941	03368	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	94.5	273	1	2088	2435

Table 94

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
3370	03942	03369	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3371	03943	03370	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3372	03944	03371	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3373	03945	03372	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3374	03946	03373	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
3375	03947	03374	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3376	03948	03375	3		0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0							
3377	03949	03376	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0							
3378	03951	03377	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0							
3379	03952	03378	2		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0							
3380	03954	03379	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3381	03955	03380	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3382	03956	03381	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3383	03958	03382	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3384	03959	03383	2		0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3385	03960	03384	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3386	03961	03385	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3387	03962	03386	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3388	03963	03387	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M76729	92.9	84	1	6245	7138	
3389	03964	03388	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0							
3390	03965	03389	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3391	03966	03390	15		0	0	0	0	0	0	0	0	1	0	0	0	0	0	9	0	0	5	0	0	0	0	0	M55618	95.5	88	1	7295	7390	
3392	03967	03391	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	L13210	100	73	1	2185	2257	
3393	03968	03392	3		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
3394	03969	03393	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3395	03971	03394	8		0	0	0	0	0	0	0	0	3	0	0	0	0	0	1	0	0	0	2	0	0	0	0	D25274	95.7	69	1	1168	1279	
3396	03972	03395	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3397	03973	03396	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3398	03974	03397	5		0	0	0	0	0	0	0	0	1	1	2	0	0	0	0	0	0	0	1	0	0	0	0							
3399	03975	03398	2		0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3400	03976	03399	5		0	0	0	0	0	0	0	0	3	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3401	03977	03400	2		0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
3402	03978	03401	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3403	03979	03402	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
3404	03980	03403	8		0	0	0	0	0	0	0	0	3	0	0	0	0	0	1	0	0	0	1	0	0	0	0	X52947	100	58	1	2981	3038	
3405	03981	03404	1		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 95

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AU	AW	AY	B	BC	BE	BF	BGBH	BI	BK
3406	03982	03405	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3407	03984	03406	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3408	03985	03407	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3409	03986	03408	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3410	03987	03409	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3411	03988	03410	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3412	03989	03411	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3413	03993	03412	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3414	04020	03413	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3415	04021	03414	4		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3416	04022	03415	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3417	04023	03416	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3418	04024	03417	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3419	04025	03418	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3420	04026	03419	9		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3421	04028	03420	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3422	04029	03421	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3423	04030	03422	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3424	04031	03423	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3425	04032	03424	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3426	04033	03425	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3427	04034	03426	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3428	04035	03427	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3429	04036	03428	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3430	04037	03429	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3431	04039	03430	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3432	04040	03431	4		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3433	04041	03432	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3434	04042	03433	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3435	04044	03434	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3436	04045	03435	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3437	04046	03436	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3438	04047	03437	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3439	04048	03438	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3440	04049	03439	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					
3441	04050	03440	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 96

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3442	04051	03441	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0						
3443	04052	03442	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3444	04053	03443	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
3445	04054	03444	9		0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	3	0	0	0	0						
3446	04055	03445	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3447	04056	03446	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3448	04057	03447	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3449	04058	03448	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M10051	100	154	1	2017	4723
3450	04059	03449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3451	04060	03450	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3452	04061	03451	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3453	04062	03452	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M88458	94.2	325	1	536	1180
3454	04063	03453	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3455	04064	03454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3456	04065	03455	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3457	04066	03456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3458	04067	03457	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3459	04068	03458	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3460	04069	03459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3461	04070	03460	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M15042	94.3	317	1	2560	2929
3462	04071	03461	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3463	04072	03462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3464	04073	03463	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3465	04074	03464	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3466	04075	03465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3467	04076	03466	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3468	04077	03467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3469	04078	03468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3470	04079	03469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3471	04080	03470	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3472	04081	03471	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3473	04082	03472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3474	04083	03473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3475	04084	03474	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3476	04086	03475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
3477	04087	03476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 97

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
3478	04088	03477	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	95.6	271	1	2937	3554
3479	04089	03478	2		0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	96.7	270	1	3174	4108
3480	04090	03479	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	99.6	264	1	594	870
3481	04091	03480	2		0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	99.2	260	1	221	480
3482	04092	03481	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	98.8	250	1	836	1104
3483	04093	03482	2		0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0					
3484	04094	03483	13		0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0	0	0					
3485	04095	03484	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3486	04096	03485	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3487	04097	03486	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3488	04098	03487	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3489	04099	03488	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3490	04100	03489	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3491	04101	03490	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3492	04102	03491	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3493	04103	03492	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3494	04104	03493	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3495	04105	03494	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3496	04106	03495	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3497	04107	03496	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3498	04108	03497	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3499	04109	03498	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3500	04110	03499	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3501	04111	03500	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3502	04112	03501	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3503	04113	03502	4		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3504	04114	03503	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3505	04115	03504	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3506	04116	03505	12		0	0	0	0	0	0	0	0	0	0	10	0	0	0	0	0	0	0	0	0	0	0	0					
3507	04117	03506	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3508	04118	03507	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3509	04119	03508	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3510	04120	03509	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
3511	04121	03510	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3512	04122	03511	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
3513	04123	03512	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BGBH	BI	BK
3514	04125	03513	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3515	04126	03514	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3516	04127	03515	4		0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0					
3517	04128	03516	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3518	04129	03517	4		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3519	04130	03518	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3520	04131	03519	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	D14705	97.4 190	1 2545	3433	
3521	04132	03520	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	M75099	97.3 186	1 377	562	
3522	04133	03521	7		0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	2	0	0	0	0	0	0					
3523	04134	03522	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3524	04135	03523	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3525	04136	03524	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3526	04137	03525	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	H34079	96.4 168	1 1172	1341	
3527	04139	03526	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0					
3528	04140	03527	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3529	04141	03528	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3530	04142	03529	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3531	04143	03530	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3532	04144	03531	11		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0					
3533	04145	03532	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3534	04146	03533	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3535	04147	03534	6		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3536	04148	03535	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3537	04149	03536	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0					
3538	04150	03537	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3539	04151	03538	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3540	04152	03539	4		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3541	04153	03540	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3542	04154	03541	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3543	04155	03542	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3544	04156	03543	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3545	04157	03544	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3546	04158	03545	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3547	04159	03546	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3548	04160	03547	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3549	04161	03548	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3550	04162	03549	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3551	04163	03550	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3552	04164	03551	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3553	04165	03552	6		0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	1	0	0	0	0	0	0	0	0					
3554	04166	03553	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	96.1	127	1	990	1116
3555	04167	03554	5		0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	96.2	132	1	533	1452
3556	04169	03555	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3557	04170	03556	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3558	04171	03557	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3559	04172	03558	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3560	04173	03559	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3561	04174	03560	4		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0						
3562	04175	03561	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3563	04176	03562	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3564	04177	03563	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3565	04179	03564	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3566	04180	03565	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3567	04181	03566	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3568	04182	03567	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3569	04183	03568	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3570	04184	03569	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3571	04186	03570	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0						
3572	04187	03571	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3573	04188	03572	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3574	04189	03573	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3575	04190	03574	10		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	2	0	0	0	0	0						
3576	04191	03575	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0						
3577	04192	03576	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3578	04193	03577	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3579	04194	03578	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3580	04195	03579	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3581	04196	03580	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3582	04197	03581	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3583	04198	03582	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3584	04199	03583	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3585	04200	03584	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						

Table 100

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
3586	04201	03585	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0						
3587	04202	03586	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3588	04203	03587	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0						
3589	04204	03588	2		0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	92.8	152	1	612	1277
3590	04205	03589	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0					
3591	04206	03590	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3592	04207	03591	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3593	04210	03592	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3594	04211	03593	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3595	04213	03594	2		0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0						
3596	04214	03595	3		0	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0						
3597	04215	03596	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3598	04216	03597	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3599	04218	03598	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3600	04219	03599	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3601	04220	03600	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3602	04247	03601	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3603	04248	03602	1		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0		95.7	328	1	767	1154
3604	04249	03603	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3605	04250	03604	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3606	04252	03605	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3607	04253	03606	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3608	04256	03607	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3609	04257	03608	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3610	04258	03609	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3611	04259	03610	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3612	04261	03611	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3613	04264	03612	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3614	04265	03613	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3615	04266	03614	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3616	04267	03615	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3617	04268	03616	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3618	04269	03617	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
3619	04270	03618	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3620	04271	03619	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
3621	04272	03620	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						

Table 101

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3622	04273	03621	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3623	04274	03622	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3624	04275	03623	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0						
3625	04276	03624	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3626	04277	03625	4		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3627	04279	03626	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3628	04280	03627	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3629	04281	03628	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3630	04282	03629	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3631	04284	03630	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3632	04285	03631	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3633	04286	03632	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3634	04287	03633	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3635	04288	03634	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3636	04289	03635	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3637	04290	03636	8		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3638	04291	03637	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3639	04292	03638	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3640	04293	03639	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3641	04294	03640	6		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3642	04295	03641	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3643	04296	03642	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3644	04297	03643	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3645	04298	03644	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3646	04299	03645	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3647	04300	03646	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3648	04302	03647	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3649	04303	03648	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3650	04304	03649	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3651	04305	03650	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3652	04306	03651	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3653	04307	03652	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3654	04308	03653	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3655	04309	03654	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3656	04310	03655	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3657	04311	03656	3		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3658	04312	03657	3		0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0						
3659	04313	03658	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3660	04314	03659	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3661	04315	03660	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3662	04316	03661	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3663	04317	03662	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3664	04318	03663	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3665	04319	03664	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3666	04320	03665	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3667	04321	03666	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3668	04322	03667	12		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3669	04323	03668	1		0	0	0	0	0	0	0	0	0	0	0	3	1	1	1	1	0	0	0	0	0	0	0						
3670	04324	03669	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3671	04325	03670	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3672	04326	03671	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3673	04327	03672	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3674	04328	03673	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3675	04329	03674	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3676	04330	03675	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3677	04331	03676	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3678	04332	03677	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3679	04333	03678	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3680	04334	03679	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3681	04335	03680	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3682	04336	03681	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3683	04337	03682	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3684	04339	03683	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3685	04340	03684	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3686	04341	03685	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3687	04342	03686	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3688	04343	03687	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3689	04344	03688	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3690	04345	03689	8		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3691	04346	03690	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
3692	04347	03691	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
3693	04348	03692	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BAB	BC	BE	BF	BG	BH	BI	BK
3694	04349	03693	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3695	04351	03694	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3696	04352	03695	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3697	04353	03696	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3698	04354	03697	4		0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	98.2	217	1	2394	2610	
3699	04355	03698	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3700	04356	03699	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3701	04357	03700	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3702	04358	03701	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3703	04359	03702	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3704	04360	03703	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3705	04361	03704	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3706	04362	03705	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3707	04363	03706	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	96.9	224	1	575	797
3708	04364	03707	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3709	04365	03708	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3710	04366	03709	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3711	04368	03710	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3712	04369	03711	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3713	04370	03712	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3714	04371	03713	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3715	04372	03714	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3716	04373	03715	3		0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0						
3717	04374	03716	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3718	04375	03717	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0					
3719	04377	03718	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3720	04378	03719	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3721	04379	03720	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3722	04380	03721	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3723	04381	03722	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3724	04382	03723	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3725	04383	03724	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3726	04384	03725	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3727	04385	03726	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3728	04386	03727	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3729	04387	03728	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						

Table 104

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
3730	04388	03729	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3731	04389	03730	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3732	04390	03731	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3733	04391	03732	3		0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0					
3734	04392	03733	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3735	04393	03734	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
3736	04394	03735	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3737	04395	03736	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3738	04396	03737	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3739	04397	03738	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3740	04398	03739	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3741	04399	03740	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3742	04400	03741	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3743	04401	03742	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3744	04402	03743	7		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3745	04403	03744	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3746	04404	03745	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3747	04405	03746	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3748	04406	03747	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3749	04407	03748	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3750	04408	03749	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3751	04409	03750	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3752	04410	03751	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3753	04411	03752	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3754	04412	03753	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3755	04414	03754	5		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3756	04415	03755	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3757	04416	03756	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3758	04417	03757	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3759	04418	03758	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
3760	04419	03759	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3761	04420	03760	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3762	04421	03761	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3763	04422	03762	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3764	04423	03763	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
3765	04424	03764	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					

Table 105

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3766	04425	03765	5		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3767	04426	03766	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3768	04427	03767	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3769	04428	03768	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3770	04429	03769	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3771	04430	03770	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3772	04431	03771	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3773	04432	03772	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3774	04433	03773	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3775	04434	03774	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3776	04435	03775	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3777	04436	03776	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3778	04437	03777	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3779	04439	03778	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3780	04440	03779	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3781	04441	03780	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3782	04442	03781	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3783	04443	03782	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3784	04445	03783	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3785	04446	03784	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3786	04447	03785	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3787	04448	03786	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3788	04449	03787	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3789	04450	03788	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3790	04452	03789	3		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3791	04453	03790	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3792	04454	03791	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3793	04455	03792	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3794	04456	03793	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3795	04457	03794	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3796	04460	03795	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3797	04462	03796	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3798	04463	03797	3		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0						
3799	04464	03798	8		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3800	04465	03799	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						
3801	04466	03800	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0						

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3802	04467	03801	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3803	04468	03802	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3804	04469	03803	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3805	04470	03804	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3806	04471	03805	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3807	04472	03806	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3808	04473	03807	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3809	04474	03808	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3810	04476	03809	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3811	04478	03810	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3812	04482	03811	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3813	04483	03812	6		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3814	04484	03813	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3815	04485	03814	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3816	04486	03815	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3817	04487	03816	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3818	04488	03817	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3819	04489	03818	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3820	04491	03819	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3821	04492	03820	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3822	04493	03821	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3823	04494	03822	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3824	04495	03823	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3825	04496	03824	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3826	04497	03825	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3827	04498	03826	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3828	04499	03827	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3829	04500	03828	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3830	04501	03829	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3831	04502	03830	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3832	04503	03831	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3833	04504	03832	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3834	04506	03833	5		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3835	04507	03834	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3836	04509	03835	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
3837	04510	03836	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 107

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
3838	04511	03837	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0					
3839	04512	03838	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3840	04513	03839	2		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3841	04514	03840	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2					
3842	04515	03841	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3843	04516	03842	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3844	04517	03843	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3845	04518	03844	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3846	04519	03845	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3847	04520	03846	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3848	04521	03847	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3849	04522	03848	1		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0					
3850	04523	03849	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3851	04525	03850	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3852	04527	03851	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3853	04528	03852	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3854	04529	03853	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3855	04530	03854	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3856	04531	03855	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3857	04532	03856	3		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3858	04533	03857	4		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3859	04534	03858	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3860	04535	03859	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3861	04536	03860	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3862	04537	03861	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3863	04538	03862	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3864	04539	03863	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3865	04541	03864	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3866	04542	03865	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3867	04543	03866	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3868	04546	03867	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3869	04547	03868	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3870	04548	03869	2		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3871	04552	03870	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3872	04556	03871	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					
3873	04557	03872	1		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0					

Table 108

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
3874	04597	03873	3		0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0						
3875	04598	03874	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0						
3876	04599	03875	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3877	04600	03876	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3878	04601	03877	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3879	04602	03878	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2	0						
3880	04603	03879	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3881	04604	03880	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3882	04605	03881	2		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3883	04606	03882	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3884	04607	03883	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0						
3885	04608	03884	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3886	04609	03885	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3887	04610	03886	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0						
3888	04611	03887	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0						
3889	04612	03888	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3890	04613	03889	3		0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0						
3891	04614	03890	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3892	04615	03891	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3893	04616	03892	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0						
3894	04617	03893	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3895	04618	03894	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3896	04619	03895	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3897	04620	03896	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3898	04621	03897	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3899	04623	03898	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3900	04624	03899	6		0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0						
3901	04625	03900	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3902	04626	03901	4		0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0						
3903	04627	03902	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0						
3904	04628	03903	3		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0						
3905	04629	03904	3		0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0						
3906	04630	03905	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3907	04631	03906	1		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3908	04632	03907	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0						
3909	04633	03908	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0						

Table 109

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AN	AS	AW	AY	BA	BC	BE	BF	BGBH	BI	BK		
3910	04634	03909	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0						
3911	04635	03910	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3912	04636	03911	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3913	04637	03912	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	562027	96.1	232	1	159	408
3914	04638	03913	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3915	04639	03914	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3916	04640	03915	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3917	04641	03916	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3918	04642	03917	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0						
3919	04643	03918	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3920	04644	03919	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3921	04645	03920	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3922	04646	03921	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3923	04647	03922	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3924	04648	03923	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3925	04649	03924	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3926	04650	03925	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3927	04651	03926	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3928	04652	03927	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3929	04653	03928	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3930	04654	03929	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3931	04655	03930	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	M22349	97.9	285	1	1990	2273
3932	04656	03931	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3933	04657	03932	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3934	04658	03933	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3935	04659	03934	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3936	04660	03935	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3937	04661	03936	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3938	04662	03937	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3939	04663	03938	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3940	04664	03939	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3941	04665	03940	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3942	04666	03941	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3943	04667	03942	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
3944	04668	03943	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
3945	04669	03944	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	L13738	92.6	269	1	4278	4545

Table 110

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
3946	04670	03945	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3947	04671	03946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3948	04672	03947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3949	04673	03948	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3950	04674	03949	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
3951	04675	03950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3952	04676	03951	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3953	04677	03952	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3954	04678	03953	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3955	04679	03954	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
3956	04680	03955	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3957	04681	03956	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3958	04682	03957	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3959	04683	03958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3960	04684	03959	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3961	04685	03960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3962	04686	03961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3963	04687	03962	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3964	04688	03963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3965	04689	03964	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
3966	04690	03965	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3967	04691	03966	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3968	04692	03967	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3969	04693	03968	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3970	04694	03969	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3971	04695	03970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3972	04696	03971	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3973	04697	03972	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3974	04698	03973	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3975	04699	03974	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3976	04700	03975	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3977	04701	03976	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3978	04702	03977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3979	04703	03978	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
3980	04704	03979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
3981	04705	03980	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						

Table 111

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK		
3982	04706	03981	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	X15088	94	3	230	1	1045	1292
3983	04707	03982	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3984	04708	03983	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3985	04709	03984	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0							
3986	04710	03985	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3987	04711	03986	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0							
3988	04712	03987	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3989	04713	03988	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3990	04714	03989	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0							
3991	04715	03990	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	1	0	0	0	0	0	0							
3992	04716	03991	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3993	04717	03992	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0							
3994	04718	03993	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0							
3995	04719	03994	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3996	04720	03995	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3997	04721	03996	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0							
3998	04722	03997	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
3999	04723	03998	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4000	04724	03999	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0							
4001	04725	04000	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4002	04728	04001	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4003	04729	04002	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4004	04730	04003	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4005	04732	04004	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4006	04733	04005	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4007	04734	04006	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4008	04735	04007	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	J02966	99	5	204	1	1057	1320
4009	04736	04008	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4010	04737	04009	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0							
4011	04738	04010	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4012	04739	04011	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4013	04740	04012	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4014	04741	04013	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4015	04742	04014	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4016	04743	04015	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	S42457	98	198	1	2483	2857	
4017	04744	04016	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							

Table 112

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BGBH	BI	BK
4018	04745	04017	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4019	04746	04018	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4020	04747	04019	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4021	04748	04020	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4022	04750	04021	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4023	04751	04022	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4024	04752	04023	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4025	04753	04024	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4026	04754	04025	8		0	0	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0					
4027	04755	04026	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4028	04756	04027	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4029	04757	04028	5		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4030	04758	04029	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4031	04759	04030	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4032	04760	04031	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4033	04761	04032	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4034	04762	04033	6		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4035	04763	04034	4		0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0					
4036	04764	04035	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4037	04765	04036	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4038	04766	04037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4039	04767	04038	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4040	04768	04039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4041	04769	04040	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4042	04770	04041	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4043	04771	04042	1		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4044	04772	04043	4		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0					
4045	04773	04044	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4046	04774	04045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4047	04775	04046	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4048	04776	04047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4049	04777	04048	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4050	04778	04049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4051	04779	04050	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4052	04780	04051	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4053	04781	04052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					

Table 113

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4090	04819	04089	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4091	04820	04090	3		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0						
4092	04821	04091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4093	04822	04092	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0						
4094	04823	04093	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0						
4095	04824	04094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4096	04826	04095	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4097	04827	04096	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4098	04828	04097	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4099	04829	04098	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4100	04830	04099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4101	04831	04100	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4102	04832	04101	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4103	04833	04102	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4104	04834	04103	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4105	04835	04104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4106	04836	04105	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4107	04837	04106	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4108	04838	04107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4109	04839	04108	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4110	04840	04109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4111	04841	04110	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4112	04842	04111	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4113	04843	04112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4114	04844	04113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4115	04845	04114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4116	04846	04115	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4117	04847	04116	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4118	04848	04117	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4119	04850	04118	5		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4120	04851	04119	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4121	04852	04120	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0						
4122	04853	04121	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4123	04854	04122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4124	04855	04123	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4125	04856	04124	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						

Table 115

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
4126	04859	04125	3		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0					
4127	04860	04126	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4128	04861	04127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4129	04862	04128	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
4130	04863	04129	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4131	04864	04130	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4132	04865	04131	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4133	04866	04132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4134	04867	04133	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4135	04868	04134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4136	04869	04135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4137	04870	04136	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4138	04872	04137	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4139	04873	04138	4		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
4140	04874	04139	4		0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0					
4141	04875	04140	5		0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0					
4142	04877	04141	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4143	04878	04142	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4144	04879	04143	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4145	04881	04144	5		0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0					
4146	04882	04145	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4147	04883	04146	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4148	04884	04147	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
4149	04885	04148	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4150	04886	04149	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4151	04887	04150	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4152	04888	04151	25		0	0	0	0	0	0	0	0	0	0	0	0	0	9	3	0	0	0	0	0	0	0					
4153	04889	04152	6		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0					
4154	04890	04153	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4155	04891	04154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4156	04892	04155	3		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0					
4157	04893	04156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4158	04894	04157	3		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0					
4159	04895	04158	14		0	0	0	0	0	0	0	0	0	0	0	0	0	13	1	0	0	0	0	0	0	0					
4160	04897	04159	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4161	04898	04160	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					

Table 116

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4162	04900	04161	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4163	04902	04162	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4164	04903	04163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4165	04904	04164	5		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4166	04905	04165	5		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4167	04907	04166	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4168	04908	04167	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4169	04909	04168	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4170	04910	04169	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4171	04912	04170	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4172	04913	04171	4		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4173	04914	04172	6		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4174	04915	04173	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4175	04916	04174	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4176	04917	04175	3		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0						
4177	04918	04176	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4178	04919	04177	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4179	04920	04178	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4180	04921	04179	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4181	04922	04180	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4182	04923	04181	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4183	04924	04182	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4184	04925	04183	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4185	04926	04184	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4186	04927	04185	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4187	04928	04186	3		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0						
4188	04929	04187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4189	04930	04188	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4190	04940	04189	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4191	04945	04190	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0						
4192	04947	04191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4193	04948	04192	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0						
4194	04950	04193	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4195	04965	04194	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4196	04985	04195	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0						
4197	04986	04196	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 117

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4198	04987	04197	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0							
4199	04988	04198	2		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0							
4200	04989	04199	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0							
4201	04990	04200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4202	04991	04201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4203	04992	04202	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4204	04993	04203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4205	04994	04204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4206	04997	04205	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4207	04998	04206	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0							
4208	04999	04207	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0							
4209	05001	04208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		93.3	270	1	2202	2626	
4210	05002	04209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		98.5	341	1	3286	3624	
4211	05003	04210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4212	05004	04211	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4213	05005	04212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4214	05006	04213	8		0	0	0	0	0	0	0	0	0	0	0	1	0	0	3	0	0	0	0	0	0	0	0							
4215	05007	04214	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4216	05008	04215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4217	05009	04216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4218	05010	04217	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0							
4219	05011	04218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4220	05013	04219	14		0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	7	1	0	0	0	0	0	0		96.3	164	1	1197	1360	
4221	05014	04220	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4222	05016	04221	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		98	196	1	1121	1763	
4223	05018	04222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4224	05019	04223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4225	05021	04224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4226	05023	04225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0		97.8	269	1	761	1032	
4227	05024	04226	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4228	05025	04227	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4229	05026	04228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4230	05027	04229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4231	05028	04230	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4232	05029	04231	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							
4233	05030	04232	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0							

Table 118

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4234	05031	04233	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4235	05033	04234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4236	05034	04235	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4237	05035	04236	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4238	05037	04237	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4239	05039	04238	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4240	05040	04239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4241	05041	04240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4242	05042	04241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4243	05043	04242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4244	05044	04243	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4245	05045	04244	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4246	05046	04245	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4247	05047	04246	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4248	05051	04247	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4249	05052	04248	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4250	05053	04249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4251	05054	04250	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4252	05055	04251	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4253	05056	04252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4254	05058	04253	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4255	05059	04254	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4256	05060	04255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4257	05061	04256	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4258	05062	04257	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4259	05063	04258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4260	05064	04259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4261	05065	04260	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4262	05066	04261	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4263	05068	04262	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4264	05069	04263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4265	05070	04264	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4266	05071	04265	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4267	05073	04266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4268	05074	04267	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4269	05075	04268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 119

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	ACA	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4270	05076	04269	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0						
4271	05077	04270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4272	05079	04271	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4273	05080	04272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4274	05081	04273	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0						
4275	05082	04274	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	X03067	95.1	246	1	815	1081
4276	05083	04275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4277	05085	04276	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4278	05086	04277	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4279	05087	04278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4280	05088	04279	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4281	05089	04280	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4282	05090	04281	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4283	05092	04282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4284	05094	04283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4285	05095	04284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4286	05096	04285	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4287	05099	04286	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4288	05100	04287	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4289	05102	04288	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4290	05103	04289	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4291	05104	04290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4292	05105	04291	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4293	05106	04292	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4294	05107	04293	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4295	05108	04294	12		0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0	0	0	0	0	0	0						
4296	05109	04295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4297	05110	04296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4298	05111	04297	16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	3	0	0	0	0	0	0	0						
4299	05112	04298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4300	05113	04299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4301	05114	04300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4302	05115	04301	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4303	05116	04302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4304	05117	04303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4305	05118	04304	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						

Table 120

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4306	05119	04305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4307	05120	04306	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4308	05121	04307	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0							
4309	05122	04308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4310	05123	04309	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4311	05124	04310	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4312	05127	04311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4313	05128	04312	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4314	05129	04313	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4315	05130	04314	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4316	05132	04315	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4317	05133	04316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4318	05134	04317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4319	05135	04318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4320	05136	04319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4321	05137	04320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4322	05138	04321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0							
4323	05139	04322	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4324	05140	04323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4325	05141	04324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4326	05142	04325	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0							
4327	05143	04326	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4328	05144	04327	3		0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0							
4329	05145	04328	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4330	05147	04329	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4331	05148	04330	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4332	05149	04331	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4333	05150	04332	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4334	05151	04333	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4335	05152	04334	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4336	05153	04335	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4337	05155	04336	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4338	05157	04337	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4339	05158	04338	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4340	05159	04339	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
4341	05160	04340	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							

Table 121

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AL	AW	AY	BABC	BE	BF	BG	BH	BI	BK
4342	05161	04341	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4343	05162	04342	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4344	05163	04343	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4345	05164	04344	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4346	05165	04345	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4347	05166	04346	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4348	05168	04347	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0						
4349	05169	04348	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4350	05170	04349	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4351	05172	04350	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4352	05173	04351	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4353	05174	04352	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4354	05176	04353	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4355	05177	04354	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0						
4356	05178	04355	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4357	05180	04356	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4358	05181	04357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4359	05182	04358	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4360	05183	04359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4361	05184	04360	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4362	05185	04361	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4363	05186	04362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4364	05187	04363	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4365	05188	04364	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4366	05190	04365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4367	05191	04366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4368	05192	04367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4369	05194	04368	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4370	05195	04369	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	L19597	90.9	55	1	3459	3511
4371	05196	04370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4372	05197	04371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4373	05198	04372	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4374	05199	04373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4375	05200	04374	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	L10284	100	51	1	3826	4117
4376	05201	04375	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4377	05203	04376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						

Table 122

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
4378	05204	04377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4379	05205	04378	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0					
4380	05206	04379	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4381	05207	04380	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4382	05208	04381	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4383	05209	04382	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4384	05210	04383	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4385	05211	04384	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4386	05212	04385	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4387	05213	04386	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4388	05214	04387	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4389	05215	04388	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4390	05216	04389	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4391	05217	04390	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4392	05218	04391	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4393	05219	04392	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4394	05220	04393	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4395	05221	04394	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4396	05223	04395	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4397	05224	04396	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4398	05227	04397	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4399	05228	04398	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4400	05229	04399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4401	05230	04400	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4402	05231	04401	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4403	05232	04402	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4404	05233	04403	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4405	05234	04404	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4406	05235	04405	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4407	05236	04406	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4408	05237	04407	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4409	05238	04408	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4410	05239	04409	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4411	05240	04410	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4412	05241	04411	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4413	05242	04412	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					

Table 123

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4414	05243	04413	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4415	05244	04414	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4416	05245	04415	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4417	05246	04416	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4418	05247	04417	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4419	05248	04418	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4420	05249	04419	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4421	05251	04420	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4422	05252	04421	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4423	05253	04422	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4424	05254	04423	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4425	05255	04424	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4426	05259	04425	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4427	05260	04426	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4428	05262	04427	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4429	05263	04428	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4430	05264	04429	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4431	05266	04430	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4432	05267	04431	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4433	05269	04432	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4434	05270	04433	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4435	05271	04434	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4436	05272	04435	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4437	05273	04436	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4438	05274	04437	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4439	05275	04438	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4440	05276	04439	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4441	05278	04440	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4442	05279	04441	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4443	05280	04442	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4444	05281	04443	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4445	05282	04444	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4446	05283	04445	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4447	05284	04446	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4448	05285	04447	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4449	05286	04448	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 124

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AL	AW	AY	BA	BC	BE	BF	BGBH	BI	BK	
4450	05287	04449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4451	05288	04450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4452	05289	04451	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	U03643	99.2	118	1	1263	1380
4453	05290	04452	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	X53799	100	290	1	792	1081
4454	05291	04453	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4455	05292	04454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4456	05293	04455	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0						
4457	05294	04456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4458	05295	04457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4459	05296	04458	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4460	05297	04459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4461	05298	04460	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4462	05300	04461	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	Z22969	98.5	130	1	3405	3786
4463	05301	04462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4464	05302	04463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4465	05303	04464	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4466	05304	04465	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4467	05305	04466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4468	05306	04467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4469	05307	04468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4470	05308	04469	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	X68148	98.354	1	2662	3031	
4471	05309	04470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	Y00971	96.9	64	1	2392	2457
4472	05310	04471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4473	05311	04472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4474	05312	04473	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4475	05313	04474	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4476	05314	04475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4477	05315	04476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4478	05316	04477	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4479	05318	04478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4480	05319	04479	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
4481	05320	04480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4482	05321	04481	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4483	05322	04482	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4484	05323	04483	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4485	05325	04484	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0						

Table 125

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4486	05326	04485	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4487	05327	04486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4488	05328	04487	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4489	05329	04488	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4490	05331	04489	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4491	05332	04490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4492	05333	04491	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
4493	05334	04492	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4494	05335	04493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4495	05336	04494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4496	05337	04495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4497	05339	04496	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4498	05340	04497	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4499	05341	04498	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4500	05342	04499	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4501	05343	04500	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4502	05344	04501	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4503	05345	04502	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4504	05346	04503	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4505	05347	04504	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4506	05349	04505	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4507	05350	04506	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4508	05351	04507	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4509	05352	04508	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4510	05353	04509	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4511	05354	04510	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4512	05355	04511	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4513	05356	04512	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4514	05357	04513	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4515	05359	04514	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4516	05360	04515	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4517	05361	04516	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4518	05362	04517	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4519	05363	04518	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4520	05364	04519	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
4521	05365	04520	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 126

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BAB	BC	BE	BF	BGBH	BI	BK	
4522	05366	04521	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	M55169	100	79	1	4363	4446
4523	05367	04522	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4524	05368	04523	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4525	05370	04524	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4526	05371	04525	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4527	05372	04526	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4528	05373	04527	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4529	05374	04528	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4530	05375	04529	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4531	05376	04530	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4532	05377	04531	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4533	05378	04532	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4534	05379	04533	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4535	05381	04534	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4536	05382	04535	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4537	05383	04536	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4538	05384	04537	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4539	05387	04538	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4540	05388	04539	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4541	05389	04540	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4542	05390	04541	32		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4543	05391	04542	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4544	05392	04543	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4545	05393	04544	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4546	05394	04545	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4547	05395	04546	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4548	05396	04547	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4549	05398	04548	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4550	05399	04549	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4551	05400	04550	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4552	05401	04551	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4553	05402	04552	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4554	05404	04553	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4555	05406	04554	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4556	05407	04555	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
4557	05408	04556	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 127

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4558	05409	04557	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4559	05410	04558	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4560	05411	04559	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0						
4561	05412	04560	9		0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0						
4562	05413	04561	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4563	05414	04562	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4564	05415	04563	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4565	05416	04564	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4566	05417	04565	5		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0						
4567	05418	04566	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4568	05419	04567	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4569	05420	04568	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4570	05421	04569	1		0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0						
4571	05422	04570	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4572	05423	04571	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4573	05424	04572	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4574	05425	04573	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4575	05427	04574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4576	05428	04575	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4577	05429	04576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4578	05430	04577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4579	05431	04578	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4580	05432	04579	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4581	05433	04580	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4582	05434	04581	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4583	05435	04582	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4584	05436	04583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4585	05437	04584	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4586	05438	04585	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4587	05439	04586	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4588	05440	04587	1		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0						
4589	05441	04588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4590	05442	04589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4591	05443	04590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4592	05444	04591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						
4593	05445	04592	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0						

Table 128

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
4594	05446	04593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4595	05447	04594	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0					
4596	05448	04595	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0					
4597	05451	04596	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4598	05452	04597	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4599	05453	04598	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4600	05454	04599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4601	05455	04600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4602	05456	04601	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0					
4603	05458	04602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4604	05459	04603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4605	05460	04604	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4606	05461	04605	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4607	05462	04606	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4608	05464	04607	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4609	05465	04608	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4610	05466	04609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4611	05467	04610	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4612	05468	04611	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0					
4613	05469	04612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4614	05470	04613	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4615	05471	04614	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4616	05472	04615	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4617	05474	04616	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4618	05475	04617	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4619	05476	04618	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4620	05477	04619	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4621	05478	04620	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4622	05479	04621	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4623	05480	04622	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4624	05481	04623	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4625	05482	04624	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4626	05483	04625	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0					
4627	05484	04626	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4628	05485	04627	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					
4629	05486	04628	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0					

Table 129

Table 130

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4666	05532	04665	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4667	05533	04666	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4668	05534	04667	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4669	05535	04668	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4670	05536	04669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4671	05538	04670	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4672	05539	04671	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4673	05540	04672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4674	05541	04673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4675	05544	04674	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4676	05545	04675	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4677	05547	04676	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4678	05548	04677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4679	05551	04678	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4680	05552	04679	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4681	05553	04680	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4682	05555	04681	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4683	05556	04682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4684	05558	04683	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4685	05559	04684	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4686	05560	04685	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4687	05561	04686	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4688	05562	04687	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4689	05563	04688	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4690	05564	04689	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4691	05565	04690	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4692	05566	04691	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4693	05567	04692	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4694	05568	04693	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4695	05570	04694	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4696	05571	04695	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4697	05572	04696	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4698	05573	04697	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4699	05574	04698	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4700	05575	04699	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
4701	05576	04700	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 131

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4702	05577	04701	4		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	809
4703	05578	04702	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4704	05579	04703	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4705	05580	04704	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4706	05581	04705	4		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	
4707	05582	04706	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4708	05583	04707	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	
4709	05585	04708	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4710	05586	04709	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4711	05587	04710	4		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4712	05588	04711	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	
4713	05589	04712	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4714	05590	04713	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	
4715	05591	04714	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4716	05593	04715	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1231
4717	05595	04716	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
4718	05598	04717	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4719	05599	04718	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4720	05600	04719	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3781
4721	05601	04720	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4722	05602	04721	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4723	05603	04722	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4724	05604	04723	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4725	05606	04724	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4726	05607	04725	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4727	05608	04726	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4728	05610	04727	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4729	05612	04728	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4730	05613	04729	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4731	05614	04730	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4732	05615	04731	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4733	05616	04732	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4734	05618	04733	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4735	05619	04734	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4736	05621	04735	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
4737	05622	04736	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

Table 132

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AL	AW	AY	BABC	BE	BF	BGBH	BI	BK
4738	05623	04737	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4739	05624	04738	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0					
4740	05625	04739	3		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0					
4741	05627	04740	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4742	05628	04741	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4743	05629	04742	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4744	05630	04743	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4745	05631	04744	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4746	05632	04745	4		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4747	05634	04746	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4748	05635	04747	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4749	05636	04748	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4750	05637	04749	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4751	05639	04750	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4752	05640	04751	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	1	0	0	0					
4753	05642	04752	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4754	05643	04753	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4755	05644	04754	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4756	05645	04755	2		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4757	05646	04756	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4758	05647	04757	5		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4759	05648	04758	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4760	05649	04759	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4761	05650	04760	4		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4762	05651	04761	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4763	05652	04762	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4764	05653	04763	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4765	05654	04764	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4766	05655	04765	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4767	05656	04766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4768	05657	04767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4769	05658	04768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4770	05659	04769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4771	05660	04770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4772	05661	04771	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4773	05662	04772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					

Table 133

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
4774	05665	04773	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4775	05667	04774	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4776	05668	04775	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4777	05669	04776	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4778	05671	04777	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4779	05673	04778	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4780	05674	04779	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4781	05676	04780	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4782	05679	04781	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4783	05680	04782	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4784	05681	04783	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4785	05682	04784	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4786	05683	04785	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4787	05684	04786	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4788	05685	04787	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0					
4789	05686	04788	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4790	05687	04789	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4791	05688	04790	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4792	05689	04791	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4793	05690	04792	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4794	05692	04793	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4795	05693	04794	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4796	05694	04795	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4797	05695	04796	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4798	05696	04797	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4799	05697	04798	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4800	05701	04799	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4801	05704	04800	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4802	05707	04801	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4803	05708	04802	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4804	05709	04803	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4805	05710	04804	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4806	05711	04805	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4807	05714	04806	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4808	05715	04807	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					
4809	05716	04808	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0					

Table 134

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AF	AG	AJ	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4810	05718	04809	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	05392	98.2	284	1	2120	2402
4811	05719	04810	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4812	05720	04811	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4813	05721	04812	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4814	05722	04813	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	K03002	95.4	306	1	327	632
4815	05723	04814	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M86667	98.4	63	1	802	1560
4816	05724	04815	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4817	05725	04816	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4818	05726	04817	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4819	05727	04818	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4820	05729	04819	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L06105	100	60	1	1297	1649
4821	05730	04820	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4822	05731	04821	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4823	05732	04822	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4824	05733	04823	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4825	05734	04824	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4826	05735	04825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4827	05736	04826	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4828	05738	04827	17		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4829	05741	04828	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4830	05742	04829	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4831	05743	04830	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4832	05747	04831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4833	05748	04832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4834	05749	04833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4835	05751	04834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4836	05752	04835	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4837	05754	04836	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4838	05755	04837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4839	05756	04838	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4840	05757	04839	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4841	05758	04840	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4842	05759	04841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4843	05763	04842	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4844	05765	04843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
4845	05767	04844	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 135

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AU	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4846	05768	04845	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	X02571	97.3	73	130	1430	1512
4847	05769	04846	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4848	05770	04847	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4849	05772	04848	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4850	05773	04849	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4851	05774	04850	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4852	05775	04851	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4853	05776	04852	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4854	05777	04853	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0						
4855	05778	04854	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4856	05779	04855	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4857	05780	04856	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0						
4858	05781	04857	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4859	05782	04858	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4860	05783	04859	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	1	0	0	0	2						
4861	05784	04860	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4862	05785	04861	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4863	05787	04862	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4864	05789	04863	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4865	05790	04864	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4866	05792	04865	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4867	05793	04866	9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4868	05794	04867	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0						
4869	05795	04868	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4870	05796	04869	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4871	05797	04870	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4872	05798	04871	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4873	05799	04872	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4874	05801	04873	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0						
4875	05804	04874	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4876	05807	04875	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0						
4877	05808	04876	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4878	05810	04877	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1	2	0	0	0						
4879	05813	04878	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4880	05814	04879	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4881	05815	04880	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						

Table 136

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4882	05816	04881	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4883	05817	04882	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4884	05818	04883	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4885	05819	04884	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4886	05820	04885	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4887	05821	04886	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4888	05823	04887	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4889	05824	04888	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4890	05825	04889	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4891	05826	04890	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0		97.8	321	1	2133	2912
4892	05827	04891	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4893	05829	04892	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0						
4894	05830	04893	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4895	05831	04894	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4896	05832	04895	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4897	05833	04896	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4898	05834	04897	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4899	05835	04898	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0		96.5	313	1	3380	3692
4900	05836	04899	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4901	05837	04900	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4902	05838	04901	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4903	05839	04902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4904	05840	04903	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4905	05841	04904	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4906	05842	04905	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0		90.7	54	1	1718	3269
4907	05843	04906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4908	05844	04907	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4909	05845	04908	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4910	05846	04909	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	1	0	0	0	0	0	0		100	135	1	941	1108
4911	05847	04910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0		92.8	223	3	125	1855
4912	05848	04911	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4913	05849	04912	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4914	05850	04913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4915	05851	04914	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
4916	05852	04915	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0		100	124	1	4132	4268
4917	05854	04916	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						

Table 137

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	SA	LA	WA	AY	BA	BC	BE	BF	BG	BH	BI	BK	
4918	05856	04917	4		0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4919	05857	04918	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0						
4920	05858	04919	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	M86667	100 168	1	376	1560	
4921	05859	04920	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	M18391	93 2 118	1	3253	3370	
4922	05860	04921	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4923	05862	04922	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4924	05863	04923	3		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4925	05864	04924	10		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	5	0	0	0	0	0	0	0	M26252	93 327	1	1817	2306	
4926	05865	04925	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0					
4927	05866	04926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4928	05867	04927	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4929	05868	04928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
4930	05869	04929	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4931	05870	04930	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4932	05871	04931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4933	05872	04932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4934	05874	04933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4935	05875	04934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4936	05876	04935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4937	05877	04936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4938	05879	04937	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4939	05880	04938	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4940	05882	04939	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4941	05885	04940	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4942	05886	04941	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4943	05887	04942	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4944	05888	04943	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4945	05889	04944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4946	05890	04945	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4947	05892	04946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4948	05893	04947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4949	05894	04948	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	M17783	98 101	1	1091	1191
4950	05895	04949	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	M21551	96 1 330	1	295	640
4951	05896	04950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					
4952	05897	04951	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0					
4953	05898	04952	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0					

Table 138

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
4954	05899	04953	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4955	05900	04954	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4956	05902	04955	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4957	05903	04956	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4958	05907	04957	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	M62994	95.2	315	1	1591	2007
4959	05908	04958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	X05803	93.8	308	1	525	956
4960	05912	04959	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4961	05913	04960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4962	05914	04961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4963	05916	04962	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4964	05917	04963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4965	05918	04964	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4966	05919	04965	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4967	05920	04966	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4968	05921	04967	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4969	05923	04968	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	X63629	99.2	126	1	3046	3171
4970	05925	04969	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4971	05926	04970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4972	05927	04971	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4973	05928	04972	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4974	05932	04973	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4975	05933	04974	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4976	05934	04975	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4977	05937	04976	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4978	05938	04977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4979	05939	04978	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4980	05940	04979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4981	05941	04980	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4982	05942	04981	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4983	05943	04982	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4984	05946	04983	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	L19183	90.2	51	1	983	2002
4985	05947	04984	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4986	05948	04985	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4987	05949	04986	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
4988	05951	04987	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	M65028	91.8	343	1	1021	1537
4989	05952	04988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						

Table 139

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AC	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
4990	05953	04989	1																								0	M37712	99.3	147	1	3717	3863	
4991	05954	04990	2																								0							
4992	05955	04991	5																								0							
4993	05956	04992	1																								0							
4994	05957	04993	1																								0							
4995	05959	04994	3																								0							
4996	05960	04995	1																								0	M27319	98.5	65	1	735	799	
4997	05961	04996	1																								0							
4998	05962	04997	1																								0							
4999	05963	04998	1																								0							
5000	05964	04999	1																								0							
5001	05966	05000	1																								0							
5002	05967	05001	1																								0							
5003	05968	05002	1																								0							
5004	05969	05003	1																								0							
5005	05970	05004	1																								0							
5006	05974	05005	1																								0							
5007	05975	05006	1																								0							
5008	05976	05007	1																								0							
5009	05978	05008	6																								0							
5010	05980	05009	1																								0	M33197	94.8	305	1	495	1268	
5011	05981	05010	1																								0							
5012	05982	05011	2																								0							
5013	05983	05012	1																								0							
5014	05984	05013	3																								0							
5015	05987	05014	2																								0							
5016	05988	05015	1																								0							
5017	05989	05016	1																								0							
5018	05991	05017	1																								0							
5019	05992	05018	1																								0							
5020	05993	05019	1																								0							
5021	05994	05020	1																								0							
5022	05996	05021	1																								0							
5023	05997	05022	1																								0							
5024	05998	05023	1																								0							
5025	05999	05024	1																								0							

Table 140

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AU	AW	AY	B	ABC	BE	BF	BG	BH	BI	BK
5026	06000	05025	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5027	06001	05026	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5028	06004	05027	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5029	06005	05028	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5030	06008	05029	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5031	06010	05030	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5032	06011	05031	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5033	06013	05032	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5034	06014	05033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5035	06015	05034	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5036	06016	05035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5037	06017	05036	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5038	06018	05037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5039	06020	05038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5040	06021	05039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5041	06022	05040	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5042	06023	05041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5043	06024	05042	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0		M60801	97.8	90	1	1279	1368
5044	06025	05043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5045	06026	05044	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5046	06027	05045	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0							
5047	06028	05046	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0							
5048	06030	05047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5049	06031	05048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5050	06032	05049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5051	06034	05050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5052	06035	05051	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5053	06036	05052	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5054	06038	05053	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5055	06039	05054	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5056	06040	05055	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5057	06041	05056	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5058	06042	05057	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0		X68314	98.1	316	1	629	971
5059	06043	05058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5060	06044	05059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							
5061	06045	05060	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0							

Table 141

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5062	06046	05061	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5063	06047	05062	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0						
5064	06048	05063	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5065	06049	05064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5066	06050	05065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5067	06051	05066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5068	06052	05067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5069	06053	05068	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0						
5070	06054	05069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5071	06055	05070	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5072	06056	05071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5073	06057	05072	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5074	06059	05073	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5075	06060	05074	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5076	06061	05075	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5077	06062	05076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5078	06064	05077	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5079	06065	05078	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5080	06066	05079	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5081	06067	05080	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5082	06068	05081	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5083	06069	05082	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5084	06070	05083	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5085	06071	05084	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5086	06072	05085	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5087	06074	05086	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5088	06075	05087	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5089	06076	05088	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5090	06077	05089	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5091	06078	05090	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5092	06079	05091	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5093	06080	05092	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5094	06081	05093	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5095	06083	05094	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5096	06084	05095	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						
5097	06085	05096	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0						

Table 142

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
5098	06086	05097	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5099	06087	05098	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
5100	06089	05099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5101	06090	05100	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5102	06091	05101	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5103	06092	05102	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5104	06093	05103	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5105	06094	05104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5106	06095	05105	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5107	06097	05106	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5108	06098	05107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5109	06100	05108	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5110	06101	05109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5111	06102	05110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5112	06103	05111	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5113	06104	05112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5114	06105	05113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5115	06107	05114	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0					
5116	06108	05115	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5117	06109	05116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5118	06110	05117	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5119	06111	05118	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5120	06112	05119	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5121	06113	05120	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5122	06114	05121	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5123	06115	05122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5124	06116	05123	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5125	06117	05124	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0					
5126	06118	05125	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5127	06119	05126	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5128	06122	05127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5129	06123	05128	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5130	06125	05129	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5131	06126	05130	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0					
5132	06127	05131	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5133	06128	05132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					

Table 143

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BGBH	BI	BK
5134	06129	05133	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5135	06130	05134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5136	06131	05135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5137	06133	05136	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5138	06136	05137	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5139	06137	05138	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5140	06138	05139	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5141	06139	05140	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5142	06141	05141	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5143	06142	05142	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5144	06144	05143	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5145	06145	05144	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5146	06146	05145	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5147	06148	05146	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5148	06150	05147	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5149	06151	05148	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5150	06152	05149	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5151	06153	05150	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5152	06154	05151	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5153	06155	05152	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5154	06156	05153	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5155	06157	05154	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5156	06158	05155	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5157	06159	05156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5158	06160	05157	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5159	06161	05158	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5160	06163	05159	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5161	06164	05160	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5162	06165	05161	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5163	06166	05162	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5164	06167	05163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5165	06168	05164	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5166	06169	05165	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5167	06170	05166	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5168	06171	05167	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5169	06172	05168	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 144

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
5170	06173	05169	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5171	06174	05170	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5172	06175	05171	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5173	06176	05172	3		0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	1	0	0	0	0	0					
5174	06177	05173	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5175	06178	05174	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5176	06180	05175	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5177	06181	05176	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0					
5178	06182	05177	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5179	06183	05178	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5180	06184	05179	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5181	06185	05180	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5182	06186	05181	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5183	06187	05182	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2					
5184	06188	05183	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5185	06189	05184	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5186	06190	05185	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5187	06191	05186	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5188	06192	05187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					
5189	06195	05188	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		723064	93.8 224	1	1152
5190	06196	05189	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0					1894
5191	06197	05190	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0					
5192	06198	05191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5193	06199	05192	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5194	06200	05193	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5195	06201	05194	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5196	06202	05195	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5197	06203	05196	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5198	06204	05197	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5199	06205	05198	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5200	06206	05199	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5201	06207	05200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5202	06208	05201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5203	06209	05202	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0					
5204	06210	05203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5205	06211	05204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					

Table 145

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5206	06213	05205	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5207	06215	05206	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5208	06216	05207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5209	06217	05208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5210	06218	05209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5211	06219	05210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5212	06220	05211	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5213	06221	05212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5214	06222	05213	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5215	06224	05214	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5216	06225	05215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5217	06226	05216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5218	06227	05217	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5219	06228	05218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5220	06229	05219	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5221	06230	05220	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5222	06232	05221	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5223	06233	05222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5224	06234	05223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5225	06235	05224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5226	06236	05225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5227	06237	05226	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5228	06238	05227	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5229	06240	05228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5230	06241	05229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5231	06243	05230	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5232	06244	05231	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5233	06246	05232	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5234	06247	05233	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5235	06248	05234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5236	06249	05235	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5237	06250	05236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5238	06251	05237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5239	06253	05238	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5240	06254	05239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5241	06255	05240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 146

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AU	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5242	06256	05241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5243	06257	05242	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	2	0	0							
5244	06258	05243	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5245	06259	05244	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	X52056	98.5	68	1	1297	1364	
5246	06260	05245	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5247	06261	05246	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5248	06262	05247	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5249	06264	05248	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5250	06267	05249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5251	06268	05250	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5252	06269	05251	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5253	06270	05252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5254	06271	05253	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5255	06272	05254	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5256	06273	05255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	M80359	93.9	181	1	2062	2914	
5257	06274	05256	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5258	06275	05257	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	2	0	0	0	M90104	94.2	173	1	1700	1879	
5259	06277	05258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5260	06278	05259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5261	06279	05260	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5262	06280	05261	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5263	06281	05262	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	M64784	95.6	338	1	638	1138	
5264	06282	05263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5265	06283	05264	11		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	X52426	100	102	1	1574	1677	
5266	06284	05265	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5267	06286	05266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5268	06288	05267	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0							
5269	06289	05268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5270	06290	05269	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5271	06291	05270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5272	06292	05271	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5273	06293	05272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5274	06294	05273	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5275	06295	05274	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5276	06296	05275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5277	06297	05276	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	M86400	92.4	197	1	1196	2834	

Table 147

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK		
5278	06299	05277	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	M74002	98.7	229	1	2508	2736	
5279	06300	05278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	J05448	98.9	176	1	1256	1766	
5280	06301	05279	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0							
5281	06302	05280	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5282	06303	05281	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5283	06304	05282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5284	06305	05283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5285	06306	05284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5286	06307	05285	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5287	06308	05286	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5288	06309	05287	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5289	06310	05288	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5290	06311	05289	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5291	06313	05290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5292	06314	05291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5293	06315	05292	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5294	06316	05293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	M69039	99	102	1	1130	1240	
5295	06317	05294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5296	06318	05295	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5297	06319	05296	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5298	06320	05297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	M59287	99.5	198	1	1549	1750	
5299	06321	05298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5300	06322	05299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	L22846	100	69	1	1698	1766	
5301	06323	05300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5302	06324	05301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5303	06325	05302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5304	06326	05303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5305	06327	05304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5306	06329	05305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5307	06330	05306	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5308	06331	05307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5309	06332	05308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5310	06333	05309	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5311	06334	05310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5312	06335	05311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0							
5313	06337	05312	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 148

[illegible]

Table 1.49

Table 150

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
5386	06418	05385	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5387	06419	05386	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5388	06420	05387	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5389	06421	05388	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5390	06422	05389	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M59040	99.3	296	1	934	1794	
5391	06423	05390	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5392	06424	05391	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5393	06425	05392	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
5394	06426	05393	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5395	06427	05394	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5396	06428	05395	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5397	06429	05396	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5398	06430	05397	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5399	06431	05398	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5400	06432	05399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5401	06433	05400	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5402	06434	05401	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5403	06435	05402	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	559184	94.9	274	1	2791	3068
5404	06436	05403	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5405	06437	05404	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5406	06438	05405	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5407	06439	05406	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5408	06440	05407	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5409	06441	05408	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5410	06442	05409	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5411	06443	05410	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5412	06444	05411	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5413	06445	05412	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5414	06446	05413	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5415	06447	05414	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5416	06448	05415	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5417	06449	05416	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5418	06450	05417	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5419	06451	05418	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5420	06452	05419	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5421	06453	05420	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 151

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
5422	06454	05421	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	L10910	95.1	205	1	2334	2595
5423	06455	05422	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5424	06456	05423	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5425	06457	05424	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5426	06458	05425	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5427	06459	05426	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5428	06460	05427	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5429	06461	05428	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	MS9465	100	183	1	4244	4426
5430	06462	05429	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5431	06463	05430	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5432	06464	05431	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5433	06465	05432	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5434	06466	05433	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5435	06468	05434	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5436	06469	05435	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5437	06470	05436	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5438	06471	05437	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5439	06472	05438	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5440	06473	05439	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
5441	06474	05440	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5442	06475	05441	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5443	06476	05442	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5444	06477	05443	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5445	06478	05444	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	XG3657	96.8	313	1	1738	2272
5446	06481	05445	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5447	06482	05446	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	X12510	95.6	250	1	760	1041
5448	06483	05447	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5449	06484	05448	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	L25610	92.8	333	1	1641	2098
5450	06485	05449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5451	06486	05450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5452	06487	05451	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5453	06488	05452	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
5454	06489	05453	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5455	06490	05454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5456	06491	05455	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5457	06492	05456	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						

Table 152

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AL	AW	AY	BABC	BE	BF	BGBH	BI	BK	
5458	06493	05457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5459	06496	05458	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0					
5460	06498	05459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5461	06499	05460	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5462	06500	05461	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	L24559	97	1	68	1 2112 2187	
5463	06501	05462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5464	06502	05463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5465	06503	05464	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5466	06504	05465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5467	06505	05466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5468	06506	05467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5469	06507	05468	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5470	06508	05469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0					
5471	06509	05470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5472	06510	05471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5473	06511	05472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5474	06512	05473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5475	06513	05474	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5476	06514	05475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5477	06515	05476	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	1	0	0	L16785	100	49	1	599	647
5478	06516	05477	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0					
5479	06517	05478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5480	06518	05479	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5481	06519	05480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5482	06520	05481	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5483	06521	05482	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5484	06522	05483	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5485	06523	05484	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5486	06524	05485	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5487	06525	05486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5488	06526	05487	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5489	06527	05488	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5490	06528	05489	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5491	06529	05490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5492	06530	05491	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
5493	06531	05492	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					

Table 153

Table 154

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
5530	06576	05529	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5531	06577	05530	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5532	06578	05531	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5533	06579	05532	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	X54925	98 203	1	1410	1970
5534	06580	05533	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5535	06581	05534	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	M58460	98.9 177	1	1364	1542
5536	06582	05535	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5537	06583	05536	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5538	06584	05537	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5539	06585	05538	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5540	06586	05539	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5541	06587	05540	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5542	06588	05541	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5543	06590	05542	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5544	06592	05543	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	M98479	92.4 250	1	1311	1557
5545	06593	05544	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5546	06594	05545	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5547	06595	05546	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5548	06596	05547	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5549	06597	05548	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5550	06599	05549	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5551	06600	05550	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	M14083	90.1 162	1	2218	2937
5552	06601	05551	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5553	06602	05552	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5554	06603	05553	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	L07590	95.1 102	1	4230	5217
5555	06604	05554	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5556	06605	05555	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5557	06606	05556	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5558	06607	05557	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0					
5559	06608	05558	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5560	06609	05559	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	M10036	95 80	43	1483	1835
5561	06610	05560	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5562	06611	05561	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	L22569	91.5 130	1	971	2286
5563	06612	05562	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5564	06613	05563	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
5565	06614	05564	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					

Table 155

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
5566	06615	05565	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5567	06616	05566	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5568	06617	05567	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5569	06618	05568	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	L11005	98.7	76	1	4882	4957
5570	06619	05569	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5571	06620	05570	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5572	06621	05571	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5573	06623	05572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5574	06624	05573	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5575	06625	05574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5576	06626	05575	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	M20472	95.4	131	1	383	1023
5577	06627	05576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5578	06628	05577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5579	06630	05578	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	X66363	95.1	184	1	1479	1745
5580	06631	05579	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5581	06632	05580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5582	06633	05581	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5583	06634	05582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5584	06635	05583	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5585	06636	05584	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	X53743	97.6	167	1	1991	2156
5586	06637	05585	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5587	06638	05586	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5588	06639	05587	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	M38258	94.9	253	1	2320	2571
5589	06640	05588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5590	06641	05589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5591	06642	05590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5592	06643	05591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5593	06645	05592	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5594	06646	05593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5595	06647	05594	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	X52678	95.8	96	1	1593	1879
5596	06649	05595	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5597	06650	05596	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5598	06651	05597	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5599	06652	05598	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5600	06653	05599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	M81757	98.6	69	17	432	510
5601	06654	05600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						

Table 156

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5602	06656	05601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5603	06659	05602	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5604	06660	05603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5605	06661	05604	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5606	06662	05605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5607	06664	05606	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5608	06666	05607	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5609	06667	05608	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5610	06668	05609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5611	06669	05610	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5612	06670	05611	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5613	06672	05612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5614	06673	05613	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5615	06674	05614	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5616	06675	05615	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5617	06676	05616	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5618	06677	05617	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5619	06678	05618	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5620	06679	05619	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5621	06680	05620	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5622	06681	05621	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5623	06682	05622	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5624	06683	05623	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5625	06684	05624	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5626	06685	05625	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5627	06686	05626	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5628	06687	05627	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5629	06688	05628	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5630	06689	05629	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5631	06690	05630	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5632	06691	05631	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5633	06692	05632	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5634	06693	05633	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5635	06694	05634	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5636	06696	05635	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
5637	06697	05636	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 157

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AU	AV	AW	BABC	BE	BF	BGBH	BI	BK
5638	06698	05637	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5639	06699	05638	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5640	06700	05639	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5641	06701	05640	5		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5642	06702	05641	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5643	06703	05642	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5644	06704	05643	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5645	06705	05644	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5646	06706	05645	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5647	06707	05646	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5648	06709	05647	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5649	06710	05648	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5650	06711	05649	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5651	06712	05650	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5652	06713	05651	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5653	06714	05652	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5654	06715	05653	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5655	06716	05654	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5656	06717	05655	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5657	06718	05656	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5658	06719	05657	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5659	06720	05658	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5660	06721	05659	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5661	06724	05660	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5662	06725	05661	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5663	06726	05662	3		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0					
5664	06727	05663	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5665	06728	05664	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5666	06730	05665	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5667	06731	05666	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5668	06732	05667	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5669	06733	05668	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5670	06734	05669	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5671	06735	05670	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5672	06736	05671	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					
5673	06737	05672	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0					

Table 158

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5674	06739	05673	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5675	06740	05674	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5676	06742	05675	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5677	06743	05676	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5678	06744	05677	2		0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0						
5679	06745	05678	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5680	06746	05679	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5681	06747	05680	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5682	06749	05681	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5683	06750	05682	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5684	06751	05683	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5685	06752	05684	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5686	06753	05685	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5687	06754	05686	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5688	06755	05687	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5689	06756	05688	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5690	06757	05689	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5691	06758	05690	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5692	06759	05691	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5693	06760	05692	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5694	06762	05693	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5695	06763	05694	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5696	06764	05695	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5697	06765	05696	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5698	06766	05697	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5699	06767	05698	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5700	06768	05699	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5701	06769	05700	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5702	06770	05701	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5703	06771	05702	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5704	06772	05703	2		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5705	06773	05704	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5706	06774	05705	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5707	06775	05706	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5708	06776	05707	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						
5709	06777	05708	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0						

Table 159

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5710	06778	05709	1		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0							
5711	06780	05710	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5712	06781	05711	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5713	06783	05712	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5714	06784	05713	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5715	06785	05714	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5716	06786	05715	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5717	06787	05716	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	005633	100 214	1 2887	3117		
5718	06788	05717	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5719	06789	05718	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5720	06790	05719	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5721	06791	05720	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5722	06792	05721	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5723	06794	05722	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5724	06795	05723	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		021163	98.3 363	1 2923	3784		
5725	06796	05724	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5726	06797	05725	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5727	06798	05726	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5728	06800	05727	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5729	06801	05728	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5730	06802	05729	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5731	06803	05730	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5732	06804	05731	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5733	06805	05732	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5734	06806	05733	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5735	06807	05734	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5736	06808	05735	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5737	06809	05736	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5738	06810	05737	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5739	06811	05738	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5740	06812	05739	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5741	06813	05740	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5742	06815	05741	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		07956	98.4 127	1 2780	2955		
5743	06816	05742	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5744	06817	05743	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		006985	93.3 195	1 1175	1550		
5745	06818	05744	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 160

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AU	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5746	06819	05745	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5747	06820	05746	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5748	06821	05747	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5749	06823	05748	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5750	06824	05749	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5751	06825	05750	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5752	06826	05751	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5753	06827	05752	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5754	06828	05753	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5755	06829	05754	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5756	06830	05755	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5757	06831	05756	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5758	06832	05757	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5759	06833	05758	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5760	06834	05759	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		105481	92.8	237	1	2363	2620
5761	06835	05760	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5762	06836	05761	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5763	06837	05762	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5764	06838	05763	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5765	06839	05764	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		103202	95.3	299	1	5002	5306
5766	06840	05765	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5767	06841	05766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5768	06842	05767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5769	06843	05768	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5770	06844	05769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5771	06845	05770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5772	06846	05771	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0							
5773	06848	05772	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0							
5774	06850	05773	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0							
5775	06851	05774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5776	06852	05775	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0							
5777	06854	05776	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0							
5778	06855	05777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5779	06856	05778	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5780	06857	05779	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
5781	06858	05780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							

Table 161

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
5782	06859	05781	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0							
5783	06863	05782	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
5784	06864	05783	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
5785	06865	05784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
5786	06866	05785	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
5787	06869	05786	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
5788	06870	05787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5789	06871	05788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5790	06872	05789	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5791	06873	05790	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5792	06874	05791	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5793	06875	05792	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5794	06876	05793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5795	06878	05794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5796	06879	05795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5797	06880	05796	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5798	06882	05797	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5799	06883	05798	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5800	06884	05799	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5801	06885	05800	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0							
5802	06886	05801	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5803	06888	05802	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5804	06889	05803	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5805	06890	05804	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5806	06891	05805	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5807	06893	05806	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5808	06894	05807	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5809	06895	05808	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5810	06896	05809	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5811	06897	05810	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5812	06898	05811	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5813	06899	05812	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5814	06900	05813	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5815	06901	05814	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5816	06902	05815	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
5817	06903	05816	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							

Table 162

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
5818	06904	05817	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5819	06906	05818	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5820	06909	05819	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5821	06910	05820	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5822	06911	05821	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5823	06912	05822	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5824	06913	05823	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5825	06915	05824	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5826	06916	05825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5827	06917	05826	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5828	06919	05827	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
5829	06920	05828	27		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 163

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
5854	06952	05853	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
5855	06953	05854	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5856	06954	05855	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1						
5857	06955	05856	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
5858	06956	05857	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5859	06957	05858	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5860	06959	05859	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5861	06960	05860	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5862	06961	05861	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					1634	1717
5863	06963	05862	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5864	06964	05863	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5865	06965	05864	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0						
5866	06966	05865	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5867	06967	05866	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5868	06969	05867	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
5869	06971	05868	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5870	06972	05869	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5871	06973	05870	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					2394	2759
5872	06975	05871	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					1731	2182
5873	06977	05872	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5874	06978	05873	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5875	06979	05874	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
5876	06981	05875	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5877	06982	05876	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5878	06983	05877	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
5879	06984	05878	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5880	06985	05879	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5881	06986	05880	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5882	06987	05881	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5883	06988	05882	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5884	06989	05883	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5885	06990	05884	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5886	06991	05885	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5887	06992	05886	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5888	06993	05887	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5889	06994	05888	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						

Table 164

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
5890	06995	05889	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5891	06996	05890	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5892	06997	05891	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5893	06998	05892	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5894	06999	05893	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5895	07000	05894	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5896	07001	05895	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5897	07002	05896	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5898	07003	05897	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0						
5899	07004	05898	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0						
5900	07005	05899	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0						
5901	07006	05900	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5902	07007	05901	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	0	0	0	0						
5903	07008	05902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5904	07009	05903	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5905	07011	05904	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5906	07012	05905	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5907	07013	05906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5908	07014	05907	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5909	07015	05908	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5910	07016	05909	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5911	07017	05910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5912	07018	05911	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0						
5913	07020	05912	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0						
5914	07021	05913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5915	07022	05914	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5916	07023	05915	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5917	07025	05916	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5918	07026	05917	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5919	07027	05918	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0						
5920	07028	05919	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5921	07029	05920	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5922	07030	05921	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5923	07031	05922	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5924	07032	05923	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						
5925	07033	05924	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0						

Table 165

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
5926	07034	05925	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5927	07035	05926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5928	07036	05927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5929	07037	05928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5930	07038	05929	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5931	07039	05930	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5932	07040	05931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5933	07041	05932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5934	07043	05933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5935	07044	05934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5936	07046	05935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5937	07047	05936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5938	07048	05937	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5939	07049	05938	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5940	07050	05939	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5941	07053	05940	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5942	07054	05941	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5943	07055	05942	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5944	07056	05943	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5945	07057	05944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5946	07058	05945	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5947	07059	05946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5948	07060	05947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5949	07061	05948	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5950	07062	05949	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5951	07063	05950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5952	07065	05951	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5953	07066	05952	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5954	07067	05953	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5955	07068	05954	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5956	07069	05955	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5957	07071	05956	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5958	07072	05957	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5959	07074	05958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5960	07075	05959	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								

Table 166

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AV	AW	AY	BABC	BE	BF	BG	BH	BI	BK
5962	07079	05961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5963	07080	05962	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5964	07081	05963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5965	07082	05964	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5966	07083	05965	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5967	07084	05966	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5968	07085	05967	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5969	07086	05968	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5970	07087	05969	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5971	07088	05970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5972	07089	05971	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5973	07091	05972	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5974	07093	05973	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5975	07094	05974	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5976	07095	05975	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5977	07096	05976	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5978	07097	05977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5979	07098	05978	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5980	07099	05979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5981	07100	05980	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5982	07101	05981	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5983	07102	05982	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5984	07103	05983	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5985	07104	05984	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5986	07105	05985	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
5987	07106	05986	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5988	07108	05987	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5989	07110	05988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5990	07111	05989	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5991	07112	05990	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5992	07113	05991	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5993	07114	05992	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5994	07115	05993	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5995	07116	05994	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5996	07117	05995	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
5997	07118	05996	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						

Table 167

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
5998	07119	05997	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
5999	07120	05998	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6000	07121	05999	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6001	07122	06000	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6002	07123	06001	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6003	07124	06002	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6004	07125	06003	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6005	07126	06004	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6006	07127	06005	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6007	07128	06006	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6008	07129	06007	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6009	07130	06008	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M16447	91.6	227	1	725	1550
6010	07131	06009	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6011	07132	06010	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6012	07133	06011	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6013	07134	06012	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6014	07135	06013	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6015	07136	06014	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6016	07137	06015	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6017	07138	06016	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6018	07139	06017	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6019	07140	06018	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6020	07141	06019	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6021	07142	06020	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6022	07143	06021	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6023	07144	06022	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6024	07145	06023	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6025	07146	06024	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6026	07147	06025	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6027	07150	06026	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6028	07151	06027	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6029	07152	06028	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6030	07153	06029	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6031	07154	06030	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6032	07156	06031	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0									

Table 168

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
6034	07158	06033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6035	07160	06034	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6036	07161	06035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6037	07162	06036	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6038	07163	06037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6039	07164	06038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6040	07165	06039	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6041	07166	06040	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6042	07167	06041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6043	07169	06042	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6044	07170	06043	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6045	07171	06044	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6046	07173	06045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6047	07174	06046	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6048	07175	06047	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6049	07178	06048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6050	07179	06049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6051	07180	06050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6052	07181	06051	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6053	07182	06052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6054	07183	06053	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6055	07185	06054	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6056	07186	06055	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6057	07187	06056	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6058	07188	06057	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6059	07192	06058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6060	07193	06059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6061	07194	06060	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6062	07195	06061	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6063	07196	06062	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6064	07199	06063	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6065	07200	06064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6066	07201	06065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6067	07202	06066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6068	07204	06067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 169

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
6070	07209	06069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6071	07210	06070	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6072	07211	06071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	19713	94.2	171	1	2239	2660
6073	07212	06072	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6074	07213	06073	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6075	07214	06074	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6076	07215	06075	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6077	07216	06076	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6078	07217	06077	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6079	07218	06078	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6080	07219	06079	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6081	07220	06080	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6082	07221	06081	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6083	07222	06082	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X68148	92.3	104	1	1502	3031
6084	07223	06083	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X65024	93.6	172	1	3234	3455
6085	07224	06084	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6086	07225	06085	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6087	07226	06086	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6088	07227	06087	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6089	07228	06088	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6090	07229	06089	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6091	07230	06090	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6092	07231	06091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	D21852	99.3	134	1	4139	4272
6093	07232	06092	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6094	07233	06093	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6095	07238	06094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6096	07241	06095	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6097	07243	06096	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6098	07244	06097	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	J05032	98.8	81	1	1573	2271
6099	07245	06098	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6100	07246	06099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6101	07249	06100	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6102	07250	06101	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6103	07251	06102	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6104	07253	06103	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6105	07257	06104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 170

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
6106	07259	06105	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6107	07261	06106	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1						
6108	07263	06107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6109	07264	06108	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6110	07265	06109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6111	07266	06110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6112	07267	06111	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6113	07268	06112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6114	07269	06113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6115	07270	06114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6116	07272	06115	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6117	07274	06116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6118	07275	06117	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6119	07276	06118	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6120	07277	06119	3		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1						
6121	07278	06120	4		0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0						
6122	07279	06121	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6123	07280	06122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6124	07281	06123	2		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1						
6125	07282	06124	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6126	07283	06125	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6127	07284	06126	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6128	07285	06127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6129	07286	06128	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6130	07287	06129	1		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0						
6131	07288	06130	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6132	07289	06131	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6133	07290	06132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6134	07291	06133	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6135	07292	06134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6136	07293	06135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6137	07294	06136	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
6138	07295	06137	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6139	07296	06138	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6140	07297	06139	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6141	07298	06140	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 171

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
6142	07299	06141	1																													
6143	07300	06142	1																													
6144	07301	06143	1																													
6145	07302	06144	2																													
6146	07303	06145	1																													
6147	07304	06146	1																													
6148	07305	06147	2																													
6149	07306	06148	1																													
6150	07307	06149	1																													
6151	07308	06150	1																													
6152	07309	06151	5																													
6153	07311	06152	1																													
6154	07312	06153	1																													
6155	07313	06154	1																													
6156	07315	06155	1																													
6157	07316	06156	1																													
6158	07317	06157	2																													
6159	07318	06158	1																													
6160	07319	06159	1																													
6161	07320	06160	2																													
6162	07321	06161	1																													
6163	07322	06162	1																													
6164	07323	06163	1																													
6165	07324	06164	1																													
6166	07325	06165	1																													
6167	07326	06166	1																													
6168	07327	06167	1																													
6169	07328	06168	2																													
6170	07329	06169	2																													
6171	07330	06170	1																													
6172	07331	06171	1																													
6173	07332	06172	2																													
6174	07333	06173	2																													
6175	07334	06174	1																													
6176	07335	06175	1																													
6177	07336	06176	1																													

Table 172

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
6178	07337	06177	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6179	07338	06178	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6180	07339	06179	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6181	07340	06180	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6182	07341	06181	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6183	07342	06182	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6184	07343	06183	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6185	07344	06184	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6186	07345	06185	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0							
6187	07346	06186	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6188	07348	06187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6189	07349	06188	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6190	07350	06189	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0						
6191	07351	06190	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0							
6192	07352	06191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6193	07353	06192	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6194	07354	06193	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0						
6195	07355	06194	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6196	07356	06195	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6197	07357	06196	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6198	07358	06197	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6199	07359	06198	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6200	07360	06199	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	D14659	95.2	147	1	885	1219	
6201	07361	06200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6202	07362	06201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6203	07363	06202	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6204	07364	06203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6205	07365	06204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6206	07366	06205	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6207	07367	06206	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6208	07368	06207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6209	07369	06208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6210	07370	06209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6211	07371	06210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6212	07372	06211	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6213	07373	06212	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0							

Table 173

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6214	07374	06213	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6215	07375	06214	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
6216	07376	06215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6217	07377	06216	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	2	0						
6218	07378	06217	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6219	07379	06218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6220	07380	06219	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6221	07381	06220	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6222	07382	06221	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6223	07383	06222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6224	07384	06223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6225	07385	06224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6226	07386	06225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6227	07387	06226	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6228	07388	06227	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0						
6229	07389	06228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6230	07390	06229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6231	07391	06230	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6232	07392	06231	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
6233	07393	06232	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6234	07394	06233	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6235	07395	06234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6236	07396	06235	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6237	07397	06236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6238	07398	06237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6239	07399	06238	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6240	07400	06239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6241	07401	06240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6242	07402	06241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6243	07403	06242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6244	07404	06243	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0						
6245	07405	06244	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6246	07406	06245	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6247	07407	06246	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6248	07408	06247	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6249	07409	06248	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						

Table 174

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6250	07410	06249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6251	07411	06250	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6252	07412	06251	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
6253	07413	06252	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0						
6254	07414	06253	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6255	07415	06254	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6256	07416	06255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6257	07417	06256	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
6258	07418	06257	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6259	07419	06258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6260	07420	06259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6261	07421	06260	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6262	07422	06261	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0						
6263	07423	06262	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6264	07424	06263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6265	07425	06264	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6266	07426	06265	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6267	07427	06266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6268	07429	06267	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6269	07430	06268	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0						
6270	07431	06269	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6271	07432	06270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6272	07433	06271	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6273	07434	06272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6274	07435	06273	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6275	07436	06274	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6276	07437	06275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6277	07438	06276	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6278	07439	06277	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6279	07440	06278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6280	07441	06279	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6281	07442	06280	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6282	07443	06281	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6283	07444	06282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6284	07445	06283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						
6285	07446	06284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0						

Table 175

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
6286	07447	06285	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6287	07448	06286	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6288	07449	06287	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6289	07450	06288	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6290	07451	06289	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6291	07452	06290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6292	07453	06291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6293	07454	06292	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6294	07455	06293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6295	07456	06294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6296	07457	06295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6297	07458	06296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6298	07459	06297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6299	07460	06298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6300	07461	06299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6301	07462	06300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6302	07463	06301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6303	07464	06302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6304	07465	06303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6305	07466	06304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6306	07467	06305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6307	07468	06306	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6308	07469	06307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6309	07470	06308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6310	07471	06309	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6311	07472	06310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6312	07473	06311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6313	07474	06312	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6314	07475	06313	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6315	07476	06314	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6316	07477	06315	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6317	07478	06316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6318	07479	06317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6319	07480	06318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6320	07481	06319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
6321	07483	06320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 176

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AU	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
6322	07484	06321	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	94.2	330	1	3032	3580
6323	07485	06322	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6324	07486	06323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6325	07487	06324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6326	07488	06325	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6327	07489	06326	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0					
6328	07490	06327	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6329	07491	06328	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6330	07492	06329	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6331	07493	06330	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6332	07494	06331	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6333	07495	06332	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6334	07496	06333	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6335	07497	06334	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6336	07498	06335	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6337	07499	06336	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6338	07500	06337	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6339	07501	06338	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6340	07502	06339	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6341	07503	06340	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6342	07504	06341	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6343	07505	06342	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6344	07506	06343	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6345	07507	06344	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6346	07508	06345	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6347	07509	06346	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6348	07510	06347	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6349	07511	06348	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6350	07512	06349	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6351	07513	06350	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6352	07514	06351	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6353	07515	06352	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6354	07516	06353	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6355	07517	06354	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6356	07518	06355	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					
6357	07520	06356	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0					

Table 177

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BAB	BC	BE	BF	BGBH	BI	BK
6358	07521	06357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6359	07522	06358	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6360	07523	06359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6361	07524	06360	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6362	07525	06361	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6363	07526	06362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6364	07527	06363	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6365	07528	06364	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6366	07529	06365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6367	07530	06366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6368	07531	06367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6369	07532	06368	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6370	07533	06369	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6371	07534	06370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6372	07535	06371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6373	07536	06372	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6374	07537	06373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6375	07538	06374	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6376	07539	06375	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6377	07540	06376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6378	07541	06377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6379	07543	06378	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6380	07544	06379	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6381	07545	06380	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6382	07546	06381	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6383	07547	06382	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6384	07548	06383	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6385	07549	06384	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6386	07550	06385	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6387	07551	06386	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6388	07552	06387	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0					
6389	07553	06388	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6390	07554	06389	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6391	07555	06390	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6392	07556	06391	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0					
6393	07557	06392	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0					

Table 178

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AJ	AK	AM	AO	AS	AW	AY	BAB	BC	BE	BF	BG	BH	BI	BK
6394	07558	06393	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M18172	97.5	161	1	674	834
6395	07559	06394	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6396	07560	06395	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6397	07561	06396	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6398	07562	06397	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6399	07563	06398	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6400	07564	06399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6401	07565	06400	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6402	07567	06401	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6403	07568	06402	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6404	07569	06403	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6405	07570	06404	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6406	07571	06405	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6407	07572	06406	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6408	07573	06407	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6409	07574	06408	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6410	07575	06409	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6411	07576	06410	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6412	07577	06411	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6413	07578	06412	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6414	07579	06413	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6415	07580	06414	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6416	07581	06415	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6417	07582	06416	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6418	07583	06417	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6419	07584	06418	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6420	07585	06419	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6421	07586	06420	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6422	07587	06421	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6423	07588	06422	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6424	07589	06423	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6425	07590	06424	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6426	07591	06425	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6427	07592	06426	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6428	07593	06427	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6429	07594	06428	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 179

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6430	07595	06429	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6431	07596	06430	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6432	07597	06431	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6433	07598	06432	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6434	07599	06433	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0							
6435	07600	06434	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6436	07601	06435	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6437	07602	06436	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6438	07603	06437	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6439	07604	06438	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6440	07605	06439	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6441	07606	06440	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6442	07607	06441	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6443	07608	06442	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6444	07609	06443	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6445	07610	06444	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6446	07611	06445	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6447	07612	06446	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6448	07613	06447	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6449	07614	06448	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6450	07615	06449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6451	07616	06450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6452	07617	06451	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6453	07619	06452	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6454	07620	06453	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6455	07621	06454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6456	07622	06455	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6457	07623	06456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6458	07624	06457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6459	07625	06458	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6460	07626	06459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6461	07627	06460	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6462	07628	06461	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6463	07629	06462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6464	07630	06463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6465	07631	06464	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							

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	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AQ	AS	AU	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6466	07632	06465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6467	07633	06466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6468	07634	06467	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6469	07635	06468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6470	07636	06469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6471	07637	06470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6472	07638	06471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6473	07639	06472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6474	07640	06473	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6475	07641	06474	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6476	07642	06475	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6477	07643	06476	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6478	07644	06477	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6479	07645	06478	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6480	07646	06479	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6481	07647	06480	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6482	07648	06481	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6483	07649	06482	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6484	07650	06483	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6485	07651	06484	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6486	07652	06485	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6487	07653	06486	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6488	07655	06487	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6489	07656	06488	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6490	07657	06489	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6491	07658	06490	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6492	07659	06491	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6493	07660	06492	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6494	07661	06493	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6495	07663	06494	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6496	07664	06495	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6497	07665	06496	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6498	07666	06497	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6499	07667	06498	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6500	07668	06499	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
6501	07669	06500	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 181

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
6502	07670	06501	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6503	07671	06502	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6504	07672	06503	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6505	07673	06504	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0					
6506	07674	06505	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6507	07675	06506	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6508	07676	06507	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6509	07677	06508	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6510	07678	06509	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6511	07679	06510	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6512	07680	06511	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6513	07681	06512	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6514	07682	06513	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6515	07683	06514	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6516	07684	06515	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6517	07686	06516	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6518	07687	06517	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6519	07688	06518	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6520	07689	06519	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6521	07690	06520	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6522	07691	06521	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6523	07692	06522	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6524	07693	06523	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6525	07694	06524	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6526	07695	06525	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6527	07696	06526	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6528	07697	06527	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6529	07698	06528	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6530	07699	06529	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6531	07700	06530	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6532	07701	06531	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6533	07702	06532	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6534	07703	06533	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6535	07704	06534	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6536	07705	06535	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					
6537	07708	06536	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0					

Table 182

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
6538	07709	06537	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6539	07710	06538	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6540	07711	06539	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
6541	07712	06540	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6542	07713	06541	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6543	07714	06542	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6544	07715	06543	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6545	07716	06544	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6546	07717	06545	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6547	07718	06546	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6548	07719	06547	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M75715	92.6	229	1	1762	2261
6549	07720	06548	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X14829	96.2	79	1	391	472
6550	07721	06549	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6551	07722	06550	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6552	07723	06551	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6553	07724	06552	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6554	07725	06553	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6555	07726	06554	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6556	07727	06555	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6557	07729	06556	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6558	07731	06557	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6559	07734	06558	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6560	07735	06559	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6561	07736	06560	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6562	07738	06561	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6563	07739	06562	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6564	07740	06563	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6565	07741	06564	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6566	07742	06565	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6567	07743	06566	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6568	07744	06567	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6569	07745	06568	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6570	07746	06569	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6571	07748	06570	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M14016	100	34	1	1164	1197
6572	07749	06571	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0												

Table 183

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
6574	07751	06573	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6575	07752	06574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6576	07753	06575	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6577	07754	06576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6578	07755	06577	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0						
6579	07756	06578	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0						
6580	07757	06579	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6581	07758	06580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6582	07759	06581	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6583	07760	06582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6584	07761	06583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6585	07762	06584	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6586	07763	06585	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6587	07764	06586	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6588	07765	06587	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	0	0						
6589	07766	06588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6590	07768	06589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6591	07769	06590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6592	07770	06591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6593	07771	06592	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0						
6594	07773	06593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6595	07774	06594	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6596	07775	06595	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6597	07776	06596	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6598	07777	06597	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6599	07778	06598	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0							
6600	07779	06599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6601	07780	06600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6602	07781	06601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6603	07782	06602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6604	07783	06603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6605	07785	06604	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6606	07786	06605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6607	07787	06606	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6608	07788	06607	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6609	07789	06608	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							

Table 184

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6610	07790	06609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6611	07792	06610	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6612	07793	06611	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6613	07794	06612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6614	07795	06613	6		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	5	0	M31732	98.5	66	1	1748	1813
6615	07796	06614	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6616	07797	06615	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6617	07798	06616	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6618	07800	06617	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6619	07801	06618	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6620	07802	06619	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0						
6621	07804	06620	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6622	07805	06621	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6623	07807	06622	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6624	07808	06623	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0						
6625	07810	06624	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6626	07811	06625	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6627	07812	06626	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6628	07813	06627	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6629	07814	06628	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6630	07815	06629	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6631	07816	06630	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	J05448	97.8	91	1	1669	1766
6632	07817	06631	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6633	07818	06632	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6634	07819	06633	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6635	07820	06634	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6636	07821	06635	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6637	07822	06636	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0						
6638	07823	06637	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6639	07824	06638	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6640	07826	06639	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6641	07827	06640	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	L07395	95.3	127	1	1265	2226
6642	07828	06641	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6643	07829	06642	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6644	07831	06643	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6645	07834	06644	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						

Table 185

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
6646	07835	06645	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0							
6647	07836	06646	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0							
6648	07837	06647	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6649	07838	06648	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6650	07839	06649	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0							
6651	07840	06650	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0							
6652	07841	06651	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6653	07844	06652	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6654	07845	06653	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6655	07848	06654	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0							
6656	07849	06655	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6657	07850	06656	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6658	07852	06657	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6659	07853	06658	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6660	07854	06659	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0							
6661	07855	06660	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		222555	94.2	278	1	2228	2566
6662	07856	06661	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6663	07857	06662	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6664	07858	06663	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		549355	94.4	284	1	1211	1558
6665	07859	06664	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6666	07860	06665	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6667	07861	06666	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6668	07862	06667	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6669	07863	06668	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6670	07864	06669	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6671	07865	06670	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6672	07866	06671	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6673	07868	06672	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6674	07869	06673	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6675	07870	06674	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6676	07871	06675	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6677	07872	06676	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6678	07875	06677	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		X63422	94.9	138	1	843	994
6679	07876	06678	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0		L20868	94.5	163	45	1043	1379
6680	07878	06679	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0							
6681	07879	06680	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0							

Table 186

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
6682	07880	06681	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	98.6	1	2360
6683	07881	06682	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6684	07882	06683	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				
6685	07883	06684	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0				
6686	07884	06685	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6687	07885	06686	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6688	07886	06687	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6689	07887	06688	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6690	07889	06689	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6691	07890	06690	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6692	07891	06691	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6693	07892	06692	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6694	07893	06693	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6695	07894	06694	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6696	07895	06695	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6697	07896	06696	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6698	07897	06697	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6699	07898	06698	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6700	07900	06699	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6701	07901	06700	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6702	07902	06701	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0				
6703	07903	06702	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6704	07904	06703	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6705	07905	06704	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6706	07909	06705	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6707	07911	06706	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6708	07912	06707	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6709	07913	06708	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6710	07915	06709	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6711	07916	06710	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6712	07917	06711	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6713	07918	06712	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6714	07919	06713	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6715	07920	06714	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6716	07921	06715	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0				
6717	07922	06716	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0				

Table 187

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
6718	07923	06717	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0					
6719	07925	06718	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6720	07927	06719	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6721	07928	06720	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6722	07932	06721	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6723	07933	06722	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6724	07934	06723	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6725	07935	06724	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6726	07936	06725	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0			91.9	62	1	3457
6727	07937	06726	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6728	07938	06727	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0						
6729	07939	06728	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6730	07941	06729	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6731	07942	06730	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6732	07944	06731	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6733	07945	06732	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6734	07946	06733	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6735	07948	06734	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6736	07949	06735	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6737	07951	06736	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6738	07952	06737	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6739	07953	06738	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6740	07954	06739	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6741	07955	06740	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6742	07956	06741	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6743	07957	06742	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6744	07958	06743	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6745	07959	06744	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6746	07960	06745	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6747	07961	06746	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6748	07963	06747	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6749	07964	06748	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6750	07965	06749	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6751	07966	06750	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6752	07967	06751	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6753	07969	06752	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						

Table 188

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AU	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
6754	07971	06753	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0								
6755	07973	06754	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6756	07974	06755	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6757	07975	06756	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6758	07976	06757	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6759	07977	06758	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6760	07981	06759	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6761	07986	06760	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	3	0	0							
6762	07987	06761	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6763	07988	06762	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6764	07989	06763	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6765	07990	06764	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6766	07991	06765	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6767	07992	06766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6768	07994	06767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6769	07995	06768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6770	07997	06769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6771	07998	06770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6772	07999	06771	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6773	08000	06772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0								
6774	08001	06773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6775	08002	06774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6776	08003	06775	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6777	08004	06776	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6778	08005	06777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6779	08006	06778	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6780	08007	06779	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6781	08008	06780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6782	08009	06781	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6783	08010	06782	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0							
6784	08011	06783	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0							
6785	08012	06784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0							
6786	08013	06785	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0							
6787	08014	06786	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0							
6788	08015	06787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0							
6789	08016	06788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0							

Table 189

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
6790	08017	06789	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6791	08018	06790	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6792	08019	06791	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6793	08020	06792	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6794	08021	06793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6795	08022	06794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6796	08023	06795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6797	08024	06796	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6798	08025	06797	27		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6799	08026	06798	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6800	08027	06799	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6801	08028	06800	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6802	08029	06801	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6803	08030	06802	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6804	08031	06803	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6805	08032	06804	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6806	08033	06805	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6807	08034	06806	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6808	08036	06807	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6809	08037	06808	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6810	08038	06809	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6811	08039	06810	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6812	08040	06811	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6813	08041	06812	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6814	08042	06813	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6815	08043	06814	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6816	08044	06815	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6817	08045	06816	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6818	08046	06817	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6819	08047	06818	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6820	08048	06819	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6821	08049	06820	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6822	08050	06821	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6823	08051	06822	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6824	08052	06823	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6825	08053	06824	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 190

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
6826	08054	06825	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6827	08055	06826	7		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5						
6828	08056	06827	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	L13463	99.5	207	1	1139	1345
6829	08057	06828	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6830	08058	06829	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6831	08059	06830	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6832	08060	06831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6833	08061	06832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6834	08062	06833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6835	08063	06834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6836	08064	06835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6837	08065	06836	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M10036	93.2	103	1	1462	1835
6838	08066	06837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6839	08067	06838	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6840	08068	06839	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6841	08069	06840	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6842	08070	06841	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6843	08071	06842	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6844	08073	06843	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6845	08074	06844	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6846	08075	06845	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6847	08076	06846	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6848	08077	06847	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6849	08078	06848	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6850	08079	06849	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6851	08080	06850	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6852	08081	06851	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6853	08082	06852	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6854	08083	06853	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
6855	08084	06854	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6856	08085	06855	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6857	08086	06856	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6858	08087	06857	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6859	08088	06858	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
6860	08089	06859	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X13425	94.4	250	1	1364	1793
6861	08090	06860	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 191

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AC	AS	AL	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
6862	08091	06861	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	013627	97.8	225	1	1597	1821
6863	08092	06862	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6864	08093	06863	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6865	08094	06864	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6866	08095	06865	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0						
6867	08096	06866	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6868	08097	06867	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6869	08098	06868	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6870	08099	06869	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6871	08100	06870	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6872	08101	06871	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6873	08102	06872	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6874	08103	06873	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6875	08104	06874	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0						
6876	08105	06875	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6877	08107	06876	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6878	08108	06877	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6879	08109	06878	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6880	08110	06879	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6881	08111	06880	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6882	08112	06881	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6883	08113	06882	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6884	08114	06883	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6885	08115	06884	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6886	08116	06885	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6887	08117	06886	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6888	08118	06887	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6889	08119	06888	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6890	08120	06889	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6891	08121	06890	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6892	08122	06891	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6893	08123	06892	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6894	08124	06893	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6895	08125	06894	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6896	08126	06895	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
6897	08127	06896	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						

Table 192

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	ABC	BE	BF	BG	BH	BI	BK
6898	08128	06897	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6899	08129	06898	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6900	08130	06899	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6901	08131	06900	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6902	08132	06901	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6903	08133	06902	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6904	08134	06903	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6905	08135	06904	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0							
6906	08136	06905	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6907	08137	06906	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6908	08138	06907	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6909	08139	06908	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6910	08140	06909	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6911	08141	06910	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6912	08142	06911	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6913	08143	06912	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6914	08144	06913	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6915	08145	06914	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6916	08146	06915	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0							
6917	08147	06916	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6918	08148	06917	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6919	08149	06918	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6920	08150	06919	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6921	08151	06920	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6922	08153	06921	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6923	08154	06922	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6924	08155	06923	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6925	08156	06924	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6926	08157	06925	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6927	08158	06926	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6928	08159	06927	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6929	08160	06928	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6930	08161	06929	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6931	08162	06930	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6932	08163	06931	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
6933	08164	06932	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							

Table 193

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6934	08165	06933	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6935	08166	06934	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6936	08167	06935	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6937	08168	06936	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6938	08169	06937	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6939	08170	06938	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6940	08172	06939	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6941	08173	06940	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6942	08174	06941	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6943	08175	06942	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6944	08176	06943	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6945	08177	06944	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6946	08178	06945	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6947	08179	06946	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6948	08180	06947	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6949	08181	06948	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6950	08182	06949	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6951	08184	06950	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6952	08185	06951	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6953	08186	06952	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6954	08188	06953	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6955	08189	06954	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6956	08190	06955	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6957	08191	06956	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6958	08192	06957	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6959	08193	06958	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6960	08194	06959	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6961	08195	06960	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6962	08196	06961	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6963	08197	06962	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6964	08198	06963	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6965	08199	06964	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6966	08200	06965	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6967	08201	06966	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6968	08202	06967	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6969	08203	06968	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 194

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
6970	08204	06969	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6971	08205	06970	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6972	08206	06971	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6973	08207	06972	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6974	08208	06973	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6975	08209	06974	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6976	08210	06975	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6977	08211	06976	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6978	08212	06977	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6979	08213	06978	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6980	08214	06979	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6981	08215	06980	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6982	08216	06981	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	M15800	98.6	69	1	983	1051
6983	08217	06982	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6984	08218	06983	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6985	08219	06984	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6986	08220	06985	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6987	08221	06986	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6988	08222	06987	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6989	08223	06988	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6990	08224	06989	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6991	08225	06990	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6992	08226	06991	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6993	08227	06992	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6994	08228	06993	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6995	08229	06994	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6996	08230	06995	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6997	08232	06996	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6998	08233	06997	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
6999	08234	06998	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7000	08235	06999	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7001	08236	07000	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7002	08237	07001	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7003	08238	07002	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7004	08239	07003	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7005	08240	07004	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						

Table 195

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	ABC	BE	BF	BGBH	BI	BK
7006	08241	07005	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7007	08242	07006	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7008	08243	07007	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7009	08244	07008	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7010	08245	07009	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7011	08246	07010	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7012	08247	07011	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7013	08248	07012	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7014	08249	07013	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7015	08250	07014	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7016	08251	07015	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7017	08252	07016	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7018	08253	07017	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7019	08254	07018	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7020	08255	07019	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7021	08256	07020	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7022	08257	07021	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7023	08258	07022	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7024	08259	07023	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7025	08260	07024	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7026	08261	07025	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7027	08262	07026	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7028	08263	07027	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7029	08264	07028	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7030	08265	07029	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7031	08266	07030	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7032	08267	07031	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7033	08268	07032	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7034	08269	07033	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7035	08270	07034	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7036	08271	07035	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7037	08272	07036	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7038	08273	07037	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7039	08274	07038	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7040	08275	07039	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
7041	08276	07040	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 196

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	ACA	AE	AG	AI	AK	AM	AO	AS	AL	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7042	08277	07041	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0							
7043	08278	07042	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0						
7044	08279	07043	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0						
7045	08280	07044	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7046	08281	07045	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
7047	08282	07046	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
7048	08283	07047	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7049	08284	07048	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7050	08285	07049	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7051	08286	07050	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7052	08287	07051	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7053	08288	07052	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
7054	08289	07053	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7055	08290	07054	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7056	08291	07055	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7057	08292	07056	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7058	08293	07057	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7059	08294	07058	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
7060	08295	07059	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7061	08296	07060	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7062	08297	07061	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
7063	08298	07062	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7064	08299	07063	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7065	08300	07064	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7066	08301	07065	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7067	08302	07066	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7068	08303	07067	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7069	08304	07068	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7070	08305	07069	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7071	08306	07070	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7072	08307	07071	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7073	08308	07072	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7074	08309	07073	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7075	08310	07074	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7076	08311	07075	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						
7077	08312	07076	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0						

Table 197

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK	
7078	08313	07077	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.8	328	1	2147	2472
7079	08314	07078	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7080	08315	07079	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7081	08316	07080	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7082	08317	07081	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7083	08318	07082	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7084	08319	07083	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4	310	1	1290	1866
7085	08320	07084	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7086	08321	07085	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7087	08322	07086	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7088	08323	07087	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7089	08324	07088	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7090	08325	07089	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7091	08326	07090	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7092	08327	07091	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7093	08328	07092	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7094	08329	07093	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7095	08330	07094	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7096	08331	07095	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7097	08332	07096	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7098	08333	07097	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7099	08334	07098	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7100	08335	07099	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7101	08336	07100	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.3	296	1	344	1182
7102	08337	07101	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.9	295	1	1293	1652
7103	08338	07102	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7104	08339	07103	9		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7105	08340	07104	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2	413	1	874	1639
7106	08341	07105	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7107	08342	07106	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7108	08343	07107	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100	297	1	34	448
7109	08344	07108	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7110	08345	07109	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7111	08346	07110	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7112	08347	07111	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7113	08348	07112	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					

Table 198

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
7114	08349	07113	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	X17519	98.4	306	1	1624	2323
7115	08350	07114	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7116	08351	07115	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7117	08352	07116	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
7118	08353	07117	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7119	08354	07118	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7120	08355	07119	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7121	08356	07120	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	M62505	97.1	204	1	2110	2328
7122	08357	07121	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7123	08358	07122	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7124	08359	07123	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7125	08360	07124	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7126	08361	07125	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7127	08362	07126	16		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16	0	0	X55720	100	85	1	2450	2546
7128	08363	07127	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7129	08364	07128	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7130	08365	07129	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7131	08366	07130	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7132	08367	07131	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	L14076	95.8	337	1	1507	2076
7133	08368	07132	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7134	08369	07133	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7135	08371	07134	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7136	08372	07135	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7137	08373	07136	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7138	08374	07137	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7139	08375	07138	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	M69043	99.3	301	1	1250	1550
7140	08376	07139	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7141	08377	07140	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7142	08378	07141	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7143	08379	07142	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7144	08380	07143	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
7145	08381	07144	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7146	08382	07145	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7147	08383	07146	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	U00115	97.2	180	1	3034	3536
7148	08384	07147	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7149	08385	07148	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						

Table 199

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7150	08386	07149	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7151	08387	07150	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7152	08388	07151	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7153	08389	07152	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1	0						
7154	08390	07153	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7155	08391	07154	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7156	08392	07155	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7157	08393	07156	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X71427	95.5	292	1	934	1678
7158	08394	07157	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7159	08395	07158	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7160	08396	07159	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	X75304	98.9	90	1	###	10300
7161	08397	07160	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7162	08398	07161	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7163	08399	07162	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7164	08400	07163	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	L08238	96.7	123	1	2681	2805
7165	08402	07164	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7166	08403	07165	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7167	08404	07166	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7168	08405	07167	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7169	08406	07168	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7170	08407	07169	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7171	08408	07170	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7172	08409	07171	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7173	08410	07172	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7174	08411	07173	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7175	08412	07174	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7176	08413	07175	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7177	08414	07176	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7178	08415	07177	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7179	08416	07178	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7180	08417	07179	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7181	08418	07180	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	M84721	99.4	345	1	3260	3680
7182	08419	07181	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7183	08420	07182	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7184	08421	07183	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7185	08422	07184	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 200

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AU	AW	AY	BABC	BE	BF	BG	BH	BI	BK
7186	08423	07185	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7187	08424	07186	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0					
7188	08425	07187	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7189	08426	07188	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7190	08427	07189	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7191	08428	07190	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7192	08429	07191	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7193	08430	07192	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7194	08431	07193	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7195	08432	07194	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0					
7196	08434	07195	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7197	08435	07196	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0					
7198	08436	07197	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7199	08437	07198	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7200	08438	07199	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0					
7201	08439	07200	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7202	08440	07201	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7203	08441	07202	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7204	08442	07203	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7205	08443	07204	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7206	08444	07205	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0					
7207	08445	07206	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7208	08446	07207	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7209	08447	07208	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7210	08448	07209	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7211	08449	07210	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7212	08450	07211	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7213	08451	07212	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7214	08452	07213	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7215	08453	07214	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7216	08454	07215	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7217	08455	07216	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7218	08456	07217	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7219	08457	07218	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7220	08458	07219	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0					
7221	08459	07220	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					

Table 201

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AU	AW	AY	BABC	BE	BF	BG	BH	BI	BK
7222	08460	07221	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
7223	08461	07222	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7224	08462	07223	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7225	08463	07224	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7226	08464	07225	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7227	08465	07226	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7228	08466	07227	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7229	08467	07228	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7230	08468	07229	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7231	08469	07230	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7232	08470	07231	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
7233	08471	07232	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7234	08472	07233	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7235	08473	07234	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7236	08474	07235	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7237	08475	07236	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7238	08476	07237	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7239	08477	07238	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
7240	08478	07239	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7241	08479	07240	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7242	08480	07241	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7243	08481	07242	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7244	08482	07243	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7245	08483	07244	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7246	08484	07245	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7247	08485	07246	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7248	08486	07247	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7249	08487	07248	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7250	08488	07249	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7251	08489	07250	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7252	08490	07251	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7253	08491	07252	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7254	08492	07253	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7255	08493	07254	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7256	08494	07255	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0													

Table 202

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK
7258	08496	07257	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7259	08497	07258	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7260	08498	07259	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7261	08499	07260	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7262	08500	07261	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7263	08501	07262	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7264	08502	07263	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7265	08503	07264	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7266	08504	07265	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7267	08505	07266	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7268	08506	07267	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7269	08507	07268	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7270	08508	07269	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7271	08509	07270	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7272	08510	07271	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7273	08511	07272	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7274	08512	07273	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7275	08513	07274	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7276	08514	07275	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7277	08515	07276	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7278	08516	07277	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7279	08517	07278	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7280	08518	07279	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7281	08519	07280	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7282	08520	07281	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7283	08521	07282	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7284	08522	07283	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7285	08523	07284	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7286	08524	07285	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7287	08525	07286	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7288	08526	07287	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7289	08527	07288	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7290	08528	07289	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7291	08529	07290	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7292	08530	07291	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7293	08531	07292	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 203

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
7294	08532	07293	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7295	08533	07294	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7296	08534	07295	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7297	08535	07296	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7298	08536	07297	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7299	08537	07298	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7300	08538	07299	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7301	08539	07300	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7302	08540	07301	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7303	08541	07302	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7304	08542	07303	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7305	08543	07304	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7306	08544	07305	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7307	08545	07306	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7308	08546	07307	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	06633	95.2	310	1	1124	1724
7309	08547	07308	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7310	08548	07309	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7311	08549	07310	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7312	08550	07311	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7313	08551	07312	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7314	08552	07313	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7315	08553	07314	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	06696	99.5	208	1	1524	1784
7316	08554	07315	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7317	08555	07316	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7318	08556	07317	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7319	08557	07318	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7320	08558	07319	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7321	08559	07320	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7322	08560	07321	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7323	08561	07322	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7324	08563	07323	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	03619	98.3	357	1	1932	2295
7325	08564	07324	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7326	08565	07325	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7327	08566	07326	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7328	08567	07327	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7329	08568	07328	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 204

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
7330	08569	07329	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7331	08570	07330	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7332	08571	07331	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7333	08572	07332	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7334	08573	07333	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7335	08574	07334	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7336	08575	07335	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7337	08576	07336	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7338	08577	07337	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7339	08578	07338	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7340	08579	07339	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7341	08580	07340	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7342	08581	07341	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7343	08582	07342	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7344	08583	07343	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7345	08584	07344	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7346	08585	07345	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7347	08586	07346	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7348	08587	07347	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7349	08588	07348	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7350	08589	07349	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7351	08591	07350	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7352	08592	07351	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		003779	96.3	375	1	4622	5508
7353	08593	07352	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7354	08594	07353	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7355	08595	07354	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7356	08596	07355	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7357	08597	07356	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7358	08598	07357	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7359	08599	07358	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7360	08600	07359	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7361	08601	07360	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7362	08602	07361	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7363	08603	07362	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7364	08604	07363	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
7365	08605	07364	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							

Table 205

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
7366	08606	07365	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7367	08607	07366	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0					
7368	08608	07367	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7369	08609	07368	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
7370	08610	07369	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7371	08611	07370	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7372	08612	07371	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7373	08613	07372	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7374	08614	07373	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7375	08615	07374	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7376	08616	07375	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7377	08617	07376	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7378	08618	07377	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7379	08619	07378	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7380	08620	07379	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7381	08621	07380	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7382	08622	07381	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7383	08623	07382	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7384	08624	07383	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7385	08625	07384	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7386	08626	07385	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7387	08627	07386	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7388	08628	07387	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7389	08629	07388	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7390	08630	07389	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7391	08631	07390	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7392	08632	07391	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7393	08633	07392	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7394	08634	07393	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7395	08635	07394	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7396	08636	07395	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7397	08637	07396	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7398	08638	07397	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7399	08639	07398	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7400	08640	07399	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7401	08641	07400	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					

Table 206

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK		
7402	08642	07401	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	016626	99.7	321	1	2765	3085	
7403	08643	07402	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7404	08644	07403	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7405	08645	07404	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7406	08646	07405	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7407	08647	07406	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7408	08648	07407	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7409	08649	07408	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7410	08650	07409	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7411	08651	07410	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7412	08652	07411	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7413	08653	07412	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7414	08654	07413	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7415	08655	07414	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7416	08656	07415	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7417	08657	07416	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7418	08658	07417	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7419	08659	07418	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7420	08660	07419	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7421	08661	07420	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7422	08662	07421	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7423	08663	07422	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	X52151	99.3	134	1	1868	2022
7424	08664	07423	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
7425	08665	07424	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7426	08666	07425	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7427	08667	07426	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7428	08668	07427	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	X59834	97.6	248	1	1124	2727
7429	08669	07428	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7430	08670	07429	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7431	08671	07430	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7432	08673	07431	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7433	08674	07432	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	M93056	94.3	353	1	955	1316
7434	08675	07433	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7435	08676	07434	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7436	08677	07435	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7437	08678	07436	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						

Table 207

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AM	AC	AS	AL	AW	AY	B	ABC	BE	BF	BG	BH	BI	BK
7438	08679	07437	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	02426	98.6	360	1	1209	1599
7439	08680	07438	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	03571	94.7	266	1	2220	2484
7440	08681	07439	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7441	08682	07440	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7442	08683	07441	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7443	08684	07442	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1						
7444	08685	07443	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7445	08686	07444	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7446	08687	07445	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7447	08688	07446	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0						
7448	08689	07447	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7449	08690	07448	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7450	08691	07449	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7451	08692	07450	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7452	08693	07451	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7453	08694	07452	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7454	08695	07453	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7455	08696	07454	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7456	08697	07455	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7457	08698	07456	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7458	08699	07457	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7459	08700	07458	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0						
7460	08701	07459	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7461	08702	07460	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	024804	100	79	1	704	782
7462	08703	07461	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0						
7463	08704	07462	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7464	08705	07463	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7465	08706	07464	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7466	08707	07465	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7467	08708	07466	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7468	08709	07467	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7469	08710	07468	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	061831	96.3	405	8	1798	2211
7470	08711	07469	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7471	08712	07470	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7472	08713	07471	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						
7473	08714	07472	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0						

Table 208

Table 209

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	B	BC	BE	BF	BG	BH	BI	BK	
7510	08751	07509	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7511	08752	07510	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7512	08753	07511	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7513	08754	07512	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7514	08755	07513	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7515	08756	07514	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7516	08757	07515	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7517	08758	07516	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7518	08759	07517	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	D00760	97.5	326	1	541	866
7519	08760	07518	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7520	08761	07519	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7521	08762	07520	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7522	08763	07521	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7523	08764	07522	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7524	08765	07523	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7525	08766	07524	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7526	08768	07525	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7527	08769	07526	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	M77836	99	303	1	1491	1792
7528	08770	07527	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7529	08771	07528	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7530	08772	07529	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7531	08773	07530	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	M27937	98.7	311	1	326	832
7532	08774	07531	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7533	08775	07532	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7534	08777	07533	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7535	08778	07534	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7536	08779	07535	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7537	08780	07536	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7538	08781	07537	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7539	08782	07538	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7540	08783	07539	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7541	08785	07540	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7542	08786	07541	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7543	08787	07542	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7544	08788	07543	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	M87339	90.3	298	1	1051	1446
7545	08789	07544	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						

Table 210

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
7546	08790	07545	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7547	08791	07546	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7548	08792	07547	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7549	08793	07548	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7550	08794	07549	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7551	08795	07550	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1					
7552	08796	07551	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4						
7553	08797	07552	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7554	08798	07553	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7555	08799	07554	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7556	08800	07555	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7557	08801	07556	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7558	08802	07557	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7559	08803	07558	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7560	08804	07559	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7561	08805	07560	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7562	08807	07561	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7563	08808	07562	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7564	08809	07563	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7565	08810	07564	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7566	08811	07565	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7567	08812	07566	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7568	08813	07567	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7569	08814	07568	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7570	08815	07569	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7571	08816	07570	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7572	08817	07571	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7573	08818	07572	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7574	08819	07573	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7575	08820	07574	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7576	08821	07575	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7577	08822	07576	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7578	08823	07577	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7579	08824	07578	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7580	08825	07579	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7581	08826	07580	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						

Table 211

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7582	08827	07581	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7583	08828	07582	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7584	08829	07583	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7585	08830	07584	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7586	08831	07585	4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0					
7587	08832	07586	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7588	08833	07587	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7589	08834	07588	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7590	08835	07589	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7591	08836	07590	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7592	08837	07591	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7593	08838	07592	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7594	08839	07593	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7595	08840	07594	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7596	08841	07595	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7597	08842	07596	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7598	08843	07597	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7599	08844	07598	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7600	08845	07599	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7601	08846	07600	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7602	08848	07601	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7603	08849	07602	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7604	08850	07603	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7605	08851	07604	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7606	08852	07605	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7607	08853	07606	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7608	08854	07607	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7609	08855	07608	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7610	08856	07609	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7611	08857	07610	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7612	08858	07611	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7613	08859	07612	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7614	08860	07613	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7615	08861	07614	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7616	08862	07615	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7617	08863	07616	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						

Table 212

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AB	AG	AI	AK	AM	AO	AS	AJ	AV	AW	AY	BABC	BE	BF	BG	BH	BI	BK	
7618	08864	07617	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0X68742	94.1	101	1	263	3453	
7619	08865	07618	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7620	08866	07619	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7621	08867	07620	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7622	08868	07621	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7623	08869	07622	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7624	08870	07623	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7625	08871	07624	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7626	08872	07625	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7627	08873	07626	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7628	08874	07627	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7629	08875	07628	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7630	08876	07629	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7631	08877	07630	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7632	08878	07631	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7633	08879	07632	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7634	08880	07633	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7635	08881	07634	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7636	08882	07635	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7637	08883	07636	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7638	08884	07637	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7639	08885	07638	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7640	08886	07639	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7641	08887	07640	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7642	08888	07641	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7643	08889	07642	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7644	08890	07643	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7645	08891	07644	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7646	08892	07645	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7647	08893	07646	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7648	08894	07647	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7649	08895	07648	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7650	08896	07649	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7651	08897	07650	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7652	08898	07651	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
7653	08899	07652	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 214

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BABC	BE	BF	BGBH	BI	BK
7690	08939	07689	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7691	08940	07690	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7692	08941	07691	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7693	08942	07692	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7694	08943	07693	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7695	08944	07694	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7696	08945	07695	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7697	08946	07696	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7698	08947	07697	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7699	08948	07698	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7700	08949	07699	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7701	08950	07700	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7702	08951	07701	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7703	08952	07702	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7704	08953	07703	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7705	08954	07704	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7706	08955	07705	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7707	08956	07706	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7708	08957	07707	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7709	08958	07708	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7710	08959	07709	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7711	08960	07710	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7712	08961	07711	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7713	08962	07712	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7714	08963	07713	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7715	08964	07714	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7716	08965	07715	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7717	08966	07716	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7718	08967	07717	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7719	08968	07718	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7720	08969	07719	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7721	08970	07720	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7722	08971	07721	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7723	08972	07722	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7724	08973	07723	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
7725	08974	07724	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0				
																							</								

Table 215

Table 216

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK	
7762	09011	07761	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7763	09012	07762	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7764	09013	07763	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0					
7765	09014	07764	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0					
7766	09015	07765	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7767	09016	07766	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7768	09017	07767	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7769	09018	07768	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7770	09019	07769	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	98.6	69	4	725	793	
7771	09020	07770	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7772	09021	07771	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7773	09022	07772	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7774	09023	07773	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7775	09024	07774	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7776	09025	07775	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7777	09026	07776	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7778	09027	07777	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	91.5	199	3	1219	1450	
7779	09028	07778	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7780	09029	07779	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7781	09030	07780	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7782	09031	07781	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7783	09032	07782	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	95.1	265	56	989	1568	
7784	09033	07783	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7785	09034	07784	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7786	09035	07785	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7787	09036	07786	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7788	09037	07787	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7789	09038	07788	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7790	09039	07789	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	93	256	1	423	683	
7791	09040	07790	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	M21302	100	123	1	1555	1681
7792	09041	07791	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7793	09042	07792	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0						
7794	09043	07793	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7795	09044	07794	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7796	09045	07795	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						
7797	09046	07796	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0						

Table 217

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BABC	BE	BF	BG	BH	BI	BK
7798	09047	07797	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	MG0047	95	261	1	103	1163
7799	09048	07798	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7800	09049	07799	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7801	09050	07800	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3						
7802	09051	07801	8		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	8	J00269	94.6	351	1	1268	1617
7803	09052	07802	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7804	09053	07803	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7805	09054	07804	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7806	09055	07805	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7807	09056	07806	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	M93150	98.8	169	1	1576	2360
7808	09057	07807	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7809	09058	07808	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7810	09059	07809	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7811	09060	07810	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7812	09061	07811	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7813	09062	07812	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	X04790	98.5	326	1	2116	2458
7814	09063	07813	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7815	09064	07814	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7816	09065	07815	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7817	09066	07816	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7818	09067	07817	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7819	09068	07818	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7820	09069	07819	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7821	09070	07820	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7822	09071	07821	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7823	09072	07822	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7824	09073	07823	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3						
7825	09074	07824	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7826	09075	07825	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2						
7827	09076	07826	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7828	09077	07827	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	X04098	93.2	325	1	1551	1918
7829	09078	07828	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	D13638	91	78	1	3793	5167
7830	09079	07829	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7831	09080	07830	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	J04605	97.6	123	1	1627	1888
7832	09081	07831	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	X02902	98.2	337	1	584	1181
7833	09082	07832	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						

Table 218

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AQ	AS	AW	AY	BA	BC	BE	BF	BG	BH	BI	BK
7834	09083	07833	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7835	09084	07834	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7836	09085	07835	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	X56976	92 287	1	3066	3419	
7837	09086	07836	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						
7838	09087	07837	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1						

Table 219

SEQ ID NO:1

LENGTH:704

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00001

SEQUENCE DESCRIPTION:

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GATCTTCAAA CAAGCATCAG CGTTTTCCAG GGCTTCCCAG AGGTCTGTGC GACTAGCCCG 60
TGCTATCAA AAGTTATTAG AGAGGATGAA GCATTAGCTT GAAGCACTAC AGGAGGAATG 120
CACCACGGCA GCTCTCCGCC AATTTCTCTC AGATTTCAC AGAGACTGTT TGAATGTTTT 180
CAAAACCAAG TATCACACTT TAATGTACAT GGGCCGCACC ATAATGAGAT GTGAGCCTTG 240
TGCATGTGGG GGAGGAGGGA GAGAGATGTA CTTTTTAAAT CATGTTCCCC CTAAACATGG 300
CTGTTAACCC ACTTGCATGC AGAAACTTGG GATGTCACTT GCCTGACATT CACTTCCAG 360
GAGAGGACCC TATCCCCAAA TGTGGAATTG ACTTGCCTAT GGCCAAGGTC CCTTGGNAAA 420
GGGAGCTTCA GTATTTGTGG GGGCNCATA AAACCATGGN TTCAAGNCAA TCCAGCCTCA 480
TNGGGNNGGT CCTGGGNACA GTTTTTTGGT AAAGGCCCTT GGCCAGNTG GGGGGAATGG 540
GCCTCCTTTT TAAGNTTGGG GNTGGAATNG TCTNGCAAAT TGGGGCTCCC ATTCNCGGG 600
GGTTTGGGGG TTTTNGGGG CCTTNCCNGG NNGGAAGGGN TGGGTTGGG GGNTNGGTTN 660
CCNTTGGGNG GGCCTGGGGN TTTGATTNA CCCGGGNCCT NGGN 704
```

SEQ ID NO:2

LENGTH:659

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00002

SEQUENCE DESCRIPTION:

```
GATCTTTAAA ATACACTC AAATCAAGAA ACTTAAGGTT ACCTTNTTC CCAAATTTCA 60
TACCTATCAT CTTAAGTAGG GACTTCTGTC TTCACAACAN ATTATNACCT TACAGAAGTT 120
TGAATTATCC GGTGCGGTTT TATTGTTTAA AATCATTCT GCATCAGCTG CTGAAACAAC 180
AAATAGGAAT TGTTTTATG GAGGCTTTGC ATAGATCCC TGAGCAGGAT TTTAATCTTT 240
TNCTAACTGG ACTGGTTCAA ATGTTGTNCT CTTCTTTAAA GGGATGGCAA GATGTGGGCA 300
GTGATGTCAC TTAGGGCAGG GACAGGATAA GAGGNTTAG GGAGAGAAGA TAGCAGGGCA 360
TGGCTGGGAA CCAAGTCCA AGCATACCAA CACGGAGCAG GCTACTGTCA AGCTCCCCTC 420
GGAGGCGGNG CTGGTTCACA GCCAGCTGGC ACCAGNTTT NTNGNGGAAG NCTTTTCAA 480
ACAGTCTCAG GNAATCCAAT NTGCAAAGAC TTGCTTNAG NAAAACCCAG NAGTTGAAAG 540
GCTCCCAAGN ATTTAAGGG NACTTNCCAA AACGGGGCCC CNGGNCCCTT TTGGGTTNG 600
GGNTCAAAA CCCCGGAGGG GTTTGGGAAG NTTTAATTG GNTTTAAAN ATNNNTNTN 659
```

SEQ ID NO:3

LENGTH:625

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00003

SEQUENCE DESCRIPTION:

```
GATCTAACTG GGTACCTGAG ATATTNACA GCTGGACCTA GTTTCACAAT CTGTTGTCTC 60
```

CAGCTCTGCA TATGTCTGGC CAGGGGGCTT CTAGGAAGTA GGTTCATCT ATCAAATGTC 120
 TCCTCTGACT TCCTTTTGAA ACTTACTGCT CTTCTGTTTT ATTTTGT TTTGAAGCT 180
 CAGAGGGAGA TGGGCAATTG ACAGGGATGC AATCCAGGGT GGGATTCTT GAGGAAGTTA 240
 CAAATAAGCT TGTACAACA TCAAGATAGA TGGAAATTGA AGGATGCTAC CAGGAGAGTA 300
 CTTACATAGT GCTCAGGAGT TTCTCTTCTT AAAATGTTA CTGCTGAAAG ATGAGCAGGA 360
 CCAGGGCGTT ATAGGCAGAG CCCTAGCCGA GAAACCTGCT GGCCTCTGCC TGTTTTATT 420
 TCCCACTTTT GGTGTTGTG GCATTACTTT CAGAATTGTC ACTTCTCTGC TTGTCATGAC 480
 TTTTTGGCA CACTTGCCAT GACGGGTGTT TCTGNGAACC ATGGAAGTTT TCGGGTAGTG 540
 CCTCCAGGGG CAGGGGGNAA GGAGNGGTG TANCTGCATT TNGTNCAAAAT AAATCCNGCC 600
 TATTGTTAAT NAACCACTCT TTTGN 625

SEQ ID NO:4

LENGTH:256

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00004

SEQUENCE DESCRIPTION:

GATCTGCCAG GCTGGGGTGT TTTCGGTATC TGCTGTTTAC AGGTCTCCAC TGTAATCCGA 60
 ATACTTTGCC AGTGCACTAA TCTCTTTGGA GATAAAATTC ATTAGTGTGT TACTAAATGT 120
 NAATTTTNTT TTGCGGAAAA TACAGTACCG TGTCTGANTT AATTATTAAT ATTNAAAAA 180
 CTTCAATCCT TAACTCTCCC TCATTGCTT TGCCACAGC CTATTCAGTT CCTTTGTTT 240
 GCAGGNTTCT GCAAAA 256

SEQ ID NO:5

LENGTH:616

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00005

SEQUENCE DESCRIPTION:

GATCAAGCTC AAGAATAAGC TGAAATATGG CCAGACTATC AGGCCCATTT NTCTCCCCTG 60
 CACCGAGGGA ACAACTCGAG CTTTGAGGCT TCCTCCAACCT ACCACTTGCC AGCAACAAAA 120
 GGAAGAGCTG CTCCTGCAC AGGATATCAA AGCTCTGTTT GTGTCTGAGG AGGAGAAAAA 180
 GCTGACTCGG AAGGAGGTCT ACATCAAGAA TGGGGATAAG AAAGGCAGCT GTGAGAGAGA 240
 TGCTCAATAT GCCCCAGGCT ATGACAAAGT CAAGGACATC TCAGAGGTGG TCACCCCTCG 300
 GTTCCTTTGT ACTGGAGGAG TGAGTCCCTA TGCTGACCCC AATACTTGCA GAGGTGATTC 360
 TGGCGGCCCC TTGATAGTTC ACAAGAGAAG TCGTTTCATT CAAAGTTGGT GTAATCAGCT 420
 GGGGGAGTAA GTGGGATGTN TGCAAAAACC AGAAGGCGGC AAAAGCAGGT ACCTGNTTCA 480
 NGGCCCCAAC TTTCACATCA NCTNTTCAA GGTNTTNCCT GGNTGAGNG GAACNTCCAN 540
 GTTGGGGGTT TTGGGTTTTT TTAAGGGGTT CNTGTTNGCA AGGGGGTTGG GNTTNNTTA 600
 NNCCTGTTNN GNACCN 616

SEQ ID NO:6

LENGTH:615

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00006

SEQUENCE DESCRIPTION:

GATCTCTGCT ATTTTANCCC CCCAAATAAG TTATTTGTCC TTAAAGGTG GTTACNNATA 60
 ATACCCTCA GTAAGATTCC AGTATTAATT TCTGGGCAGT TTGTCTCTG TATACAATTG 120
 CAAATGATAA QCATTTTGT GAGTGACCAC CTTTGCAATA TGTTGTAA TTNTTCATGT 180
 TGGGTCTTT CTGAAATGTA CATCTTTACA TAAAAACCTC ACATTCTACT TGATTACAC 240
 TTCCTAGTCT ACATTACATG TGGTTGAAGG TTTTATACAT TCTATATGCT TTTACTAAAT 300
 ATACAAGATT TACTACTAGA AATTGGAGA AAGAACACTA ACACATGTAC TTGTGATTG 360
 TTCATGTTAT ATTA AACCT TGAGATTGT GTATTTATGT AGGGGGGGT ATTGNCCAGG 420
 NCTGNTGGT TTTTGCTCCN TGGGGCTATT NTAATAAANC NGGGGTATNG GGTGNTGGC 480
 CTNGTTTGG GCCTAAANTT GGATATATNT GGGGTTCTT NGNTTTACC AAAATNGNTT 540
 TTGGTTGTA GGGTNTTAT TGGACCCNNT CCTGGGCTG GGATAATNG GCNGNTTCCC 600
 NGGANAAAAAN NCCCN 615

SEQ ID NO:7

LENGTH:608

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00007

SEQUENCE DESCRIPTION:

GATCAAACCA AAGGAAAAGT GTTGCTAGAG AAAATTGGGG AAAAGGTGAA AAAGAAAAA 60
 TGGTAGTAAT TGAGCAGAAA AAAATTAATT TATATATGTA TTGATTGGCA ACCAGATTTA 120
 TCTAAGTAGA ACTGAATTGG CTAGGAAAAA AGAAAACTG CATGTTAATC ATTTTCCTAA 180
 GCTGTCCTTT TGAGGCTTAG TCAGTTTATT GGGAAAATGT TTAGGATTAT TCCTTGCTAT 240
 TAGTACTCAT TTTATGTATG TTACCTTCA GTAAGTTCTC CCCATTTTAG TTTTCTAGGC 300
 TGAAAGGATT CTTTCTACA TTATACATGT GTGTTGTCAT ATTTGGCTTT TGCTATATAC 360
 TTTACCTTCA TTGTTAAATT TTTGTATTGT ATAGTTNCTT TGGNGGTATC TAAAAACCT 420
 ATTTTGAAC ACCAACCTTG GCTTTGNTAA NCATTTGGGC CGCTTGGTA NGTCCGGACC 480
 TNNCCTTNC CCCNAGGGCC TGTCAGGAGN GCCGNTNN CCGGGNGTT GGNCCGNG 540
 CCTTCCGAT TTTTNGGGT TGGTCCTN GGTNCCGC NTCTGTANG GGTNCNCTT 600
 TTNNCCN 608

SEQ ID NO:8

LENGTH:606

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00008

SEQUENCE DESCRIPTION:

GATCGCTTCC TAGAAATAAG CAACACCTCT CCCAAAAAGC AGCCACAAG GCAGGGGCCA 60
 GCAGCCAGC CATCACTCAT CTTNAGGAA ATNAGTTGGT AGCCTCTGTG CACTGTTTGG 120
 TGGCCACATC ANNGGTGATG TCCTGTTAC ATACCTGCTT GTATTTAAAG CCCTCAGTCT 180
 GTCCTGTTGT GTGGGGCGAA GTGATGGACT CTGCCAGGTG GACATGCTGT GGGTGGATGT 240
 TCCCGCGTG TGCCGGCTG AATGGACAGG GGTCACTTCA CAAGCATGTC AGGGAAATC 300
 ACTGTCACAC AATCCAATG GATTTTGTGC TCTTTTGAA AAAAAAAT TCTTTAGCGT 360
 AAACCATGNA TTTTTCAT ATGTAGNCCC TTGGGGANTG AANTGAAAT TTGGGCTTCT 420

TCANATNCGN AAAATNAAAT TTTTACCCCT GAGGGGGGGA GCCCCTTCT GAAAGAAGGT 480
 NTGGGCCAAA AGCCCTTTTA ATGNTTGCTG GCCNTTGNTG GTTTNANNG TCCANTTGC 540
 TTGGGGCGAA NGCCGNNNTG ANAAAGGTGG GTTTCNCTGG NGGNTTAAAG GNGGTGGTTT 600
 GNTTTN 606

SEQ ID NO:9

LENGTH:606

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00009

SEQUENCE DESCRIPTION:

GATCTTCANN NGTTAAGCAC TTGCTCTNAA GATTAAATTT CCTTTCTTT TTAAGGTAA 60
 GGGTGTGTAC GTATGGCAGT GATGTCTATG TTGAGATTAA CTTATGTATT GAGGAAAATT 120
 TGAAGTTTAT TTTTTCGATG AATAAGGCTG TCAAATNATT TAGTATAGAT TAATGACATC 180
 TTTTITAGAA ATATTAAAGT GAGTATTCCT CATTATGTCA TCATTCTGA TAATTAGAGT 240
 GCTAATTTGA ATGTTAGATA ATGNTTCCAC ATCTATACCT ATTTCTTCT AGGGCACTTC 300
 TGACCCTGGG GCTTGGGGAT GGCCTTTAGG CACAAGTAGT GTCTGTGTTA AGTTCATAA 360
 ATGTGTATTT AATGAGAAAC ATTCCNATGT AAAAATGTGT GTATGTGAAC GTATGCNNAC 420
 ATTGTTATTG TGCACCGTA CATTGTGAAG AAGTAGTTN GAAATTTGT AANGCACAAC 480
 CCTTAANGNG GTGTGGAGTT ATTAAANTGN TGTAGGCNCA AATGTAATGT TTAGCCTATA 540
 AAAGGCCCTC CTATTGTCCN TNGGCAAGGC TTTGNCNCTT GNAANTAAAN CCCGTNTTGT 600
 TTTAAA 606

SEQ ID NO:10

LENGTH:606

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00010

SEQUENCE DESCRIPTION:

GATCAGGGGA GACCCCAACT GCCAGATATA TTTAATGTA CAAAACTGAA ACCAGATGAA 60
 ATAATGTTCT GTCACGTGAA ATATTTAAGT ATATAGTATA TTTATACTCT AGAACATGCA 120
 CATTTATATA TATATGTATA TGTATATATA TATAGTAACT ACTTTTATA CTCCATACAT 180
 AACTTGATAT AGGAAGCTGT TTATTATTC ACTGTAAGT TATTTTTCT ACACAGTAAA 240
 ACTTGTAATA TGTTAATACC TTGTCCTATG TCAATTTGTA TATCATGAAA CACTTCTCAT 300
 CATATTGTAT GTAAGTAATT GCATTTCTGC TCTTCCAAAG CTCCTGCGTC TGTTTTTAAA 360
 GAGCATGGAA AAATACTGCC TAGGAAAATG CAAAATGGAA ATAGGAGAGA GTAGGTTTTT 420
 CAGCTTAGTT TTGAGGGGGG CCGGTTACCT TGTATATTCC CCCATTCA TTTGGTGTCC 480
 ATGTGTAGGG GAAGGTAAAG GGGTGGTTCC ATAATCAAGT TCCCCGTGGG GTGTNCCCCC 540
 TGTTAAATGT CCCTGGTTTG GTGTTACCCG GGCTTTATGG GNCCTTTCA TTATTCCGG 600
 TNGGGN 606

SEQ ID NO:11

LENGTH:598

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00011

SEQUENCE DESCRIPTION:

GATCAACAAA AGATAAACAA ATTTGCACGG AATACAAGTA GAATCACAGA GCTGAAGGAA 60
 GAAATAGAAG TAAAAAAGAA ACAACTCCAA AACCTAGAAG ATGCTTGTA TGACATCATG 120
 CTTGCAGATG ATGATTGCTT AATGATACCT TATCAAATTG GTGATGTCTT CATTAGCCAT 180
 TCTCAAGAAG AAACGCAGAA ATGTTAGAAG AAGCAAAGAA AAATTTGCAA GAAGAAATTG 240
 ACGCCTTAGA ATCCAGAGTG GAATCAATTC AGCGAGTGTT AGCANGATTT GAAAGTTCAG 300
 TTGTATGCAA AATTCGGGAG CAACATAAAC CTTGAAGCTN GATGAAAGTT AAACATTTTA 360
 TAATACTTTT TTTATTTGNT TTAATAANCT TGATTATTTG TTAAANATGG TAATTTTCC 420
 TTCTTCANAT GGCNNNGGT NAGCAAANCT TTCTTTTTTT AAAAAATTTT CCANTTGT 480
 AATGGGGAAC TTTGCCNTT TTCCNCATGG CNTGNTNATT NATTTTNTNT TTTAAAGGG 540
 GGGCCAGTTT TCCCCNNGG TTTTGTGNT TNNCGGTNT TNCAGGNNTN GGGGGTCN 598

SEQ ID NO:12

LENGTH:597

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00012

SEQUENCE DESCRIPTION:

GATCGACAGA CCTGAAGCCA TCAGTGAAGA GAGGTTGCGA GAGATGTTG GTTTATATGG 60
 TCAGACAACA GGAAGGGGA GTATATCTCT GAAAGAACTG AATGCCCGAC CCTTAGAAGT 120
 TTTTATGTGT AGTGTGCTCA AAAGACAAGG TTACGGAGAA GGCTTCCGCT GGATGGCACA 180
 GTACATTGAT TAACACAAAC TCACATTGGT TCCAGGTCTC AACGTTTCAGG CTTACTCAGA 240
 GATTTGATTG CTCAACATGC ATAACCTGAA TTCAATAGAC TTTTGCTNGG TTATAAAACA 300
 GATGTTTTTT AGATTATTAA TATTAANTCA ACTTAATTG ANTNGAATT NGAAANCTGA 360
 TTCAAGTAAG NTTTGAGTAT CACANTGTTA GCTTTCCTAA TTCCATAAAN GTACCTTGGG 420
 TTTTNTCAG NTTTATAAAT CTGGCCATCA NCCCCNGCGG CCTTTTNGTA AAGGGGCACC 480
 TTTTCCNGCA GGCATTGTTG NAGCNCTTTT TTAACCACTT TGGGNTTTTT AACCTTTTT 540
 TNAAGGGNCN NCNTGGTTAA NTTTNTTNT GGGCCTTNC NGGGCCTGGT NTTAAN 597

SEQ ID NO:13

LENGTH:593

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00014

SEQUENCE DESCRIPTION:

GATCTTCCAA AGCACTATTT GTTGTAATAA CTTTTCTAAA TGAGTGCCCT TTAAAGGAAA 60
 AATGAACACA GGAAGTGAC TTTGCTACAA ATAATGTTGC TGTGTTAAGT ATTCATATTA 120
 AATACATGCC TTCTATATGG AACATGGCAG AAAGACTGAA AAATAACAGT AATTAATTGT 180
 GTAATTCAGA ATTCATACCA ATCAGTGTTG AAACCTCAAAC ATTGCAAAAG TGGGTGGCAA 240
 TATTCAGTGC TTAACACTTT TCTAGCGTTG GTACATCTGA GAAATGAGTG CTCAGGTGGA 300
 TTTTATCCTC GCAAGCATGT TGTATAAGA ATTGTGGGTG TGCCTATCAT ACCANTTGT 360
 TTCTGTATCT TGA AAAAGTA TTCTCCACAT TTTANATGGT TTTATATTNG GGGATTCTT 420
 TAATGCCCCC TTGGNCAAT TTATATATAT GGGCCCCATN GTTNCNTTT NAATTTTNG 480
 GTTTTNGGGT GTAAGGGNCN TGCNCNTATG GTGGGGGCCT CCCAAAANTG GGANCANGNT 540

TTTNCCTNNG GACNCCCNNT TGGTTGTNA GGGGGGCCAA TTTTCNTNC CCN 593

SEQ ID NO:14

LENGTH:574

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00015

SEQUENCE DESCRIPTION:

GATCGTNTG CAGTGGGAGC GTGTGACTGC GGAAGTTGTG AAGCCACGGG AAAC TCGGAG 60
 CCTAGAGCAG CAGCTCAGCG CTTCTATGGG AAGCGGTCTC GAGCAGAAGC CCCACTGAAG 120
 TGTCCTCTGG CAGACACCCA CATGAACTCT TCCGAGAAAC TCCAGTTCTA TAAAGAGAAA 180
 GCCCCAGATT GCCATGGGCC AGTNTTGAAA CACGAAGCTA TCTCAAGCCA GGAGTCAAAG 240
 AAGAGCAAGA AGAGACCTTT TGAGGAGTCA GAGACAGAAC AGAATAACTC TTCACAACCT 300
 TCAAAGCAGA AATATGTATG TTTTGCTGTG GAAGACTGGG GACTTGTTAA ATTCCTATTG 360
 ATTAAGTAGA TACAAGTTGA CCTTTCTCTG GCCCCAGCT CTAGTGTGTTG AGTAAAGGGA 420
 GACTNAGGGT GGGTTTACTT TTTTNGGTTT GNATTANCC TATTGGCATT TAGNCATAGG 480
 TAAGGCGGTN TTTTCNNCT TTTNTTGGNT TTGGGNGGGG GATTNTNTNN GGGGNNNNA 540
 AAAANTTNC ANGGGNTTTT TCCAAANCA NGN 574

SEQ ID NO:15

LENGTH:573

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00016

SEQUENCE DESCRIPTION:

GATCAGCCCA GAGGAATGCT GAGAAATCAC CTGGAGGAGG GAGCAGAAAG AGAAGGTTTT 60
 TAAGGAGGGG CTTCTGAATA CTTGGGAGAT ACGGAACGGA CCAAGGACCA CACTCCAGGG 120
 TGCATTCTGT GCTCCCTGGG GCACCACTTC TGGATTACAG TGTGCCAGGT CCTTTGGAGG 180
 CCCTACCCCT TCCCCATTCA TTGCCACCAG TGAGAAATNG GGGTGCCCT GTGTAAAGAA 240
 ACCTACCAAA GGTTTACATT TGCACCTTAG CCTCAATAGC TACGAACCCT AGAGAAGCAG 300
 CTAGCTGGAG CTCATGTGCA ACTCCTGATT CTCAGGAGAA AGATGGATTT TAACCNAAAA 360
 TTATGAGTNA GCTGTTAACT CTAATATGTA CTTNGGGAGA TAGGGCCAAG NGAGAGGTCA 420
 TGGGCCAACT TAAGTGTTAT CCNGTAGGAA AGNCCAGGTA NCACTGGNTT TTTTTTTNNA 480
 GGGTTGCTNT TNCCTTNTNC TAAANGGATT TGNTANTTCC NTGGGGNTNG NATTTAAATT 540
 GGGTTNTAAA AAGNTTNGAC GTGANAAAAA TTN 573

SEQ ID NO:16

LENGTH:567

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00017

SEQUENCE DESCRIPTION:

GATCAAAACA GTCTCACCAG CACCATATCC ACATTCTAGC CCATGGAAAG GGTAAAGAAA 60
 AGAAAGTGGA AGATATTAGT TTCCATTAA GGAAGTGACA TGGAGNTAAT ATAAGTCACC 120
 TGTGTTTACA TTCCACTGGC AAAAATTTCAG TCACAGGAAT GTACTTAGCT GCAGAGGAGG 180

CTAGGATATG CCCTCCAAAA ACTCAGGGGG GATGTCCTAC TTGTAAAAGG AAGAAATGAA 240
 AANTGGACAC TGAGAGGAAA TCAGCAGTCT CAGAGGTAAT ATACTTACAC AAGTTTTTTA 300
 AAAACCATAA AATGATGCAG AATGAAGTTT CCACTCTATT CACCATCTAT CCAGTCCTCA 360
 TGCCTCCCAN CANGNGGTAA ATNCTTTATT ATTGTGTCAT GGTATCTTTC CAGGGTTTTT 420
 CTAAGCAATT TTGCAACNGN TTTTAATTAT GTATCCTNAT TTCCTACNTT ACCCCNTTTT 480
 TGTCCATGNA NGGNANANTN TCCTGNGGNN TAACCTTCNT GTNTCTTTTT TTCCCCTNAT 540
 ATTTTTTGGC GGTNCCNTNN NTTTGGN 567

SEQ ID NO:17

LENGTH:552

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00018

SEQUENCE DESCRIPTION:

GATCTTACCC GTGACAAAAT GTGTTCCATG GTCAAAAAT GGCAGACAAT GATTGANGCT 60
 CACGTTGATG TCAAGACTAC CGATGGTTAC TTGCTTCGTC TGTNCTGTGT TGGTTTTACT 120
 AAAAAACGCA ACAATCAGAT ACGGAAGACC TCTTATGCTC AGCACCAACA GGTCCGCCAA 180
 ATCCGGAAGA AGATGATGGA AATCATGACC CGAGANNNGC AGACAAATGN CTTGAAAGAA 240
 GTGGTCAATA AATTGATTCC AGACAGCATT GGAAAAGACA TAGAAAAGGC TTGCCAATCT 300
 ATTTATCCTC TCCATGGNTG TCTTCGTTAG AAAAGTAAAA ATGCTGAAGA AGCCCAAGTT 360
 TGAATTGGGA AAGCTCATGG AGCTTCATGG TGAAGGCAGT AGTTCTGGAA AAAGCCACTT 420
 GGGGNCCGNG ACAGGTGCTT AAAGGTTGAA CCGNGCTNGA TTGGTTNTGA ACCCACCAGT 480
 CCCAGGAATT CTGTGTTAAA GTTCCAGNCN TTCAATTAGT TGGCAAATTA AAAANGTGCT 540
 TTTTTGNGGA AA 552

SEQ ID NO:18

LENGTH:581

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00019

SEQUENCE DESCRIPTION:

GATCGCCGTT CTGGTAAAAA GCTGGAAGAT GGCCCTAAAT TCTTGAAGTC TGGTGATGCT 60
 GCCATTGTTG ATATGGTTCC TGGCAAGCCC ATGTGTGTTG AGAGCTTCTC AGACTATCCA 120
 CCTTTGGGTC GCTTTGCTGT TCGTGATATN AGACAGACAG TTGCGGTGGG TGTCATCAA 180
 GCAGTGGACA AGAAGGCTGC TGGAGCTGGC AAGGTCACCA AGTCTNCCCA GAAAGCTCAG 240
 AAGGCTAAAT CGAATATTAT CCCTAATACC TGCCACCCCA CTCTTAATCA GTGGTGGAAG 300
 AACGGGTCTC AGAACTGTTT GTTCAATTG GCCATTAAAG TTTTAGTAGT AAAAGACTGG 360
 TTTAATGATA ACAATGCATC GTAAACCTT CANGAAGGNN AANGGAGGAA TGNTTTTG 420
 GGCCCACTTT GGGTTTNTCT TTTTNCGGT GTNGGCAGTT TTTAAGGTTN TTAAGTTTTT 480
 TNAAAATNCA GGACCTTTTT TAANTGGNAA CCAACTTTGG CCCAAAAATT TTGTCACCAG 540
 ATTTTTTNGG GCCCCNTTTA AAAANGTNTT NATNNGGGAA A 581

SEQ ID NO:19

LENGTH:556

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00020

SEQUENCE DESCRIPTION:

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GATCAGCAGG GTTCTTTGTA AATAGTATTT TGAGACACTA AGATGTTTCT ACTGCTACGG 60
AATGTATTTT AAACACATAT CGTTTCTTTT TCTTGAAAA AAAGTTGATT AGGACCACAG 120
NNNNGGTTTA GAAAGGGTAA TATTTTGAAA TACTACAAGG TTTAGACAGT CCATGAAATC 180
GACCTGTTTA ATAATTTACC ATCCTGAAAG TCCAGAATTA AAATATGGAA GCAAGAACTA 240
TATAATTGAT TAGGATGCTT GGTAGGTTTT TTTCATTGTT CAAATATTCA TTGCACAGTG 300
GATTGTTTTG ATTAGTTAGT ATGCTTTTTT TTTAATTAAT TCAGTCTTCT GTTAATTTTT 360
AAGNTTGGT TAGTGCCACA AGGAATTNA CTTNTTGATT TGTATAATNG GAACCTGACC 420
TNGGGATTNG TAGCGGGGNT TTGAAGGGTG GGGACCTNCC CNCAAAATAA GGGGGAGGTT 480
TCCAAANNNT CCNCTGGCCG NCCNNNNATC CCAGGTAAAG GGGGTNGAAA TANTNNGGGN 540
NCCCCCAGG GGAAAN 556
```

SEQ ID NO:20

LENGTH:555

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00021

SEQUENCE DESCRIPTION:

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GATCTGGTAC GAGTGTGTGA AAACATCCCC ATTGTGTGTG GTGGCAACAA AGNGGATATT 60
AAGGACAGGA ANATGAAGGC GAAATCCATT GTCTTCCACC GAAAGAAGAA TCTTCAGTAC 120
TACGACATTT CTGCCAAAAG TAACTACAAC TTTGAAAAGC CCTTCCTCTG GCTTNCTAGG 180
AAGCTCATTG GAGACCCTAA CTTGGAATTT GTTGCCATGC CTGCTCTCGC CCCACCAGAA 240
GTTGTCATGG ACCCAGCTTT GGCAGCACAG TATGAGCACG ACTTAGAGGT TGCTCAGACA 300
ACTGCTCTCC CGGATGAGGA TGATGACCTG TGAGAATGAA GCTGGAGCCC AGCGTCAAGA 360
AGTCTAGTTT TATAGGGAAG TTGTCCTGTG ATGTCAGCGG TNCAGCGTGT GTNCCACNTC 420
ATTATTATCT AGCTAAGCGG ACATGTNTTC ATCTGTGGGN TCTTAAGGAG NTGAGTNGNN 480
TNGGNGTNAT NTGGANTTAA AAATAACTTC ATTNTTNGGC CNNATATTTA NGTNTTTTNG 540
CCCGNTTNT CCCTN 555
```

SEQ ID NO:21

LENGTH:544

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00023

SEQUENCE DESCRIPTION:

```
GATCGATACA TGCAAATTTA ATGTAGTAAC TCACTTTTCC ATATATTTTN AATGTATATT 60
TCTATTTATG AATACCAATT TATAAAAAAT AATTACACAG AAAAAAATGG AATAGGAAAA 120
ATTATGCATC TAGCACATTT AAAGTGTGCA AATATGAAAA TTTTTCGAGG ATTACATTTT 180
NTNNNTAGGC TGCATATTTT AACTGGCTTT AAAACTGTAA CACATCACAT AAAAGTACTT 240
TACCCGGTAT GTATTGCATT ATATCATTGC AATAATTATT GGAGTCTAGA TATCGAGCCA 300
TCCCAGGTGT TGGGCGGGGG GAGGGTTGTG GCAAGTTGTC TTTTCAATTT NGNGNGTTTT 360
CCTGTNGCTC CAGGGCAAGT ACCGGTTTGG AAAGCTGCCT GTAAGCGTTG GCACCTTCAT 420
AGNGTAGTGT TTNGGTGNCT TTTTNTTCG GTTCTTGTA ATTNGGTNCG GTNGGTGGTG 480
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TTCAGATGNT TTTTNCNCT NGTTCAGCAA CTTNCCNNT NNCTTGTCTT GATAGGGNAC 540
NTCN 544

SEQ ID NO:22

LENGTH:538

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00026

SEQUENCE DESCRIPTION:

GATCTCTATC CAGTTGGACA CTTAATTGCT TTCTTCATTC AGAAAGATAG TCATGTTTAC 60
TGGTATATTT GGTCACTCTT AGAACCTGTC CTTACATAT GTTTTTTATG GGACCCATGA 120
ATGGTTAGCC TTTCTGTACT ATTGTAGAAG GAAATAAATA GCGGTAAAAA GACCATTGTA 180
GTAAATAAGT TCAAGGGGAA CTTGGGACCA GAAACCACTG GTATGTACAA AAAAGCTGGC 240
AATTGAATA ACCTCAAGTT TGACAATAAT TTTTAAATTT GAACAGTTAT GATAAATTC 300
AGTAGTTTTA TACACTAGAT GTGCCTAGAT GGTCTCAAG GCTTATAGGA CTGGCTCACA 360
GTTCAACATT TCTAGTGGCT TTTCTTGGCT TTGGGTCTGG GGGGCTGGGG GCAATGGGCT 420
TTTTTCCTTG GGTGCGCAAT CGGTTTCTCT GGTGCTCAG TTTCCAATCC TTNGGGGGGT 480
CNTTGTGNTN TTNNCNGCCC NGNNNGGTNN GTCCNGGGTG TTNGCCGGGN NCNTTTTN 538

SEQ ID NO:23

LENGTH:535

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00028

SEQUENCE DESCRIPTION:

GATCCTGGAA TATGTCGAGG TTATATTACC AGGTATTTTT ATAACAATCN GACAAAACAG 60
TGTGAACGTT TCAAGTATGG TGGATGCCGT GGCAATATGA ACAATTTTNA GACTCTGGAA 120
GAATGCAAGA NCATTGTNA AGATGGTCCG AATGGTTTCC AGGTGGATAA TTATGGAACC 180
CAGCTCAATG CTGTGAATAA CTCCTGACT CCGCAATCAA CCAAGGTTCC CAGCCTTTTT 240
GAATTCACG GTCCTCATG GTGTCTCACT CCAGCAGACA GAGGATTGTG TCGTGCCAAT 300
NNGAACAGAT TCTACTACAA TTCAGTCATT GGGAAATGCC GCCCATTTAA GTACAGTGA 360
TGTGGGGGGA AATGAAAACA ATTTTACTTC CAAACAAGGA ATGTCTGAGG GGCATGTAAA 420
AAAGGGTTTC ATCCAAAGGA TTTCANAAGG GNGGCTNATT TAAAACCANA NGGAANNGGN 480
AGGAGGCNGG NNGTGAATTT GNNTTTTGGN GGAANTTTTT GNTTNAANNT TNTGN 535

SEQ ID NO:24

LENGTH:528

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00029

SEQUENCE DESCRIPTION:

GATCTACACT TGGATGGATG CAACTTTGAA AGAACTGACA AGTTTAGTAA AAGAAGTCTA 60
CCCAGAAGCT AGAAAGAAGG GCACTCACTT CAATTTTNC AATCGTTTTA CAGATGTAA 120
AAGACCTGGC TATCGAGTTA AGGAGATTGG CAGCACCATG TCTGGCAGAA AGGGGACTGA 180
TGATTCCATG ACCCTGCAGT CGCAGAAGTT CCAGATAGGA GATTACTTGG ACATAGCAAT 240

TACCCCTCCA AATCGGGCAC CACCTCCTTC AGGGCGCATG AGACCATATT AAATTCTATT 300
 TACTATTTGT TGAATTTATT TTTCCGTCAG TTATGTAAAA TAAACATACT CTNCCTTCCT 360
 CCCCTGGATT TATTGCCATT TAAGGCTTTT AAAATTCTAA TCAANNTTGG TNANTGCAAT 420
 CATCTGTTTN GGGNGTTNNG TTTTGGGATG TGCTTTTTGN NTGGNTTNCG GNTTAGNCTT 480
 GGNTTGTTTT AATGGCCNTT CNNGTNANAT TTGGNGGNAA NNGGCTTN 528

SEQ ID NO:25

LENGTH:528

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00030

SEQUENCE DESCRIPTION:

GATCAAGGTA TAATGGAAAA ATATACCTAT TCTTGAAGTA GTTTATTATN GTTTCAAAT 60
 TGATTTATAC CATTATTAAC CTGATGTGGT CTGCTTAAAA AATGAATATA TCAGTATTTA 120
 GAAATAAATT GCAAAGGTGG GAATATATAC TTAAATAATT TGTCTTAAGT AAATTAGCAT 180
 TTGGTAGTCT GANATGGTGA CAGATTACTT GTTAAAATTG TGAAANCTCT GTTGTGTCCT 240
 CTCTNCCTAC ATTTGTCCCT GAGAGTNCTC CACGATTACT AGGTTCTTGA TTCCCTTATA 300
 TGGCAATCAG GCAGAGGCGT TCCTTAAGCA TTAGAGAGTT CTGAAGCTTA AGATTGTTT 360
 TGGTTGGATG AANGTCCTTA GTACAGTTGA AAANCAGAGC ATTAAAGNCT ANTCANTTTG 420
 TTTTGNCTC ACCAGTCATT TAAAAATNNG TNGGAATNCT TNTTNCTCA GTGCTTAAAN 480
 NTTCCNTTG TTTCAANCTG NNGGGGGTTN GGATTAAACC AGGCCNCN 528

SEQ ID NO:26

LENGTH:527

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00031

SEQUENCE DESCRIPTION:

GATCAGAATG CCCCTCCACT CATGAGACTC TTCATTTTGT CCACTTTGAC AGGAAAAGTG 60
 GGAATGTATG CAGAGCTCTC AAAAGAAACA AAAAAGGCCA AAACGGTGCC TTCAGCCACA 120
 TCCTCTGAAT TGGCCCTGAC TTGGACTAAA TGCACTAATG CAAAATCCCT TGACAAAAGC 180
 GCATAGGTTA TTTCAAACCA GCATTGTTTT TTATGTAACC TGTTTTACCG CATCTTCTCA 240
 GCAGCTTCTG ACCACTGCTC AATTTTCTCC TTTACAGCCA TTGTTCTGGT GGACAAATAA 300
 CCTAGGTACT CCAAATCCTG GCAGGAAAAA TATACAGCAT TATGAANCAG CACTCANGTA 360
 ATCCTAAAT GGATTTCCTA AGCTGGTTAC ACATGGCCCT GGNAANGTCN TATTGANTTT 420
 ANANGGGCTT TCTTCNTTTC AGGAGTTTNG GTCAACGGTG GCAAATCCNT GGGGTNNTTA 480
 ANTGGNNNGG TTNNTTAANT TNTGNTANTT TCNTNGGGGC CANAGGN 527

SEQ ID NO:27

LENGTH:520

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00033

SEQUENCE DESCRIPTION:

GATCAAAATG GTTGGTGAAC CTCCACATGT CCAGTTCTGT TGCCAAACTT TCCATTCAGA 60

GTATTTGGTG GAGTTTGAAT TTGAGCAAAC TAAATGCCTT CATCTTAGGT AGAAAGGGCC 120
 TGAATCTTCC ATTTTATATT CAAACCTCAT TGTATTGG CTAAGTAAA AAGTCAGATT 180
 TCATTTCCAT TTACCTGAGT TCGCTTTAAA GAGCTTTTCA AAGAGAGCTT TATAGACACC 240
 CACAATTGTC CCCAATCTCT TCATGATGTT GCATTAATAG TTGTTTTTGT CCCTTTCTTG 300
 GAAATGTAA TGCCAAAGNT TGCCTGAACA TTNGGGCGGG TTTCTTAAA TTTGAANGTN 360
 TAAAAATTTT NTAANGGGGG AATTNCCAAA NGGGTATTTA AAAGGGTTNG TTTTAACCAG 420
 GTATTGTNGT GGGGGGATGG TCCAATAATC CTCNNGGGGG AGGGCTTTCA AGGGAAATCC 480
 CNTTTTNGGG GAAATAAAAA NNGGGTTAAA ANNNNTTTN 520

SEQ ID NO:28

LENGTH:514

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00034

SEQUENCE DESCRIPTION:

GATCAGCGAG GCCGACAAGA AGAAGGTGCT GGACAAGTGT CAAGAGGTCA TCTCGTGGCT 60
 GGACGCCAAC ACCTTGGCCG AGAAGGACGA GTTTAAGCAC AAGAGGAAGG AGCTGGAGCA 120
 GGTGTGTAAC CCCATCATCA GCGGACTGTA CCAGGGTGCC GGTGGTCCCG GGCCTGGGGG 180
 CTTGGGGGCT CAGGGTCCCA AGGNAGGGTC TGGGTCAGGC CCCACCATTG AGGAGGTAGA 240
 TTAGGGGCTT TTCCAAGATT GCTGTTTTTN TTTTGAGCT TCAAGACTTT GCATTTCTTA 300
 GTATTTCTGT TTGTNAGTTC TCAATTTCTT GTGTTTGCAA TGTTGAAATT TTTGGTGGA 360
 AGTACTGAAC TTGCTTTTTT TCCGGTTTCT ACATGCAAGA GATGAATTTA TACTGCCATC 420
 TTACCGGCTA TTTCTTCTTT TTTAATTCCA CTTAACTCAG GCCATTTTTT AAAGTTGGGT 480
 ACTTGCAAAG TAAATAAAAC TTTAAAAATT CAAA 514

SEQ ID NO:29

LENGTH:513

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00036

SEQUENCE DESCRIPTION:

GATCATCATT CTTCTGACTC TAGATGGGAC ACTTGACAGT GACTTGAAAC ATTTGCATAT 60
 TCAGGAATGC ATGAGATTTC AAGAGAGCCT ACAGTATGAA ATCATTTC AAAAAAAGC 120
 AGCTTGCTTC TGAATGCTG TCTTTCCAG TAGCTACTCA CCTGCCTCTG GTGGCTGGGA 180
 TTCAGATGCC AAAAACTGT CAGTATCTAT AGACCAGGTC TGTGCCACCT CCTCTCTCCT 240
 CTGTGCTCAG TGAGGAGGCA GTAAATGAAG TTACAGGCTA GCACAATACC TAACTCATGT 300
 TTCCCAGTAC ACCTGTTGGA TATTNCTGT NCCTTTTAAT GGTTCCTCAAG GGANTTAGGT 360
 TTTTNCCTG TTTCCAGNGG TTTCCAGGTT TTCTTTGGGT NCTTTTNAA TTTTNAANTT 420
 CCNAGGGGGG GGGNNTTTGG GGNAAGGGGG GGGCAAAGGG GNTTTTTTTT TTNTGGGCC 480
 NNGNTTTTTG GGGGGAAANC CTTTNGGTN NCN 513

SEQ ID NO:30

LENGTH:512

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00037

SEQUENCE DESCRIPTION:

GATCTAAATT GTTACATTTT ACCATTTCAT TCCGAAGTTG GTTTTACTTT ATTAAATGAA 60
 GATTTAGTTT TCATATCGTA TACATAGCTG TATAGATTTC AAAATNAGGT TGTTAATTTG 120
 TGTCACTTAC TATTTTGTG TTGGTAATGC TTAAATGCA TACTTAAAAA TGAAGTACTG 180
 TTATCTAAGC TACTGTGTTT AGAAAATGTT AAGAATGAGC AGAAATTTT ATAGAAAAGT 240
 ATAACCGGAA GANGAGAGAA GATACTGCGA ATAGGCCCTC AANCTTAAAA NAGAAAAACC 300
 TTTGCCAGTT TTANGGACAT ATTTTGATTG TTTTCNGTATT CTTAACACCT TTTTAAACAA 360
 NGTTCTTGAT AGTACCCACT ATTATTGGGT TTGTTTTATG CCATTATTTG ATTCTTGGAT 420
 ATTCAAGCAT TTNCAATGTG GCATATTTNG NTTCCNNTN NCCTTNCNTT TTTTNGGNCN 480
 NCNTTACCCT TTCCNTTGA AAGNCANTTN GN 512

SEQ ID NO:31

LENGTH:510

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00038

SEQUENCE DESCRIPTION:

GATCAGCCAG GCACAGAATC TCCAGAACAA CCTAGAGAGT GAATGCTAAT TTGTAGAGCG 60
 AACTTCCATT TGGCCCATNA TTTGTAAGT TGTAAGTCT CCAAGTGCCA GANTGCTTAC 120
 ACGTTAAAGC AGCACCTTTC CATTGCCCCA CATATTCTTC TTGCACACCC CTCCATTAC 180
 TGCTGAATAG GACATTGCAT GGAAGAGTA CAGAGGTGGC AGANTGANGC TAGAGTGGGC 240
 AGGNCTAAAG ACTGAGCCCC AGAGTGCTCC CAGCAACCGC CACGTACANG GTCTGNAATG 300
 NCANGGGCAN GNGTGAGATT GGAANCTGTG TGTGAANGGT AAGCCCTTGC AGTNTTTCTG 360
 CCTCCCTTTC TTTCTGCCTT TCACCCCNCT TANTTGTNTG GTTNTTGGTT TGCCCGTTCT 420
 TCTCTTGGTG GNTGCNCATT TGTTANATGG TGTTAGGGGT GTGGGGNTGA GGTTTTCCCC 480
 TTTGATGTGG GNTTNTCCN TTGGGTTTAN 510

SEQ ID NO:32

LENGTH:507

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00039

SEQUENCE DESCRIPTION:

GATCGTGAAG CCCAATGGCG AGAAGCCGGA CGAGTTCGAG TCCGGCATCT CNCAGGCTCT 60
 TCTGGAGCTG GAGATGAACT CGGACCTCAA GGCTCAGCTC AGGGAGCTGA ATATTACGGC 120
 AGCTAAGGAA ATTNAAAGTT GTGGTGGTCG GAAAGCTATC ATAATCTTTG TNCCCGTTCC 180
 TCAACTGAAA TCTTCCAGA AAATCCAAGT CCGGCTAGTA CGCGAATTGG AGAAAAAGTT 240
 CAGTGGGAAG CATGTCGTCT TTATCGCTCA GAGGAGAATT CTGCCTAAGC CAACTCGAAA 300
 AAGCCGTACA AAAATAAGC AAAAGNGTCC CAGGAGCCGT ACTCTGACAG CTGTGCACGA 360
 TGCCATCCTT GAGGGACTTG GTCTTTCNA AGCGGAAATT NTNGGCAAGA GGANTCCNGN 420
 GTCAAACCTT GNTTGGCANG NCGGGCTCAT AAANGTTCA TTTTGGNCA ANNGACNAGN 480
 AGGNCCAATT NTGGGNCAAA NAGGNTN 507

SEQ ID NO:33

LENGTH:508

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00040

SEQUENCE DESCRIPTION:

```
GATCAGAAAC TCACCCTAAA TCTNAACGGG TGCCGCTATA ATNGTNACA TCTGGCAAGA 60
TTTCCCTTTA TGTATATATT TAAACAATCC GCTTGGACAC GAACAAAGCC ACACTTCTAA 120
CTGCTTCTGG CGAACTGATT TAATTTTNAA TTTTNNCAA TAAAGATATT CTTAGATACT 180
GAAAGAAATA GTTAATGAGT TTNCATTTGT CCTTGAGAAA ATTTGGCTCA AGTCCATTG 240
GCTGTAGTGT CAACGATGTT TCCAGTAGTG TTAGGATTT GGTGTCTCA AAGGTAGTTG 300
ATTAAACCAA GTGTGTCTTT AATATCTTGT ATCAGAATAA CTTTGTATGT TACCAACTTA 360
AATTGCTAGA ATAAGGGTAA ATTGGATACA CAACTGCTGA TTTTAAATT AGGANCTTTG 420
ACCNATTTT GGGGTTTCA AANCCGTTT TGGNTGCTNT GTATCCTAT GCTGTTTGGT 480
TNATTCCAN TAAAAANTTC ACNCGNGN 508
```

SEQ ID NO:34

LENGTH:505

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00041

SEQUENCE DESCRIPTION:

```
GATCTGTAAG TAACCTCACA TAAAAAATG AAATATTTT TAATTAAAG CTTACTCTGT 60
CCATTTATCC ACAGGAAAGT GTTATTTTA AAGNNAGGTT CATGTAGAGA AAAGCACACT 120
TGTAGGATAA GTGAAATGGA TACTACATCT TAAACAGTA TTTCATTGCC TGTGTATGGA 180
AAANCCATTT GAAGTGATCC TGTGTACATA ACTCTGTAAG ANCACTGAAA ANTTATACTA 240
ACTTATTTAT GTTAAAGAT TTTTTTAAT CTAGACAATA TACAAGCAA AGTGGCATGT 300
TTTGTGCATT TGTAATGCT GTGTTGGTA GANTAGGTTT TCCCCTCTT TGTTAAATAA 360
TATGGCTATG CTAAANGGT TGCATACTGG GGCCAAGTAT AATTTTNTG GTAATGTGTG 420
GNAAGGATG NCCAGTTATT GGTTACCNT TTANGNNATC CNNTAANGG AACCTCCCC 480
TNGTTAAAA NCANGNGTA NANNN 505
```

SEQ ID NO:35

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00042

SEQUENCE DESCRIPTION:

```
GATCTGAAA GAGCTGTTT GGATGAATGC AGTATAAAT GTAAANCCC TGCTAAATGA 60
AA 62
```

SEQ ID NO:36

LENGTH:503

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00043

SEQUENCE DESCRIPTION:

GATCGAAAAGG CACTCCATGA GCTAAAACTG GAAGAGTGGG AAGGCAGACT ACAAGTTACT 60
 GAGCACCTCC CTGAGAAAAT TGAAAGTAGT TTACAGGAAG ATGAACCTGA GAATGNTGCT 120
 AAGAAAATTG AAGCACTGCT AAACCTTCCT AGAAACCCTT CAGTAATAGA TAAACAAGAC 180
 AAGGACTGAA AGTGCTCTGA ACTTGAACT CACTGGAGAG CTGAAGGGAG CTGCCATGTC 240
 CGATGAATGC CAACAGACAG GCCACTCTTT GGTGAGCCTG CTGACAAATT TAAGTGCTGG 300
 TACCTGTGGT GGCAGTGGCT TGCTCTTGN TTTTCTNGN CTNTTAACT AAGAATGGGG 360
 CTGTTGTACT CTCACCTTAC TNATCCNTAA ATNTAAATAC ATACTGATGN TTTGTATTAA 420
 TCGNTCCAAT ATATGNNTAC ATGNANTATA TCNACNCNCC TTNGATNTTT AAGCANGTAA 480
 ATAAAACCAT TNGCAATGG AAA 503

SEQ ID NO:37

LENGTH:497

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00044

SEQUENCE DESCRIPTION:

GATCGATAAA GAATTGGCTA GTGGTGAATA CTTTTTGAAG GCAAATCAGA AGAAGCGGCA 60
 GAAAATGGAA GCAATAAAGG CTAACAAGC AGAAGCCATC AGTAAGAGAC AAGAGGAAAG 120
 AAACAAAGCA TTTATTCCAC CTAAGGAAAA ACCAATTGTG AAACCTAAGG AAGCTTCTAC 180
 TGAAACTAAA ATTGATGTGG CCAGCATCAA GGAAAAGGTT AAGAAAGCAA AGAATAAGAA 240
 ACTGGGAGCT CTTACAGCTG AAGAAATTGC ACTTAAGATG GAGGCAGATG AAANGAAAAAN 300
 GANGAAAAAN NAGTANCATA CCCAAANCTC CTTGNCTNGG ACCTATCTCC TTTTNGTAA 360
 AGGGGTTTTT TGGGGTTTTT AGGCCTTAG GTTNCCCTTT TTTGNGGGA AANTTTNTT 420
 GGGGGGGTTT TTTNNCTTT TTTNGGGGGG GGNGGGGGTT TTNNTCCTTG GGNGGGGGTT 480
 TCTTTNAAA AATTTN 497

SEQ ID NO:38

LENGTH:498

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00045

SEQUENCE DESCRIPTION:

GATCTTATGG ATGCTGAGCA TGTCTGCAC TGGTGCTAAT GTCTAATATA ATNTTATATT 60
 TACACACATA CGTGCTACCC AGAGATTAAT TTAGTCCATA TGAACATTG ACCCATTGTT 120
 CATTGAGACA GCAACATACG CACTCCTAAA TCAGTGTGTT TAGACTTTTC AAGTATCTAA 180
 CTCATTTCCA AACATGTACC ATGTTTTATA AACCTCTGA TTTCCAGCAA CATACTATAG 240
 AAAACACCTG CTACTCAAAA CACAACCTCT CAGTGTGATC CATTGCTGTC GTGAGAGACA 300
 ACATAGCAAT ATCTGGTATG TTTGCAAGCT TTCAAGATAG CCTGAACTTA AAANGTTGGT 360
 GCATTAGTTG TATCTGATGG NTATAAATTT TGCTCCTAG GTTCACTTTG GTGTCCAGGN 420
 GCTAAACCTG TGGANCCTAA CTTCCCTN ATTGGGGGGG GAATAACCTG GAAAATAAAG 480
 GGTTTTTTTC CAGGGNTN 498

SEQ ID NO:39

LENGTH:494

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME ____ DE ____

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DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME ____ DE ____

NOTE: Pour les tomes additionnels, veuillez contacter le Bureau canadien des brevets

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THIS IS VOLUME 2 OF 8

NOTE: For additional volumes please contact the Canadian Patent Office

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00046

SEQUENCE DESCRIPTION:

```
GATCTGTGCT GTAGAAAAAC ATTAACCCCT GTTCAAAAAA GAAATGGATA ANCTTGGCCT 60
TTCTAAGTGG TAAGAATGAC CTGTCACTAT AATATACTGT ATGTTTACAT TTNATTAAAA 120
TTTAATCTCT TATGTATAGG GTGATAACCT TCCCCAGAAA CAACAGTGAT TGCNATTGTT 180
TTCTAGAAAC TNCTTTAAAG TGCCACATTT GGCAGTACAA ATGAGTCTGA GTGTAATAGC 240
CCAGAGATTT ATATATAGTT GAATGTCTAA NATGGTAAAA TGTGCCACTG TGTCAAGTTA 300
CAGTGGCTTA TGTTTTTCAT AGTAATTCAN ATGANCTTCC TATTTTTGNT AGTAAATGGC 360
CATTTAATAG NATTCCTTGG CCATTGAGG CTCACTGGCA AATTTTAGGT GCNGGGGGNG 420
GAANCCANTT TTTTANATGG NAATCCTTGG GTTTTNNCCN CCNTNNTNCC TGGNCCNTTC 480
CCCCAAAAAN CCTN 494
```

SEQ ID NO:40

LENGTH:244

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00047

SEQUENCE DESCRIPTION:

```
GATCAGTTGA CAGTGGCAAT TAAACTGTAA ATAACCTGCC CTGGGGGCCT TTTTTTAAAA 60
AACAAAAACC ACAAAAATTC CCAAACCATA CTTGCTAAAA ATNCTGGTAA GTATGTGCTT 120
TTNTGTGGGG GTGGGATTG GAAGGGGGGT TGGGTGGGC TGGATATCTT TGTAGATGTG 180
GACCACCAAG GGGTGTGTA AACTAATTG TATTAAATGT CTTTGTATAA GCCTTCTGCT 240
CAAA 244
```

SEQ ID NO:41

LENGTH:283

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00048

SEQUENCE DESCRIPTION:

```
GATCACTGTA AATGAACCTC CCTGTTGGCC GCTCTGTGGA TGANACTTTA AGACTAGTTC 60
AGGCCTTCCA GTTCACTGAC AAACATGGGG AAGTGTGCCC AGCTGGCTGG AAACCTGGCA 120
GTGATACCAT CAAGCCTGAT GTCCAAAAGA GCAAAGAATA TTTCTCCAAG CAGAAGTGAG 180
CGCTGGGCTG TTTTAGTGCC AGGCTGCGGT GGGCAGCCAT GAGAACAAAA CCTCTTCTGT 240
ATTTTTTTTT NCCATTAGTA AANCACAAGA CTTGAGATTC AAA 283
```

SEQ ID NO:42

LENGTH:486

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00049

SEQUENCE DESCRIPTION:

```
GATCAGTTTT CNTTGTAACA CTGGGTTTAA TCTGAATGGC GCTGATTCTN CCAAGTGCAC 60
```

TGAGGAAGGA AAATGGAGCC CGGAGCTTCC TGTCTGTNCT CCCATCATCT GCCCTCCACC 120
 ATCCATACCT ACGTTTGCAA CACTTCGTGT TTATAAGCCA TCAGCTGGAA ACAATTCCT 180
 CTATCGGGAC ACAGCAGTTT TTNAATGTTT GCCACAACAT GCGATGTTG GAAATNATAC 240
 AATTACCTGC ACGACACATG GAAATTGGAC TAANTTACCA GGAATGCAAG GGAAGTAAAA 300
 TGCCCATTC CATCAAGACC AGNCAATGGA TTTGTGGNAC TATCCTGCAA ANCCCAACAC 360
 TNTNTTCCA AAGNNTTAAA GGCCACATTT TGGGTTGGCC ATTGGTNGGG TTATTNTCT 420
 TGGGAGTTGG GCCCCGGANG GAANTTTGNN TNTGTTNCCN NAANCTTGGG GAACCCTTGG 480
 GTTTNN 486

SEQ ID NO:43

LENGTH:470

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00050

SEQUENCE DESCRIPTION:

GATCCACCAG CTGAGAATTC GTCCGCTCCC GAGGCTGAGC AGGGCGGGGC TGAGTAAATG 60
 CCGGCTTACC ATCTCTACCA TCATCCGGTT TAGTCATCCA ACAAGAAGAA ATATGAAATT 120
 CCAGCAATAA GAAATGAACA AAAGATTGGA GCTGAAGACC TAAAGTGCTT GCTTTTGCC 180
 CGTTGACCAG ATAAATAGAA CTATCTGCAT TATCTATGCA GCATGGGGTT TTTATTATT 240
 TTACCTAAAG ACGTCTCTTT TTGGTAATAA CAAACGTGTT TTTAAAAAA GCCTGNGTTT 300
 TTCTCAATAC GCCTTTAAAG GTTTTAAAT TGTTTCATAT CTGGTCAAGT TGAGATTTT 360
 AAGNCCTTCA TTTTAAATTT GTAATAAAN GTTTACCACC TTGGATTTT TCAANAAAGG 420
 TCAACCAANC TGCAANGCAC CTGTTAATAA NGGGTCTTTA ANTAATTTAA 470

SEQ ID NO:44

LENGTH:479

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00051

SEQUENCE DESCRIPTION:

GATCTGTAAG TAACTTCACA TAAAAAATG AAATATTTT TAATTAAAG CTTACTCTGT 60
 CCATTTATCC ACAGGAAAGT GTTATTNTNA AAGGAAGGT CATGTAGAGA AAAGCACACT 120
 TGTAGGATAA GTGAAATGGA TACTACATCT TTAANCAGTA TTTATTGCC TGTGTATGGA 180
 AAANCCATTT GANGTGTACC TGTGTACATA ACTCTGTAAA ANCACTGAAA AATTATNCTA 240
 ACTTATTAT GTTAANNAT TTTTTTAAT CTAGACAATA TACAAGCCAA AGTGGCATGT 300
 TTTGTGCATT TGTAATNCT GTGTTGGTA GAATAGGTTT TCCCCTCTT TTGTTAANTA 360
 ATATGGCTAT NCTTTAANGG GTTGCNTACT GGGCCAGGTN TAATTTTTG TAATGGNGTG 420
 AAAGGGTGCC ATTTTTTGT CNCACTNNG GGGTCTCANT GGGGGGNTTC TNNCNGGGN 479

SEQ ID NO:45

LENGTH:477

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00053

SEQUENCE DESCRIPTION:

GATCTCTAAG GAACTCCTGT TGCTAAATAT GAAGAGTATG GAACATTCAT ATAGTCTCTG 60
 TGAAGCATGG GGGGAGGGAA GACATTCTT TTTCTTATAG GCTTTATGCT CAAATGTCAT 120
 AGTCTCCTTT CAAAGAATTG TGTTGCATTT TAAATGCACC CAGCTTAAGT AGAAGACATT 180
 GAAGGATGCA TTAATTTTCA GGAACATTTT TGAATTATGA AAAGATTCCC AATTGAAAAA 240
 NTTATTCAAC AAGTAAAAGC TAAGAAATTT CATTGAAATC ATAAGGCAGT TTAAGCATAA 300
 NTTGATAAAA ATAGCTGTGT ACTACTAATT AATAGAAAAT CATTCAACCA AGAGANGAGT 360
 CANGTGAATA TCGTTTGTGTT ATTTGCTAGT GAGTTTCTTT GTAACGTTGG ATTTTATTAA 420
 NTGGTTAATN TTTGGTTAGG TATGTCCTAT GTTANTNAAA ANTGGNCCAA NTTTAAA 477

SEQ ID NO:46

LENGTH:476

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00055

SEQUENCE DESCRIPTION:

GATCACCATT AGCAAATGGA AATNACATTT GAAAGCCATT AGACTTATAG GTGATGCAAG 60
 CATCTAAGAG AGAGGTAAAT CACACTATAG AGGCATAAGT GGTATCAGTT TTCATTTTCN 120
 TAATTGTTTA ANCTGTGTTT TATACCAGTN TTTGCAAGTA ATTGGGTGTT AGCTTGAGAT 180
 GGTTAAAGGT GGTTTGGGGA GGGACTTCGT TGTAATGGTT TTCCTGTAAA ANATGTTTCC 240
 AACTCCNCTG AAATGTTGCT GAAAAGCATG GTGCTGGTAA CAGTTCAACA ATCCCGTGGC 300
 TGCTCATTCT TGGCCTACTT TTACTCTCCC ACTTGNNAGC AGGTTAGCGT TTGAAGGGTG 360
 GTATGGGAAA AGCCTNGCAT TGCCTGGGCC AAATTCCTTT TGGGGTCTN CTCNTTCCC 420
 CNCTCNCCN TNCCTTCCT TTCCCCNTN ANGTCCNNCC NCTTNCNTTA GGTTCN 476

SEQ ID NO:47

LENGTH:472

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00056

SEQUENCE DESCRIPTION:

GATCAAATCT GCACTGTGTC TACATATAGG AAAGGTCCTG GTGTGTGCTA ATGTTCCCAA 60
 TGCAGGACTT GAGGAAGAGC TCTGTTATAT GTTCCATTT CTCTTTATCA AAGATAACCA 120
 AACCTTATGG CCCTTATAAC AATGGAGGCA CTGGCTGCCT CTTAATTTTC AATCATGGAC 180
 CTAAGAAGT ACTCTGAAGG GTCTCAACAA TGCCAGGTGG GGACAGATAT ACTCAGAGAT 240
 TATCCAGGTC TGCCTCCCAG CGAGCCTGGA GTACACCAGA CCTCCTAGA GAAATCTGTT 300
 ATAATTTACC ACCCACTTAT CCACCTTTAA ACTTGGGGAA GGNNGCNTTT CAAATTAAAT 360
 TTAATCNTNG GGGGNTTTTA AACTTTAACC CTTTNCNT TNTNGGGGTN GGNANTTGNC 420
 CCCNTTAAAG GGGGNCCCC TNCNNGGGG AATAAAACAA NTTNNTTTT TN 472

SEQ ID NO:48

LENGTH:472

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00057

SEQUENCE DESCRIPTION:

GATCAAANCT GCACTGTGTC TACANATAGG AAAGGTCCTG GTGTGTGCTA ANGTTCCCAA 60
 TGCAGGACTT GAGGAAGAGC TCTGTTATAT GTTCCATT CTCTTTATCA AAGATAACCA 120
 AACCTTATGG CCCNTATAAC AATGGAGGCA CTGGCTGCCT CTTAATTTTC AATCATGGAC 180
 CTAAGNNGT ACTCTGAAGG GTCTCAACAA TGCCAGGTGG GGACAGATAT ACTCAGAGAT 240
 TATCCAGGTC TGCCTCCCAG CGAGCCTGGA GTACACCAGA CCCTCCTAGA GAAATCTGTT 300
 NTANTTTAGC AACCCAGTTA TCCNCNTTAA NNCTGNNGGAG AGTGGTCTTT ACATCTTAAT 360
 TTTATTCNTG TGGTGGTTNT TACCTTTAAC CCGGTTTCTT ATTTTGGGT TTGTTATTGG 420
 CCCTTTTtag GGGTGGTCCC TTTCCNGGT TGGNTTCCC TTTTTTGTG TN 472

SEQ ID NO:49

LENGTH:319

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00060

SEQUENCE DESCRIPTION:

GATCTCATGG TCCGGAATGA CACCCCTGT GGAACCACCA TTGGACCTAT CTGGGCTTCT 60
 CGGCTGGGGC TCGGGGTGCT GGATTTAGGC AGCCCNNAAC TGGCCATGCA CTCTATCCGG 120
 GAGATGGCCT GCACCACAGG AGTCCTCCAG ACCCTCACCC TCTTCAAGGG CTTCTTTGAG 180
 CTGTTCCCTT CTCTAAGCCA TAATCTCTTA GTGGATTGAG CCCTCTTGA AAGACTTCTC 240
 TGCCATCCCT TTGCACCTGA GAGGGGAAGT TCTCAGCTGA GCTGAAGCTG GATTATTAAA 300
 GTGGATTGTC ACTCAGAAA 319

SEQ ID NO:50

LENGTH:461

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00061

SEQUENCE DESCRIPTION:

GATCTTCCTC TAATTGACAG CCTCATTACG GGTCTTACAA AATATGGAAC AGTGTGAGAA 60
 AAAACCAGAG AACTCGGCAG AGTCTAACAC AGAGGAAACC TAAAAGGACT GATTTAACCC 120
 AAGATGATT CCACCTGAAA ATCTTAAAGG ATATTTTATG TGAATTTCTT TCTAATATTT 180
 TTCAGGCATT AACAAAGGAG ACGGTGGCTC AGGGAGTAAA GGAAGGCCAG TTGAGCAAAC 240
 AGAAGTGTT CTCTGCATTT CAAAACCTTC TTCCTTTCTA TAGCCCTGTG GTGGAAGATT 300
 TTATTGAAAA TCCTACGGTG AAGTTGATAA GGCCTTTGCT TGGATGGGCT TGGGATAAAA 360
 ACCCTTTCCC AAGTTTAAA GGGTTTCAGG TCTTTAAATC CCTGAAATTT TGGGATTTCT 420
 TTCTTGTTCC AGGTGTTTA AACCTTTTAT TTTTCTCTCC N 461

SEQ ID NO:51

LENGTH:458

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00062

SEQUENCE DESCRIPTION:

GATCTAGCAT ATTTACTAT TCTGTGGATG AATACATAGT TTGTGGGGAA AACAAACGTT 60
 CAGCTAGGGG CAAAAGCAT GACTGCTTTT CCCTGTCTGG CATGGAATCA CGCAGTCACC 120

TTGGGCATTT AGTTTACTAG AAATNCTTTA CCTTAAGCAG CACACACATT TACTACACAC 180
 ACAGNCCTAA CAAAGCACTG TGCTTAGAGG GTAAAAAGGA ATCACAAAAC AAGAATCTTT 240
 CCAAAGTTGT CTCATTACAG AATGTTAAGG CATCTGTATC AAATTATTTT GGATGTAAAG 300
 ATTCCTGTGT CTCATAATAT GAATGTATTT TTTGATATAC AAGGAAACTG GCCATAAAAA 360
 TGGTGNGGNA ANCCGCCCN TAATTTNCC CCTGGGGCCC CAATTGGTNN NNTCNANTCT 420
 NGGNTTNAGC NTTTGTCTC AAATGGGATN CANTNNN 458

SEQ ID NO:52

LENGTH:459

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00064

SEQUENCE DESCRIPTION:

GATCTATCAC CCAAACATCG ACGAAAAGGG GCAGGTCTGT CTGCCAGTAA TNAGTGCCGA 60
 AAACCTGGAAG CCAGCAACCA AAACCGACCA AGTAATCCAG TCCCTCATAG CACTGGTGAA 120
 TNACCCCCAG CCTGAGCACC CGCTTCGGGC TGACCTAGCT GAAGAATACT CTAAGGACCG 180
 TAAAAAATTC TGTAAGAATG CTGAAGAGTT TACAAAGAAA TATGGGGAAA AGCGACCTGT 240
 GGACTAAAAT CTGCCACGAT TGGTTCAGC AAGTGTGAGC AGAGACCCCG TGCAGTGCAT 300
 TCAGACACCC CGCAAAGCAG GACTCTGTGG AAATTGGCAC GTGCCACCGN CTGGCGTTCG 360
 NTTGTGGCAG TTACTAAGTT TTCTACAGTT TTCTTAATCA AAAGTGGTCT TAGGTAANCC 420
 TGTAAGGNA AGGGGTTTAN NAATTTTANG GTTGGTCTN 459

SEQ ID NO:53

LENGTH:458

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00065

SEQUENCE DESCRIPTION:

GATCAGCTGG CCAACTCAGC CAATCCGCAC ATTTAGCTCT CCAACTACCA TACAACGTGC 60
 TTGGTTTAGG TCGGAGCGCA AATNTNCTTG ACCATCTCTA CGTTGGTATT CCCCGTCCAT 120
 CTGGAGAAAA ATCTATACGA AANCAAGAGT GGACTGCAAT NATTCCAAAT NCCCAGCTAA 180
 TTGTCATTCC ATACCCTCAC AATGTCCCTC GAAGTTGGAG TGCCAAACTG TATCTTACAC 240
 CAAGTAATAT TGTNCTGCTT ACTGCTATAG CTCTCATCGG TGTCTGTGTT TTCAATCTTT 300
 GGCAATAAAT TGGCATTTTA CCATTTGNCA GGGAAAAGGA AAGGCNGGTT GGNTTGGGGG 360
 GAAAACCGGC CAAGGGANGG CCCCCCGGG TTTTCNATTT TTGGNNGGNT TTTTGGGNNT 420
 TTTGCCTTTT TAAANTTTTT CCNAANAAAN NGGGANTN 458

SEQ ID NO:54

LENGTH:454

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00066

SEQUENCE DESCRIPTION:

GATCAGTTNC GTGTCCGCNG GAGCAGGCCT TGCTGAGTGA AGACACTGGN ACTAGCTGGG 60
 TCCTGGGGTG ACTTGGAGGC TTTGGGCCTA AAAGGGCAGC CTGAACCTGG AGTCTTATCT 120

CCCCCAGGAG CCGAAAGCAC TTTTCTTGAT TTCCCCCAGG AAATCAAGCG CTGCTTCTCA 180
 GCTCCTGTGG TTTTAGTATT TATATATCTG TATCTTCTTT GTAGAAATTT ATTTATTTT 240
 GAATAAGAAT ACCTGCCTGG AAAAAATTA AAAGGACGGG AGGGCGAANT GCAAGGGAAG 300
 GCCTCTCCTA TGCCGNCCCA GAGNAGCACT GTACCAATTT CATGTGATTC CTTAACTCTG 360
 TTTAAGGAAG CTCTGAAACT GTCATTTCTT TTGCAGATTG TTNTGAACCT GGAAACCCNG 420
 AATTTATNGN TAANNCTCAN TTNCCACCNG GAAA 454

SEQ ID NO:55

LENGTH:505

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00067

SEQUENCE DESCRIPTION:

GATCGTTGGG GAACCCAGCC CCTTGGAAC TGGAGACCC GTGTTTCCTG GACCGCGAAT 60
 CAGTGTGTTG GGCATCAGTG TTTTCTGCAA GGGTTGTGAC CTGAAACTTT TAAAAACCA 120
 CCCACCTTTG GGAAGCATT TCTGAATTA TCCATCACCA ACCATTTCTT CTTGGATACC 180
 ATCAAGTAAC AGCTATTATT TGCCAAGTGG AGCTGTCATT TAATTTGATG CACCTCTGGN 240
 TTCAGATGAA ACATTAAATT GTCTTCCTCG ATTCTCCATC GGGTGTAGAG TTTTAAACT 300
 ATCANTGGCA TTTCAAGTCT TCTGANACAA CATGGCTGTA TGTGCGTGGT CCATAGCACA 360
 GTACATGCAG CATCTAATAA GNGTTTCCAT TTGTAGAATT NTTTTCNCA NACTTNTAGT 420
 TAAANNCAAA ATTTTTTAAT TTGNAANAA GNGNTGNGTT GGTTATTTNN GNTGTTNTT 480
 GTNTNTGGTT GNTNTGTTTA TTNTN 505

SEQ ID NO:56

LENGTH:450

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00068

SEQUENCE DESCRIPTION:

GATCAGAGAC TGGAGAGGTG GAGTGAGAAG TCTCCGCTGC TCGGGCCCTC CTGGGGAGCC 60
 CCCGCTCCAG GGCCTGCTCC AGGACCTTCT TCACAAGATG ACTTGCTCGC TGTTACCTGC 120
 TTCCCCAGTC TTTTCTGAAA AACTACAAAT TAGGGTGGGA AAAGCTCTGT ATTGAGAAGG 180
 GTCATATTTG CTTTCTAGGA GGTGTTGTGT TTTGCCTGTT AGTTTTGAGG AGCAGGAAGC 240
 TCATGGGGGC TTCTGTAGCC CCTCTCAAAA GGAGTCTTTA TTCTGAGAAT TTGAAGCTGA 300
 AACCTCTTTA AATCTTCAGA ATGATTTTAT TGAAGAGGGC CGCAAGCCCC AAATGGAAAA 360
 CTGTTTTTAG AAAATATGAT GATTTTTGAT TGCTTTTGTA TTAAATTCTG CAGGTGTTCA 420
 AGTCTTAAAA AATAANGATT TNTANCAGGN 450

SEQ ID NO:57

LENGTH:447

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00069

SEQUENCE DESCRIPTION:

GATCTTTGAT AGTNGAGAAA ATTATGCAAA GTTCCTCAGA AGTNGGTTAT NATGCTATGG 60

CTGGNGATTT TGTGAATATG GTGGAAAAAG GAATCATTGA CCCAACAAAG GTTGTGAGAN 120
 CTGCTTTATT GGATGCTGCT GGTGTGGCCT CTCTGTAAAC TACAGCAGAA GTTGTAGTCA 180
 CAGAAATTCC TAAAGANGAG AAGGACCCTG GAATGGGTGC AATGGGTGGA ATGGGAGGTG 240
 GTATGGGAGG TGGCATGTNC TAACTCCTAG ACTAGTGCTT TACCTTTATT AATGANCTGT 300
 GACAGGAAGC CCAAGGCAGT GTTCCTCACC AATAACTTCA GAGAANGTCA GTTGGAGAAA 360
 AATGANGAAA AAGGGCTGGC TTGAAANTCA CTNTTAACCN NTTANGGTTG CTTGGGTTTC 420
 ANGTTGGCCA NAGTTTTNNN TNNTGGN 447

SEQ ID NO:58

LENGTH:445

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00070

SEQUENCE DESCRIPTION:

GATCACTGAG CAGTTTTCCC AGAGCTCCAT GGAAGGCAA GCTCTCCCTC CCAATGGGAG 60
 CCCCCTGTC ACTAACTGTA AACTCAGGCT CAGGCTTCAN CTGCCTACCC CCATCCTCAT 120
 ATTTCTGTCT GTCCCAGCAC CTCAGGAGCA TTCTCATTGT GGCCGGCTAA CTCCGCCTGG 180
 ATGTGAACAG GCAAGCACAG TGGGAAATNA GTCACGTA CTGTATTGCAC AGTGGACACC 240
 TCTAGAGGTC CATTGGTTTA AAGGGATAGG GAAGGAGGAG GGATGAGACC ATCTCCCCCT 300
 CCCAGGAAGT AAATCTAAGT ATCTAAGGTT TTCTTTATNG CCTTNGAGTC AACTANTAA 360
 CTGGCTAGTA CGGGAGGTGT NTGCTNGGTT TNTTCGGGT GGTTTTTTCC TAATGNAATA 420
 AACTTCATTT NTTGCTGNT TGGNN 445

SEQ ID NO:59

LENGTH:459

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00071

SEQUENCE DESCRIPTION:

GATCTTCGGT GGCCTCATGT AAACGTGGCA GCCAGCCTCT TCTAGAACCC TAGCCCAGGG 60
 ACTGGAGCAG GAAAGGGACC TTCAAAGTGA AGACTGCCTT GTCCCGCAGC TCCTTCTGGC 120
 TTAGATTGAA ACATGGGCTT CCTAATGGGT TAAATCCTTT AAAACAAGGA GTTGTGGGGG 180
 AAGGGTGTCTG TGCACTCCTA GAGAAAGGTA CACAGTTGCC CGGTTGGGAA TGTGCTTGGC 240
 GCTGACCCTG CGGGCATCTG ACTGGTCTTC CAGCTCAGGA AAAAGAATTT GAAAGAGGCT 300
 TAGCGTGAAG GGAATCAAAA GAGGAGGTTG TNATTNGGT CGAAGGTGCC TTGGTTAAG 360
 TCCTNGTAAT TTGTNCTTAT TAATTTTTTT TNATATAATA TNATTTTNTT GGGGGGTAAA 420
 CCATTTTAA ATTAAACCAA CCATTTGTCT TNCTNGAAA 459

SEQ ID NO:60

LENGTH:441

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00072

SEQUENCE DESCRIPTION:

GATCAGACAC TTCAAGGTCT AGGCTAGACA TGGCAGAGAT GAGGAGGTTT GGCACAGAAA 60

ACATAGCCAC CATTITTTCC AAGCCTGGGC ATGGGTGGGG GGCCTTGTCT GCTGGCCACG 120
 CAAGTTCACA TGCNATCTAC ATTAATATCA AGTCTTGACT CCCTACTTCC CGTCATTCCCT 180
 CACAGGACAG AAGCAGAGTG GGTGGTGGTT ATGTTTGACA GAAGGCATTA GGTGACAAC 240
 TTGTCATGAT TTTNACGGTA AGCCACCATG ATTGTTTCT CTGGCCTCTG GGTGACCTT 300
 AAAAAACCC ATTTGGAAC TGNNGACTTT GAAANGGTGC TCTTGCTTA AGGCTTTNAT 360
 ATNGNGCCTT GTTTAATTGG GANGGTCNCT TNAAGGCC NTTTCCTTA NTTAANGNG 420
 GGGTTNTTAN GGNTGTAGAA A 441

SEQ ID NO:61

LENGTH:436

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00073

SEQUENCE DESCRIPTION:

GATCCGTCAC TCTTCCTTGT GGTAAATCCCT AGACTGGGAG CTCAGGTACT CTTTATGTCA 60
 TCTTTGTATG TCTTTAGCAG AGTTCTTGAC ATGTGGTAGG TGCTTAATAA ATNTTGTG 120
 TTTATCAAAT TTTATGGTAG GGAGAGTAAG TCAGCATCGG TATAAAATCG CTTACTCCAC 180
 GTAACCTTC TTCTGATAGG GTTTGATTTT CTATTAGAAG CTCAATTTA GTTTTTTTC 240
 ATATTATAAC TAAATATGTT TCCTGAGAGA TAAGAGAAAT AATGTTCTTA CAATAGTTGT 300
 ATGTATCTAA GATAAGACAT ATAGATGCTT AAGACATTT GTTTCATTG CTATTCATA 360
 GTGTAATTGA ACCATGGTCA TTTTAGCCC TTTTCCTAGG GACCATGCTT ATTTCTCAAT 420
 AAGGAAATAC CTTCCN 436

SEQ ID NO:62

LENGTH:434

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00074

SEQUENCE DESCRIPTION:

GATCTTTTTC CATCCAGCAG TGGAGTTTAG TACTTAAGAG TTTGTNCCCT TAAACCAGAC 60
 TCCCTGGATT AATGCTGTGT ACCCGTGGGC AAGGTGCCTG AATTCTCTAT ACACCTATTT 120
 CCTCATCTGT AAAATGGCAA TAATAGTAAT AGTACCTAAT GTGTGGGGTT GTTATAAGCA 180
 TTGAGTAAGA TAAATANTAT AAAGCACTTA GAACAGTGCC TGGANCATAA AAACACTTAN 240
 TAATAGCTCA TAGCTAACAT TTCCTATTTA CANTTCTTCT AGAAATAGCC AGTATTTTGT 300
 TGGAGTGCC TACNATGTTAG TTCCTTNTAC TAGTTGCTT ACATGGATTA TCTTNATATC 360
 CTGTTTTAAA GNTTNTTCAC AGGTACCAGG TTTTCATGGA ATTTTCCTT NANTAAANGG 420
 GGAGGNNAAN GNTN 434

SEQ ID NO:63

LENGTH:433

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00075

SEQUENCE DESCRIPTION:

GATCTGTGAA TCTTGGCTGG GACTTCCTCT GAGTGATGCC TGAGGGTCAG CTCCTCTAGA 60

CATTGACTGC AAGAGAATCT CTGCAACCTC CTATATAAAA GCATTTCTGT TAATTCATTC 120
 AGAATCCATT CTTTACAATA TGCAGTGAGA TGGGCTTAAG TTTGGGCTAG AGTTTGACTT 180
 TATGAAGGAG GTCATTGAAA AAGAGAACAG TGACGTAGGC AAATGTTTCA AGCACTTTAG 240
 AAACAGTACT TTTCTATAA TTAGTTGATA TACTAATGAG AAAATATACT AGCCTGGCCA 300
 TGCCAATAAG GTTCCTGCTG TGTCTGGTTA GGCAGCATTN CTTTGTATGC AAATTTCTTA 360
 TTGGNCCCTN TTTTNTCCA AAAAGGTAAA TGNCTNNAT TNCCCGGTTA AAAAATNNTT 420
 CCCNGGNNAT TTN 433

SEQ ID NO:64

LENGTH:432

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00076

SEQUENCE DESCRIPTION:

GATCCTGGAG GTCITTTCTA GTCTGAGCTT CTTAGCTAG GCTAAAACAC CTGGGCTGT 60
 TATTGCCTCT ACTTTGATTC TNATAATGCT CACTTGGTCC TACCTATNAT CCTTCTACTT 120
 GTCCAGTTCA AATAAGAAAT AAGGACAAGC CTAACCTCAT AGAAACCTCT CTATTTTAA 180
 TCAGTTGTTT AATAATTTAC AGGTTCTTAG GCTCCATCCT GTTGTATGA AATTATAATC 240
 TGTGGATTGG CCTTAAAGCC TGCATTCTTA ACAAACCTTT CAGTTAATTC TTAGATNCAC 300
 TAAAANTCTG AGGAACTCTA CATGTAACCTA TTTCTTCAGA GTTGTGCATA TACTGNTTGG 360
 CATCTGAATG GCTACTCAGC ATTTGGTTAA CATNGNGTA AATTTGGAAT AAANTTCCCC 420
 AGTAAGCCAT TN 432

SEQ ID NO:65

LENGTH:459

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00077

SEQUENCE DESCRIPTION:

GATCCATCGC AGAGTCCTAA AGAAGAACC ACTGAAAAAC TTGAGAATCA TGTGAAGCT 60
 AAACCCATAT GCAAAGACCA TGCGCCGGA CACCATTCTT CGCCAGGCCA GGAATCACAA 120
 GCTCCGGGTG GATAAGGCAG CTGCTGCAGC ANCGGCACTA CAAGCCAAAT CAGATGAGAA 180
 GCGCGCGGTT GCAGGCAAGA AGCCTGTGGT AGGTAAGAAA GGAAAGAAGG CTGCTGTTGG 240
 TGTTAAGAAG CAGAAGAAGC CTCTGGTGGG AAAAAAGGCA GCAGCTACCA AGAAACCAGC 300
 CCCTGAAAAG AAGCCTGCAG AGAAGAAACC TACTACAGAG GAGAAGAAGC CTGCTGCATA 360
 AACTCTTAAA TTTGNTTATT CCATAAAGGT CAAATCATTT TGGNCAGCTT CTTTTTTGAA 420
 TAAAAGNCCT GNTTATACC AGGGCAGTGA GGAACCAA 459

SEQ ID NO:66

LENGTH:626

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00078

SEQUENCE DESCRIPTION:

GATCTACAAA GGCCATGGGA AAAATTCAGA GAGTTAGGAA GGAAAAACCA ATAGCTTTAA 60

AACCTGTGTG CCATTTTAAG AGTTACTTAA TGTTTGGTAA CTTTATGCC TTCACTTTAC 120
AAATTCANGC CTTAGATAAA AGAACCGAGC ANTTTTNTGC TAAAAAGTCC TTGATTTAGC 180
ACTATTTACA TACAGGCCAT ACTTTACAAA GTATTTGCTG AATGGGGACC TTTTGAGTTG 240
AATTTATTTT ATTATNCCC TTTNGTTTAA TGTCTGGTGC TNNCTATCAC CTCTTCTAAT 300
CTTTTAATGT ATTTGTTTGC AATTTTGGGG TAAGACTTTT TTATGAGTAC TTTTCTTTG 360
AAGTTTtagc GGTCAATTTG CCTTTTAAAT GANCATGTGA AGTTATACTG TGGGCTATGC 420
ACCAGCTCTC ACCTACNGGG GGNCTTACCT TGGGGGTAGN GNCCATACCA GNCCACTGTA 480
TGTTTACTTC CTCACCCATT TGGNGTTGCC CCANCTTGGT TNAACACTNG GGCANCATTN 540
TGGTTTnagg GGNCCTTAGG GTTNACCAGN TCNTTTTAA NGGNTATTNN CCCGGGGTTT 600
TTTNAANTG GCCCAAAATN CTTAAA 626

SEQ ID NO:67

LENGTH:534

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00079

SEQUENCE DESCRIPTION:

GATCAACAGT TCTAGTACTC TTCTTTGTCA GTATATCAAC CTACAGCTAT TGAATGCAAA 60
GCCACAAGAG TGTTTAATGG GGACAGTGGG CACTCTCCTG CTTGAAAACC CACTTGGGCA 120
GAATGGACTC ACCCAACCAAG GTCTTCTGTA TGAAGCAGCC AAGGTGTTTG GCCTTCGGAG 180
CAGGAAGCTA AAGCTGTTTC TGAATGAGAC CCAAACGCAG GAAATTACAG AAGACATCCC 240
CGTGAAGACT TTGAATATGA AGACTGTGTA TGTTCCTGTG TTACCAACAA CAGCAGACTT 300
CTAGCATGTA CTTATCAATG TTGTTCCGTC AGCCCTTCCC TAATTACACC TATCCCCTAC 360
ACATACATGC ACATAGNCAC ACACATGNAC ACACTTGAAG GTATTTCCCT CAAGGTGTGT 420
GTAAAAATAT GCTGCTTGGN TTTGAATTCA AATGGGGTTG NTTAGGTCAA GTACTTTNG 480
GCCTNANAGG NATCTTCACA CTTAACCTTA GGCACTTTG ANGCA TTGTT GGGN 534

SEQ ID NO:68

LENGTH:417

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00080

SEQUENCE DESCRIPTION:

GATCTTAGTT GATATTTTGG GCTTGGGGCA GTGAGGGCTT AGGACACCCC AAGTGGTTTG 60
GNAAGNAGG AGGGGAGTGG TGGGTTTATA GGGGGAGGAG GAGGCAGGTG GTCTAAGTCC 120
TGA CTGGCTA CGTAGTTCNG GGCAATCCT CAAAAGGGA AAGGGAGGAT TTCCTTAGAA 180
GGATGGCGCT CCCAGTGA CTCTTTTGAC TTCTGTTTGT NTTACGCTT TCTCAGGGAA 240
AAACATGCAG GTCCTCTAGT GTTTCATGTA CATNCTGTNG GGGGGTGACA CCTTGGTTCT 300
GGTTAAACAA GCTGTACTTT TAATAGCTGT TNCAGGAAG GTTAAGGCCA ACTACAAATT 360
AATGTTGGTT GCAATGTAG TGTGGTTCCC TAACTTTNCG GGGTTTCTCT GAGGAAA 417

SEQ ID NO:69

LENGTH:417

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00081

SEQUENCE DESCRIPTION:

GATCTGCCTG CCCACCAACT GGTGATGGAA GGTACAAGT GGCACCTCAA TGAGACGGTG 60
 CTCACGTGTG GGTCCGCACC AACTACTGCT ACCGTGTGGG AATGTGGCAG CATCTTGGAG 120
 CTGGACGAGC ATCTCCAGAA AGATTTCATC ATCTTTGAGC TGCTCCCAAG AGCACGGGGC 180
 ATCCCTCCAA GAGCCGTGCC GCTATTCCTG TGACCCGCCG GCCTGCCCTC ACCTTTGGCT 240
 CGACATGTGC TTGCATTTCT AGCGAGCTGG CGTGGGGGCT GTCTGGTGT GTCCCAAGAG 300
 GTGTTGAGGT AGGTNTTGAG AGCTGAGACT AGTCATGTCT CTCTTCCAT TACATGAGTT 360
 CATATTTTNN TTTTCTNTTT TGTGTTAGTA ATTTGGAAAT GAAATTATAA GGAATGN 417

SEQ ID NO:70

LENGTH:415

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00082

SEQUENCE DESCRIPTION:

GATCTTTCTG GGAACACAGC CCNGCTGGCG GCTAACCTGC TGTGTTGAGT GCTATGTGCT 60
 CTCCCCAAAG TGACAACCGT CTGAGTCTTG TGCTCTTCAA GACAAAACAG ATTGCGTCGC 120
 TGACAAGTTC TCAAGAAGAA CTTATGAGTA AGCAGTCTGA GAACTAAAGA GTTTATGCCA 180
 AGAAAACTTT CTGCTGAAAG TGTCATTGCT GGCTGTGAAG TCGGGATAAT CAGTAGAATT 240
 CTCACCCAAA CAGCAACATT TCTAAGGAAC TTGGATTAAT TGGGGGAAAA AAAANGGGGT 300
 ACTTGACTG CTTTGATTG TTTTCCTTG GNTGAAAAGN TGGGGGGTTA AANGGGGGAT 360
 NGTGAGGGGG ANTTNCTTN TNNAGGGNTT TTTNTNANC CCATTNNGN NTNCN 415

SEQ ID NO:71

LENGTH:415

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00083

SEQUENCE DESCRIPTION:

GATCAGAATC ATTAATAAAT ATTTTGTGTT AGTAAGTTG AAGATTCNN GCTTNNAGGC 60
 CTTTCTATT TTGTCCATT TATTTTNCA GGCAATCTTT TCCATGGAGG GCAGGGTATC 120
 CATTCTTTAC CATGGGTGTA CCTGCTTAGG TAAAAATCA TACCAAGGCC TCATACTTCC 180
 AGGTTTCATG TTGCGTCTG TTGAGGGAGG GAGAGCAGGT TACTTGCAA CCATATTGTC 240
 ACCTGTNCCT GTCACACATC TTGAAAAATA AAACGATAAT AGANCTAGTG ACTAATTNC 300
 CCTTACAGTT CCTGCTTGGN CCCACCCNAC TNGGGGTNGG CTCCATTGGT NNGTCCGGG 360
 GCCGTNNTTT AGGGGGNANT TGGGGGNTCG GTTAGGCCTN TNGGTTTGGG GAAAN 415

SEQ ID NO:72

LENGTH:410

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00084

SEQUENCE DESCRIPTION:

GATCTCCCN CTCTAGGGGT CAGGCTCCAT TAGGATTGTC CCCTCCCAN CTCTCCTAC 60

CCAACCACTC AAATNAATCT TTCTTTACCT GAGACCAGTT GGGAGCACTG GAGTGCAGGG 120
 AGGAGAGGGG AAGGGCCAGT CTGGGCTGCC GGGTTCTAGT CTCCTTTGCA CTGAGGGCCA 180
 CACTATTACC ATGAGAAGAG GGCCTGTGGG AGCCTGCAAA CTCACTGCTC AAGAAGACAT 240
 GGAGACTCCT GCCCTGTGTT GTATAGATGC AAGATATTTA TATATATTTT TGGTTGTCAA 300
 TATTAAATAC AGACACTAAG TTATAGTATA TCTGGACAAG CCAACTTGTA AATACACCAC 360
 CTCACTCCTG TTACTIONT AAACAGATAT AAATGGCTGG TTTTAGAAA 410

SEQ ID NO:73

LENGTH:406

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00085

SEQUENCE DESCRIPTION:

GATCGTGACG CTGAATAAAT GTCTTTTTTT TAATGTGCTG TGTAAGTTA GTCTACTCTT 60
 AAGCCATCTT GGTAAATTC CCCAACAGTG TGAAGTTAGA ATTCCTCAG GGTGATGCCA 120
 GGTTCATTTT GGAATTTATA TACAACCNGC TTGGGTGGAG AAGCCATTGT CTTCGGAAAC 180
 CTTGGTGTAG TTGAAGTAT AGTTACTGTT GTGACCTGAA GTTCACCATT AAAAGGGATT 240
 ACCCAAGCAA AATCATGGAA TGGTTATAAA AGTGATTGTT GGCACATCCT ATGCAATATA 300
 TCTAAATTGA ATAATGGTAC CAGATAAANT TATAGATGGG AATGAAGCTT GTGTATCCAT 360
 TATCATGNGT AATCAATAAA CGGNTTNAAT TCNCTTGGAN TGGAAA 406

SEQ ID NO:74

LENGTH:408

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00086

SEQUENCE DESCRIPTION:

GATCACATTG TAAACTATG GATGGTCTGA TAAGGCTTN ACTGACCCCA CTGACTTCAG 60
 AGTTATACTC TGTTTGCNAC ATCATAATGC TGGTTTTCCT GACTTTTGT NTTTTAATAT 120
 ATTTATAAAA AAAGAAAAAG TTGGTGATTG CATTGGGAAA TTCCAGGGT ATTACTGGAC 180
 CTATGTGGTG TATTGTTAAA CCAGTGTCTT TGTNACTG TTGCTCTGA TGTCCTGAT 240
 ACAGGTAAGG ANGCAATTGG TCAACTCTNA TACAAAGTAT ATATACAGTT CAGTATTGTC 300
 TCTGTTCAAT TTGTTTAAAT TTCATTGGNC AAANTCAANC CAGCATTCCT CATTGTGTA 360
 AATAAATGAT TTTCTGGAA TAAAAGGNA AGGNCCTNAA ATTCCAAA 408

SEQ ID NO:75

LENGTH:407

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00087

SEQUENCE DESCRIPTION:

GATCAAACTA GCTCAGGCCA AACTTTAAGT TCATACCTGA GCTAAGAAGG ATAATTGTCT 60
 TTTGGTAACT AGGTCTACAG GTTNCATTT TTCTGTGTTA CACTCAAGGA TAAAGGCAAA 120
 ATCAATTTTG TAATTTGTTT AGAAGCCAGA GTTTATCTTT NCTATAAGTT TACAGCCTTT 180
 TNCTTATATA TACAGTTATT GCCACCTTG TGAACATGGC AAGGGACTTT TTTACAATTT 240

TNATTTTATT TTCTAGGTAC CAGCCTAGGG GATTTCGGGT TAGGTACTCA TTTTGTATTC 300
 ACTGTCACCTT TTTCTCATG GTCCTAATTA TAAATNGNCC CAAAATCAAG GNTTGCCTNA 360
 AAAAGGGGGN AAAATGGTTG GCCCCNNGGT TTTTNGNNNC CCCNGTN 407

SEQ ID NO:76

LENGTH:413

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00088

SEQUENCE DESCRIPTION:

GATCTACCGA CTCACTTCTG AGAATATTTT TNACAGATTA TCTTTGGGCC TTTCCATTAG 60
 AAAGCTGTTT GTTTGTCCCC CTGTTGGTAC ATTTGGTTAC CTCATTTTGC CGTTTCAAAT 120
 TGTAAGAGCT CACAGGGGTG TTTTGTGAA TCATTGCTG AGTCATTTTC TCAAATCATA 180
 TTCCATTGTA TCAGTTAACA TATAGTTTTA AATGTATGTA TTATAAATNT CTGTANCCAA 240
 ATCATTGAA GGCTTGATAA ATTTNTAACA ANGTTGTAC ATTTNTCATG AAAGTCACTA 300
 GTAATGCTNG GNGNGGTAGT GCAATGGANT TTTCCNTTTT TCNTCCCTGT GCCCATTTTG 360
 GAGTTGAGAG GGTGTNGGT AATNAACTGT ATGGTGTA CA NTGNANCCNA NNN 413

SEQ ID NO:77

LENGTH:417

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00089

SEQUENCE DESCRIPTION:

GATCGGCAAG CCNCACTG TCCCTTGCAA GGTGACAGGC CGCTGCGGCT CTGTNCTGGT 60
 ACGCCTCATC CCTGCACCCA GGGGCACTGG CATCGTCTCC GCACCTGTGC CTAAGAAGCT 120
 GCTCATGATG GCTGGTATCG ATGACTGCTA CACCTCAGCC CGGGGCTGCA CTGCCACCCT 180
 GGGCAACTTC GCCAAGNCA CCTTGATGC CATTCTAAG ACCTACAGCT ACCTGACCCC 240
 CGACCTCTGG AAGGAGACTG TATTCACCAA GTNTCCCTAT CAGGGAGTTC ACTGACCACC 300
 TCGTCAAAGA CCCACACCAG AGGTCTCCGT GCAGNGGACT TCAGGNTNCA GNTTGTGGTT 360
 ACAACATAGG GGNTTTTAT ACAANGGAAA NGTAAAGGTG NNNTTAAAGN GGTGAAA 417

SEQ ID NO:78

LENGTH:404

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00090

SEQUENCE DESCRIPTION:

GATCAGAAGA AACACTCCAA AAATTGAGAT GAAATGTTGG TGCAGCCAGT TATAAGTAAT 60
 ATAGTTAACA AGCAAAAAA GTGCTGCCAC CTTTATGAT GATTTTCTAA ATGGAGAAAC 120
 ATTTGGCTGC ATCCACATAG ACCTTTATGT TTTGTTTCA GTTGAAAAC TGCCTCCTTT 180
 GGCAACATTC GTAAATNAAG CAGAATTTT TTTTCTCTT TTTCCAAATA TGTTAGTTTT 240
 GTNCTTGTA GATGTATCAT GGGTATTGGT GCTGTGTAAT GAACAACGAA TTTTAATTAG 300
 CATGTGGTTC AGAATATNCA ATGTTAGGTT TTTAAAAAG TATCTTGATG GTTCTTNTTC 360
 TATTTATAAT TTCNGACTTT CATAANGTGT ACCCANGANT TTCN 404

SEQ ID NO:79

LENGTH:622

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00091

SEQUENCE DESCRIPTION:

```
GATCCCCGCA ACTCGCTTGT CCTTGGGTCA CCCTGCATTC CATAGCCATG TGCTTGTCCTC 60
TGTGCTCCCA CGGTTCCAG GGGCCAGGCT GGGAGCCCAC AGCCACCCCA CTATGCCGCA 120
GCGGCCCTAC CCACCTTCAG GCAGCCTATG GGACGCAGGG CCCCATCTGT CCCTCGGTCG 180
CCGTGTGGCC AGAGTGGGTC CGTCGTCCCC AACACTCGTG CTCGCTCAGA CACTTTGGCA 240
GGATGTCTGG GGCCTCACCA GCAGGAGCGC GTGCAAGCCG GGCAGGCGGT CCACCTAGAC 300
CCACAGCCCC TCGGGAGCAC CNCACCTCTG TGTGTGATGT AGCTTTCTCT CCCTNAGCTG 360
CAAGGGTCCC GATTTTGCCA TCGGAAAAG ACAACCTCTA CTTTTTNCCT TTTGTATTTT 420
TGATAAACAN TTGAAGNTTG GAGCNTGTTA AAATTTATTN TTTGGGGGGA AACCTNAAGA 480
ACTGGGNCTT AATTNGNGG TTCGTGGGAC CCTNTTANNT GGTTTTNAAT NAANCGGTTA 540
NGGAATTAAT CTGTTTGGGA ANANTTGGTT TAAAGNTTAA AAATTTTGGG AAAAAAAGGG 600
GCTTTTAAAT TTTTGGGT TN 622
```

SEQ ID NO:80

LENGTH:400

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00092

SEQUENCE DESCRIPTION:

```
GATCTTCCTT TTTCTNTGA ATNGCTCTG TTGNCTTTT CTCTTTTTC TCATGTGTTT 60
TTCCCTCCAC CTCCACCCCT TTCTTTCTT CTCTCTCTGA TTGAGAGGCA TTNAATTACG 120
TTTTAGTAG TACAGGCTTC TTGCCGATAT GAAGGGAAGT TTTCAGAAAG AGACCTACTC 180
TGGGTCATTT AATTTTGAAT ACAGTTTCA ATCGTTCAAG TTTTGGNNNG NTTATATCTA 240
ATGTGTGTTT CATTTTTTG GAAAGCTATA TTTTGTATTT AGGAAATGGT ATACTATTTT 300
GCTATTTGTA CTGAGTGAGT ACATTGGCAT AAATATAGAA ATTTATATAT ATACATATAT 360
ATAACTGTGC TNNTGCCCT TTTNNTGNG GGAAATTGGN 400
```

SEQ ID NO:81

LENGTH:396

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00093

SEQUENCE DESCRIPTION:

```
GATCAGACTG TGGCATTGTA AATGTCAACA TTCCAACAAG TGGGGCTGAG ATTGGAGGTG 60
CCTTTGGAGG AGAAAAGCAC ACTGGTGGTG GCAGGGAGTC TGGCAGTGAT GCCTGGAAAC 120
AGTACATGAG AAGGTCTACT TGTACTATCA ACTACAGTAA AGACCTTCCT CTGGCCCAAG 180
GAATCAAGTT TCAGTAAAGG TGTTTTAGAT GAACATCCCN NAATTTGAGG GTGTCCAGC 240
AGCTGTTTTT GGAGAAGACA AAGAAAATTA AAGTTTCCC TGAATAAATG CATTATTATG 300
ACTGTGACAG TGAATAATCC CCCTATGACC NNAAGNCCT GATTAAATCA AGAGATTCTT 360
```

TTTTTAAAAA TCAANTAAAA TTGTNACACC ATAAAA

396

SEQ ID NO:82

LENGTH:400

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00094

SEQUENCE DESCRIPTION:

GATCGATGGT TGACAATCCA GAGTGGTGAA CAGCCCTACA AGATGGCTGG TCGATGCCAT 60
 GCTTTTAAAA AAGAATGGAT AGAATGTGCA CATGGAATNG GTTATACTCG GGCAGAGAAA 120
 GAGTGCAAGA TAGAATATGA TGATTTCGTA GAGTGTTCGTTTC TCGGCAGAA AACGATGAGA 180
 CGTGCAGGTA CCATCAGGAA GCAGCGGGAT AAGCTGATAA AGGAAGGAAA GTACACCCCT 240
 CCACCTCACC ACATTGGCAA GGGGGAGCCT CGGCCCTGAA CAGAGCAGCT GCTGATGTCT 300
 GGAGGCTGAT TTTCTGTTC TCTGTTCTCC ACTGGAAAAGG TTGTTTACGA CAAACCTCCT 360
 TGTCAAAGTN TGTAAAAATA AAGGATTGCT CCATCCTAAA 400

SEQ ID NO:83

LENGTH:397

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00095

SEQUENCE DESCRIPTION:

GATCTGGGCA CTGTACTTNA GCCTGGGCGA CAGAGAGACC CATCTCAAAN AAAAAATTGG 60
 AACCTGAGAA GGGGGTCGTG GGGTCCCCGG GGCCACCGT CTGCACTGG NATCTNAAGT 120
 CGGGGTGGNC TTGTGGGACT NACCCNTTAC CCTGTGGGTT CTGTACTAGC TCCGGGNAAT 180
 TGGTGACAGA NTCGAGTTAA ATTGTAGGAC ATCGCGTTGG TGTCTGAGAG GGAGTTGGAG 240
 AGCTGGTTGG TGTGGAGGGA AAGGNTTACA CACATGTNAT TTCAGAAGCG TTCTGTGGGT 300
 AGAGGAATCG TTTTCTCTTT GAGACTGTTA TGAGTATGTA CAAATTTTAT TTCCTGTAAA 360
 AATATTTNCA TTTTTTAAAN TGGTTATTTT CTAGAAA 397

SEQ ID NO:84

LENGTH:390

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00096

SEQUENCE DESCRIPTION:

GATCGAAGAT TTATCCCAGC AAGCACAACT AGCAGCTGCT GAGAAATTCA AAGTTCAAGG 60
 TGAAGCTGTC TCAAACATTC AAGAAAACAC ACAGACTCCA ACTGTACAAG AGGAGAGTGA 120
 AGAGGAAGAG GTCGATGAAA CAGGTGTAGA AGTTAAGGAC ATAGAATTGG TCATGTCACA 180
 AGCAAATGTG TCGAGAGCAA AGGCAGTCCG AGCCCTGAAG ANCAACAGTA ATGATATTGT 240
 AAATNCGATT ATGGAATTAA CAATGTAACC ATATGGANGC AACTTTTTTT TGGTGTCTCA 300
 NAGGNGTAAC TGCAGCTTGG TTTGAAANTT TGTTACCTTG TTTCTTATCA TAAATNAAN 360
 NGTTATTNGC TTCCTTTTTT GGNTTGGAAA 390

SEQ ID NO:85

LENGTH:392

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00097

SEQUENCE DESCRIPTION:

```
GATCACTTTC ACTNTCAATT ATTTGCCAGG NCTCACAGAA CTCAGAAAAG CTCAGANCAC 60
TCATGGTTAC TATTTAGTAA AGCAAAAAGA CACAAATNAA AATNAGCAAG TTTGGCCGGG 120
ATTGCAGGCA TGAGCCACTG AGCCCGGCCC CCAACTGTTA CATCAAAATA TTATTTGAGA 180
GTATATGTGT CCTCACGTCC CTAAACACT AGAAACTGTC AANCTTTTAA TCTTTGTCAA 240
ACTCTCAAAA GTAGTATCTC TGCATTTGCA TGCCTTTGNG TNCTAATAAG GTTGAGTACT 300
GCTTTAAAAG TTTGCTGGNC ATCTNTTGN TTTTTTAAAG GACCTGCCGT GGNNAGGCC 360
NTTCAANANA TTNTTTCNTT AATTNGGGCC TN 392
```

SEQ ID NO:86

LENGTH:393

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00098

SEQUENCE DESCRIPTION:

```
GATCAGTCTG GCTGGTGGTT TAACAGGTGT CACTCTGCAA ACCTGAATGG TGTATACTAC 60
AGCGGCCCCCT ACACGGCTAA AACAGACAAT GGGATTGTCT NGNACACCTG GCATGGGTGG 120
TGGTATTCTC TGAATCTGT GGTATGAAA ATTAGGCCAA ATGATTTTAT TCCAAATGTA 180
ATTTAATTGC TGCTGTTGGG CTTTCGTTT TGCAATTCAG CTTTGTTTAA AGTGATTGTA 240
AAAATACTCA TTCTGAACAT ATCCATGCGC AATCATGATA ACTGGTTGTG AGNAGTGCTT 300
TTCATTCTTC TCACTTGCCCT TTGTTACTTA ATGTGCTTTC AGGACAGCAG ATATGCAATA 360
TTCACCAAAT AAATGTAGGC TGGTGGTAAT AAA 393
```

SEQ ID NO:87

LENGTH:391

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00099

SEQUENCE DESCRIPTION:

```
GATCCAGAAA TACTTAACAC GTGAATATTT TGCTAAAAAA GCATATATAA CTATTTNAAA 60
TATCCATTTA TCTTTTGAT ATCTAAGACT CATCCTGATT TTAATATCA CACATGAATA 120
AAGCCTTTGT ATCTTCTTT CTCTAATGTT GTATCATACT CTNCTAAAAC TTGAGTGGCT 180
GTCTTAAAAG ATATAAGGGG AAAGATAATA TTGTCTGTCT CTATATTGCT TAGTAAGTAT 240
TTCCATAGTC AATGATGGTT TAATAGGTAA ACCAAACCCT ATAANCCTGA CCTCCTTTAT 300
GGTTAATACT ATTTANGCAA GGANTGCAGT ACAGATTTGG NTACAGTACG GATTTGNCCA 360
AATAANTTCA NTAAGCCT TAAAGCTGAA A 391
```

SEQ ID NO:88

LENGTH:390

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00100

SEQUENCE DESCRIPTION:

GATCAACCCA CAGAACAAAG CGGATTTCCT AGGCATCTCC CCAGAGCGAG CCTTGCTGA 60
 TTTTCTCTTT GCCAGCACCA TCCTGCACCT TGTGTGTCATG AACTTTGTTG GCTGACTCAT 120
 TCTCATTAC TTAATTGAGG AGTAGGAGAC TAAAAGAATG TTCACTCTTT GAATTTCTG 180
 GATAAGAGTT CTGGAGATGG CAGCTTATTG GACACATGGA TTTTCTTCAG ATTTGCACTT 240
 ACTGCTAGCT CTGCTTTTTA TGCAGGAGAA AAGCCCAGAG TTCACTGTGT GTCAGAACAA 300
 CTTTCTAACA AACATTTATT AATCCAGCCT CTGCCTTTCA TTAAATGTAA CCTTTGCCT 360
 TCCAAATTAA GGACTCCATG CCACTCCTCN 390

SEQ ID NO:89

LENGTH:390

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00101

SEQUENCE DESCRIPTION:

GATCTTTCTN AATGTGTATT GATTGGTCTT TTCAGCTACT CTGAACAGAT TACTAAGGCC 60
 ATCTCCTCAT CTCTAAGGGA GAAAAATAGT CTGTAGATGA ATAATGTAAG GTAAAGAGTT 120
 GCATGTCAGT CTTTGTAATN ATTTACACTT TAACTTTCTC CAGAACTCAG ACATGATTTC 180
 AACATGGTGT TAGATTTGTG CATTNATTT TCCTGACCAC CTCATTCCAG CCAATGTATG 240
 GTTATCCACT CTGTGTGCNA AANCCAATCA TGCNTTTCAC GGCCCTTTAG TTCAGAGAAG 300
 TTCTGCACTG ATTTTATGTC TCTTGATGTC TCAATCTTAC ATGTATACCA ATCACAATGG 360
 AATAAAAAGT GTTTGAGGTT GTACTGTGGN 390

SEQ ID NO:90

LENGTH:391

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00102

SEQUENCE DESCRIPTION:

GATCCGAGGA GGGGGAACAA GTCCACGGAG TCCCNNGCAG GCCAACGTGC AGCGGCTGAA 60
 GGAGTACCGC TCCAACTCA TCCTCTTCCC CAGGAAGCCC TCGGCCCCCA AGAAGGGAGA 120
 CAGTTCTGCT GAAGAACTGA AACTGGCCAC CCAGCTGACC GGACCGGTCA TGCCCGTCCG 180
 GAACGTCTAT AAGAAGGAGA AAGCTCGAGT NATCACTGAG GAAGAGAAGA ATTTCAAAGC 240
 CTTGCTAGT CTCCGTATGG CCCGTGCCAA CGCCCCGNTC TTCGGCATA GGGCAAAAAG 300
 AGCCANGNAN GCCGCAGANC AGGATGTTNG TAAGGAAANN ATTTANAGCC CCTCCTGGGN 360
 GACCTTTGGG ATTCAGTCGN CAGTCAATAA A 391

SEQ ID NO:91

LENGTH:391

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00103

SEQUENCE DESCRIPTION:

GATCTGTGCC AAGCTCAGGG TGTAGCGCTG CAAACGATGA AGCAAGAGAT TCTCATTAA 60

CTTGTGAAGC AAAAGCCACA AATAACAGAG GAACAACTTG AGGCTGTCAT TGCAGATTTC 120
 TCAGGCCCTGT TGGAGAAATG CTGCCAAGGC CAGGAACAGG AAGTCTGCTT TGCTGAAGAG 180
 GGACAAAAAC TGGNGNCAAA AACTCGTGCT GCTTTGGGAG TTTAAATTAC TTCAGGGGAA 240
 GAGAAGACAA AACGAGTCTT TCATTCGGTG TGAACTTTC TCTTTAATTT TAACTGATTT 300
 AACACTNTTT GGTGAATTA TGAAATGNTA AAGACTTTTT ATGTGAGATT TTCCTTATCA 360
 CAGAAATNAA NTNTCCTCCA AATGTTAATA N 391

SEQ ID NO:92

LENGTH:385

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00104

SEQUENCE DESCRIPTION:

GATCTTTTCC CCTGGCCAAA GGAAGTTGT ATTAGTCTGT GACATCTTGT GATGCTGTTT 60
 ATCTTGTTTT GACATTGGAG ATACGCTAGT AACTGTGATA CCATACTATA AAACAGAAGA 120
 ATTTTCTGCT ACTAAAACT GCCTTTTAC AAAATGACTG TAAATATTG TAAAAATAAA 180
 TAACACTAAA CTTTAAGCCC AAAAGGAGAG ATAGAGCCAT GTGTTGAGTT GTGGACCTGT 240
 CCGTGGGGCA CAGTGCCACC CCATCACAGT GTTGCTGTCA TCAGGCAAAN GTGAATGTTT 300
 GTTTATGGCA AATTGNCCTT TTGCGAATGG CTTANTTCTG ACACTACCTT TCTGGGAAAT 360
 GTTAATANAT TTTTAATTNT TCAA 385

SEQ ID NO:93

LENGTH:381

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00105

SEQUENCE DESCRIPTION:

GATCTTTGAT AGTTTGGTG AACTCTCTAA AATACATTCA CTGTGGGTCC GACGCAATTT 60
 AAAAAATNA TGTACTCAAG AAGGGAGACC TGTTGTGTTT ATTTCTCATC TGTTTGGGAG 120
 ATGATTTTAG AGCACTAGAA AGGCACTGGG GAGATTCTCA GCTTAAACA TCCAGCAGTT 180
 TGAAGTATGA TTAGGTACAT CAGGGCTGCA TTGTCAATNT TCTCTTAAAG TCTTTTAA 240
 TTTATAGCAA TTTTTTTTT CCCGGAGAGT TTAGGTTGCA AGTTTGGGT TTCTTGTTG 300
 TTTTGTTTT GCTTCCTGCT TTAATNCTN AATTNCACT CATTACTGGT ATTGAAAAAT 360
 AAAATATCTT TAAANCANNG N 381

SEQ ID NO:94

LENGTH:380

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00106

SEQUENCE DESCRIPTION:

GATCTAAGAG ACTCAAGAGC TGGGTTTCTT TCAGCACTCT GTACTGTCCC AAATAGCAAA 60
 CAAATNACTT TGTAGCCAGA TTTCTGAATG GAAATNAGAA ATTGAATTCT CCATGGACTT 120
 TTAGGTTTAT GGGGGAGTTT TAGCTGTGTT TCTTGGTTTT ATTCAGCCA AACATGTCTG 180
 CTTTGTATTT TTTTTTAA GTATAAGTGG TCTATATATA TGTTACCTT TAAATGTAA 240

ATGTTTAAAA AGTAAGCATT TATGTGTTTC CATAACTGAC ATCTGATGCA GACCTCATT 300
 TCTCCCCCTC TTCTACCCTC CTCTTTTCCC CCTTTTCAAT ACTCTTGAT TGGGTTCTAA 360
 TAAAATGGGT TGCTTTTTCN 380

SEQ ID NO:95

LENGTH:379

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00107

SEQUENCE DESCRIPTION:

GATCCATACT TGGATGATAT TGATGATGAG ATGGACCCAG AGATAGAAGA AGCTTATGAA 60
 AAGTTTGTGTT TGGAAATCAGA GCGTAANGNA NAACAGTAAA GTTAAATTTC AGCATATCAG 120
 TTTTATAAAG CAGTTTAGGT ATGGTGATTT AGCAGAACAC AAGAGAGCAA GAAAATGTGT 180
 CACATCTATA CCAAATTGAG GATGTTGAGT TATGTTACTA ATGTATGCAA CTTTAATTTT 240
 GTTAAACACT ATCTGCCAAA ATAACTTTA TTCCCTATAA CTAAAAATGT GTATATATAT 300
 ATAATAGTTT ATTATGTACA GTTAATTCTA CTGTTTGGC TGCAATAAAA TCGATTTTGG 360
 AAATAAATGG AATGTTGGN 379

SEQ ID NO:96

LENGTH:384

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00108

SEQUENCE DESCRIPTION:

GATCTTTGCT GGCAAGCAGC TGGAAGATGG ACGTACTTTG TCTGACTACA ATATTCAAAA 60
 GGAGTCTACT CTTCATCTTG TGTGAGACT TCGTGGTGGT GCTAAGAAAA GGAAGAAGAA 120
 GTCTTACACC ACTCCAAGA NGAATAAGCA CAAGAGAAAG AAGGTTAAGC TGGCTGTCCT 180
 GAAATATTAT AAGGTGGATG AGAATGGCAA AATTAGTCGC CTTCGTCGAG AGTGCCCTTC 240
 TGATGAATGT GGTGCTGGGG TGTTTATGGC AAGTCACTTT NGNCAGACAT TATTGTGGCA 300
 NATNTTGTCT GACTTACTGG TTNCAACAAN CCCAGAAGNC ANGTTAACTG TNTGANGTTN 360
 ATNAAAAGNC ATGTNCTGAA CAAA 384

SEQ ID NO:97

LENGTH:583

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00109

SEQUENCE DESCRIPTION:

GATCCTCATG AATGACTATC CTAAATTTAA GTATGCAGTT CTNTTTTTGC TGGGTTTATT 60
 CGTGCTGGTT CATCGNGAGT NAGANGCCTG CCTTGCTGTT CCTGGGAAGA TGCCATAGTT 120
 TTCGTTACTG GATGTTTGA GATAGACTG GTCTGTNATT GGTGGAATGG AGAACACACG 180
 TGTTGGTGCT TCTGGGTAGC ACTGGTTTGC ATTAGTTTAT GTTCCATGC CAGAGTTTGT 240
 GTGGCGGGC GCATGTCCAC CACAGAGTGC ACTCGAGGGG ACTTTCAGTC ACAGGATTTTC 300
 ATAATTGTNA TTGTCACACT TTCAAATTTT TGTACATCAG TGAATTTTTT TTATATTTAA 360
 AGGTTGAGCC AAAGCCCCCA GTGTTTGTGA TTTTGAAGCC AAGCTTCACT TCTAAAAGTG 420

CCTACAGAGG ACTTGTA AAA TGGAAAATGC AGCTCTGCAC GGAGTTTGAA ACCGTCATAC 480
 CTCCTTCTAT TAGGGAATNG GCATATACTG AGGGTGGTCC GGAAGNNNTT AACTTCCTAA 540
 AATTTTAAAA TAAAAGGCCT TTGCACCATT GGACCCCN TT AAA 583

SEQ ID NO:98

LENGTH:370

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00110

SEQUENCE DESCRIPTION:

GATCAAGAAA AGCAACTTAT GGAAACAAC TACAGAATTTA CAAAAAAGGA TACTCAAACC 60
 AAAAGTATTA TTTCAGAGAC CAGTAATAAA ATTGACGCTG AAATTGCTTC CTTAAAAACA 120
 CTGATGGAAT CTAACAAACT TGAGACAATT CGTTATCTTG CAGCTTCAGT GTTACTTGC 180
 CTGGCAATAG CATTGGGATT TTATAGATTC TGGAAGTAGT ATTAATGCTC ATCCTGCTGT 240
 GGCTGTTGGC TTCTTAGAAC ACCAAACCGG GAGAGATTTA CTTTGAACAT TGTCAGTTGC 300
 AGCAAAAATT TACTACACAA GATTATTCGA AGTGTATACG GACTAAAAGA GGAAGTGTTT 360
 TAGAATGAAA 370

SEQ ID NO:99

LENGTH:384

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00111

SEQUENCE DESCRIPTION:

GATCTGAAGA GCGTCCTGGG TCAACTGGGC ATCACTAAGG TCTTCAGCAA TGGGGCTGAC 60
 CTCTCCGGGG TCACAGAGGA GGCACCCCTG AAGCTCTCCA AGGCCGTGCA TAAGGCTGTG 120
 CTGACCATCG ACGAGAAAGG GACTGAAGCT GCTGGGGCCA TGTTTTAGA GGCCATACCC 180
 ATGTCTATCC CCCCCGAGGT CAAGTTCAAC AAACCCCTTG TCTTCTTAAT GATTGNCCAN 240
 AATACCAAGT CTNCCCTCTT CATGGGAAAA GTGGTGAATT CCACCNAAAA ATAAGTGNCT 300
 GTNGGTNCTC AACCCCTTNC NNTTCATCCN TGGGCCCN TN GGCTTGATN GANAATTAAA 360
 AGAAGGGGTT GNGGCTNGGG NAAA 384

SEQ ID NO:100

LENGTH:374

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00113

SEQUENCE DESCRIPTION:

GATCTTTGAA ACCTTGGTCC CGTAACTTA CTAGTCACAT TGACCAATGT TTTATAGAAA 60
 TGCCTAGAAT TTTGAGACTA ATNGTAGTTA TCCATTAACA TTCCAAAAGT TTTGTNCTTT 120
 TNAAAAATTG TTTGGTAAT TATCACATT NNCCTCTTA CCTTCCTTTA AATGGCCACA 180
 GTGTGTACTG CTGGANTGTN CCATCCAAAA GATGTAGCTT CAGANGCACA GTGATTGCCC 240
 CAGGGTCCAT GAGATATTGT TTGTATTATG ANGTTGGAGT GCTGTCTACT GAAATTATAC 300
 TCTTAAATAA NTATGTATGT NGTGTGTAAT ATTCCTAAT AAATNCTTTN GATAAACTAA 360
 AAAACTNNNG CTNN 374

SEQ ID NO:101

LENGTH:382

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00114

SEQUENCE DESCRIPTION:

GATCTGTGCA AGGTATTAAC GTGTCAGGGC TGAGTGTCT GGGATTCTC TAGAGGCTGG 60
CAAGAACAG TTGTTTGTG TTGCGGGTCT GTCAGGGTTG GAAAGTCAA GCCGTAGACC 120
CAGTTTCCTT TCTTAGCTGA TGTCTTGGC CAGAACACCG TGGGCTGTTA CTTGCTTTGA 180
GTTGGAAGCG GTTTGCATTT ACGGCTGTAA ATGTATTCAT TCTTAATTA TGTAAGGTTT 240
TTTTTTGTAC GCAATTCTCG GATTCTTTG AAGNAGATGA CAACAAATTT NGGTTTCTA 300
CTTGTTATGT GAAGACCATT AAGGCCCAA GCAACAAGNC AATTNTGTAA GGGAAANTNA 360
AAGTCCTTG CNGTAANCCA AA 382

SEQ ID NO:102

LENGTH:368

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00115

SEQUENCE DESCRIPTION:

GATCTGTCTC TGCTGTTAA CTTCAATTGA TTAATCAGCT GGTTCAACT CTAAGCGAA 60
ACAAAAATAG CTCCTTAAAA GTACTGTTCT CCTTCAGTGG CATGTAGTTA TCTAATCAAG 120
ACACCTCATT CAAACAAAAC CTGCCTTAGG AAAATTTAAT ATATTNAAA TNATTTTAAA 180
AGAAATACAA CATCTTATTC TTTAGCTTC TTAATCGGTG CTTTATGGAG GCCAGTGTA 240
CGNTACATGA CTCGTTGAGA AAGTTGAGGA ATTTCTCTA CCACCTTTGT TGCTGAAGA 300
AAAACATGTC TTTCAAAAT GAGAGGCTTT CATTGAAGAA AAGAAAAAA CAACAGTTAA 360
AAGCTAAA 368

SEQ ID NO:103

LENGTH:367

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00116

SEQUENCE DESCRIPTION:

GATCTCGGAT GACCAAACCA GCCTTCGGAG CGTTCTCTGT CCTACTTCTN ACTTTACTTG 60
TGGTGTGACC ATGTTCAATNA TAATCTCAA GGAGAAAAA AACCTTGTA AAAAAAGCAA 120
AATGACAACA GAAANCAAT CTTATCCGA GCATTCCAGT AACTTTTTG TGTATGTNCT 180
TAGCTGTACT ATAAGTAGTT GGTGTGTATG AGATGGTTAA AAAGGCCAAA GATAAAGGT 240
TTCTTTTTT TCCCTTTTT GTCTATGAAG TTGCTGTTA TTTTTTGGG CCTGTTTGAT 300
GTATGTGTGA AACANTGTN GTCCAACATT AANCAGGANT TTTATTTTNC NGAGTNGTNC 360
TANCAA 367

SEQ ID NO:104

LENGTH:366

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00117

SEQUENCE DESCRIPTION:

GATCTTAGTA ACTATGNATG AAGATGGTGC TTGGCCTGTN CTTCTTGATG AATTGTTGA 60
GTGGCAAAAA GTCCGTCAGA CATCATAGCA AGAACTATGT GAAGAAAATG CAAACCTTTC 120
AATTCCCACG TGTATACAAG CTAATGTGAT GAGGGGGAAA AAAATCCAAC GGGTGCATT 180
TCATTCATAT GAAAGACTTC TCATAGTACT TTTTTCCTN TTTTAAAAA GGAGGTTTTT 240
CTTGTTACAT GTGATGGGCA TTGAGCCACA CCNNTCTTA GACTGAATAT NGAAGTTTTT 300
GTTTTGAGTT ATGTTTATAA CATTATTTC AGAACANTAA TGATTCAGAT TTGTGACAAA 360
GGCAAA 366

SEQ ID NO:105

LENGTH:122

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00118

SEQUENCE DESCRIPTION:

GATCCCCGAA ATTGGTGGGC TTGACCTCCT GGCAAATTGC TCGTCTTTC CACTTGCTGT 60
TCAGGACCAC TAAATGCTGA AATNTGGATG CATACCGAAA TAAAAGNAAT TCATTGTGTA 120
AA 122

SEQ ID NO:106

LENGTH:364

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00119

SEQUENCE DESCRIPTION:

GATCTTCAAT ATGAAGACAT GAGCTTTTCT CGCAGGAAAT TTTCTTTTC ACAGAACTGG 60
TGTCAGGAAT CACTGAAGGG CTAACCGTGA TAGTCCTGC AAGTAAGTCA AGGTTTATC 120
CTGATTGGAA ATAGAAGACA TTTCCGGTTG AGAGAACAGA TTCGTTGGAA GCTTAACTTT 180
TGTTGCCTCT TAACGCCACC AAATTTTAGG GTAATTTGAT TATGAAAGAG TGAATTTTC 240
TGGACAGAAA AGGGAGAGCT ACCAAATTGT TTTTCTTT TAAAAGGAA GTTTAATGTC 300
CGTTGTATCA CAAATCAGTG TAAAACACC AGAACTTAG CAAAATAAA TGTCTTACAT 360
TACN 364

SEQ ID NO:107

LENGTH:358

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00120

SEQUENCE DESCRIPTION:

GATCAGCAGG GAGTTTATTT GAGGACATCA GTCACCTTTG GGGTTGCCAT GTACAATNAG 60
ATTATAATC ATNATACTCT TCGGTGGTAG TTTCAAAGA CACTACTAAT ACGCAGGAAG 120
CGTTCCAGCT ATTTAATGCT GGCAACTACT GTTTAATGGT CAGTTAAATC TGTGATAATG 180

GTTGGAAGTG GGTGGGGTTA TGAAATTGTA GATGTTTTTA GAAAACTTG TGAATGAAAA 240
 TGAATCCAAG TGTTCATGT GAAGATGTTG AGCCATTGCT ATCATGCATT CCTGTCTCAT 300
 GGCAGAAAAAT TTTGAAGATT AAAAAATAAA ATAATCAAAA TGTTTCCTCT TTNCTAAA 358

SEQ ID NO:108

LENGTH:430

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00121

SEQUENCE DESCRIPTION:

GATCTGTCTC TGGGGTCCCN CATAACAGAGA AATGCATCTT GCTGAACAAG TGACCAATAA 60
 TCTTAAAGAA CTTGCACAGC AAGTAACTCC AGGTGATATC GTAAGCACGT ATGGAGTTGC 120
 AAAAGCAATG GGGATTTCCTA TTCCTTCCCC CGTCATGGAA AACAACTTN TGGATTGAC 180
 AGANGNNCT GAAGAACCTA AAAAGACGGA TGTGCTGAG TGTGGACCTG GTGGAAGTTG 240
 AGGCTGCCTG GTATTGATT ATATATTATG TACATACTTT TTCATTCTTA ACTTAGAAAT 300
 GCTTTTCAGA AGATATTAAA TATTTGTAAA TTGTNTTTT AATTAACTT TGGAACAGCG 360
 AATTTGNGTG TTCCAGAGGT TGGGCCTTGT ATTAGGGAAA TAAAGCTTG GACCTGGGGC 420
 CTCGTGAAAA 430

SEQ ID NO:109

LENGTH:357

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00122

SEQUENCE DESCRIPTION:

GATCACTNGA TATTTTAGTC ATTCTGCTC TCATCTAAAT ATTTCCATAT NCTGTATTAG 60
 GAGAAAATNA CCCTCCCAGC ACCAGCCCC CTCTCAANCC CCAACCCAA AACCAAGCAT 120
 TTTGGAATGA GTCTCCTTTA GTTTCAGAGT GTGGATTGTA TAACCCATAT ACTCTTCGAT 180
 GTACTTGTTT GGTTTGGTAT TAATTNGACT GTGCATGNCA GCGGCAATCT TTTCTTTGGT 240
 CAAAGTTTTC TGTTTATTTT GCTTGTCATA TTCGATGTAC TTTAAGGGTG TCTTTTATGA 300
 AGGTTTGCTA TTCTTGCCAN TTAAGNTTTT TTAGNCTTT TAAANGNGN ANNNAAA 357

SEQ ID NO:110

LENGTH:356

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00123

SEQUENCE DESCRIPTION:

GATCAAGGGA CGGCTGAACA GACTTCCCGC TGCTGGTGTG GGTGACATGG TGATGGCCAC 60
 AGTCAAGAAA GGCAAACCAG AGCTCAGAAA AAAGGTACAT CCAGCAGTGG TCATTCCACA 120
 ACGAAAGTCA TACCGTAGAA AAGATGGCGT GTTCTTTTAT TTTGAAGATA ATGCAGGAGT 180
 CATAGTGAAC AATAAAGGCG AGATGAAAGG TTCTGCCATT ACAGGNCCAG TAGCAAAGGA 240
 GTGTGCAGAC TTGTGGCCCC GGATTGCATC CAATGCTGGC AGATTGCATG ATTCTCCAGT 300
 ATATTTGTAA AAANTAAAAA AAAGCTAAAC CCATTAAAAA GTATTTGTTT TGCAAA 356

SEQ ID NO:111

LENGTH:375

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00124

SEQUENCE DESCRIPTION:

GATCCTACCT ATCAAGCACT AAAAAGTTGA ACCATTATAC TTTATATCTG TAATGATACT 60
GATTATGAAA TGTCCCCTCA AACTCATTGC AGCAGATAAC TTTTGTGAGT CATTGACTTC 120
ATTTTATATT TAAAAAATTA TGGAATATCA TCTGTCATTA TATTCTANTT AANGTTGTGC 180
ATAATGCTTT GGAANAATGG GTCTTTTATA GGAAAAAACC TGGGATAACT GATTCTATG 240
GCTTCAAAG CTNAAATATN TAATATACTA AACCANCTCT AATATTGCTT CTTGTGTTTT 300
ACTGTCAGNT TAANTTACAG CTTTATGGG TGGTAACTT TTCGTNCATT TTCAAAAAAN 360
CCNGGGGNNN NNNNN 375

SEQ ID NO:112

LENGTH:356

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00125

SEQUENCE DESCRIPTION:

GATCTCTGTT TTGTTGTGTA AAATTCATTT GTATACTTTT GTTTNTACT AGGACTTCAT 60
GTTTTTTNAA AGCACTGGCA GCCAGGAACA AAAATCAGGA GTGTGGTAGT GGATTAGTGA 120
AAGTCTCCTC AGGAAATCTG AAGTCTGTAT ATTGATTGAN ACTATCTAAN CTCATACCTG 180
TATGANTTAA GCTGTAAGGC CTGTAGCTCT GGTGTATAC TTTTCCTTTT CAAATTATAG 240
TTTATCTNCT GTAACTGA TTTATAAAGG TTTTGTACA TTTNTNAATA CTCATTGTCA 300
ATTTGAGAAA AAGGACATAT GAGTTTTTNC ATTTATTAAT GNAACTNCCT TTGAAA 356

SEQ ID NO:113

LENGTH:351

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00127

SEQUENCE DESCRIPTION:

GATCACATTA TNATAAATAA ATGAAAAAAT GATTTAATCT GTAATAAACT GGTTTATTGT 60
GCAGTGACTG TAATATACTA GAGTTATAAT AAATTGTTTA CTCTGCCTCA CCAAACACAT 120
GCTAGGATAT AACCCCAAAA ATAAGTATTT AACTTTGCAT TAGGTATAAA GGAGACTGGG 180
TGCTATAATN AGATTATTTT GAGGCAGACA GAGAGCTGTT ATCCTAACTG ATTTAGTATG 240
TTCTGTAATT GAGAAAATGT TCACCAAATN ATACTTTTGA GTGATTTACA TGTACATTTT 300
ATAGGGGACA TGTCTGTGT ATAGCGAATA AATAACTTTT ATAGTATCAC N 351

SEQ ID NO:114

LENGTH:352

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00128

SEQUENCE DESCRIPTION:

GATCTTGAAC CTGGTGCTCC ATCCATGGNA GCNNAAGCC TTTGCATCCC CTTCAAACCA 60
 CTCTGTGAAC TGCAGCCTGG AGCCAAATNT GTCTGTGGCA AGAACCCCTGC CAAGTACTAC 120
 ACCTTATTTG GTCGCAGCTA CTGNGGGATG NACGAAAGCC CCCTCTTCAA CTCCTCTCAC 180
 TTTTAAAGC ATTGATATTA GTATCTTCTC AGATACAGAC CGTTTTATGA TTTTAAAAA 240
 AGTAAAGTT CTAAATGAA GTCACACAGG ACAATTATTC TTATGCCTAA GTTAACAGTG 300
 GATAAAGAC TTTTCTGTAA ACAACTCCAG TAATAATAT CATGNACTNA AA 352

SEQ ID NO:115

LENGTH:348

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00129

SEQUENCE DESCRIPTION:

GATCAAGTCG TGCTCCTGGC AGGCGCGCCC CTGGAGGATG AGGCCACTCT GGGCCAGTGC 60
 GNGGTGGAGG CCCTGACTAC CCTGGAAGTA GCAGGCCGCA TGCTTGGAGG TAAAGTCCAT 120
 GGTTCCTTGG CCCGTGCTGG AAAAGTGAGA GGTCAAGNTN NTNAGGTGGC CAAACAGGAG 180
 AAGAAGAAGA AGAAGACAGG TCGGGCTAAG CGGCGGATGC AGTACAACCG GCGNTTGTGC 240
 AACGTTGTGC CCACCTTTGG CAAGAAGAAG GGCCCCAATG CCAACTCTTA AGTCTTTTGT 300
 AATTCTGGGC TTTCTTCTAA TAAAAAGCC ACTTNAGTTC AAGTCAAA 348

SEQ ID NO:116

LENGTH:344

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00130

SEQUENCE DESCRIPTION:

GATCTCCAC AATTAATTTA TCTTTTGACA AAGGGGATAA AGAGTTTCAG TTTAGCTCCT 60
 TTTGATTGTA TATNATTTTT TCCTTTTNA TTGTGAAAAG AGGTAGGTTT TATTTGTGGA 120
 GAGAGAGTTG AAGATTAGGG AACCAGTGAT TTAAATTATG CTACTTTTCC TTCTAAGAGA 180
 TAAATTGATA TATCATTGAG TGTCATGAAA AACATGAATG TNGTACAATT TTCTNCCTCA 240
 AAAAACTTTT TAAATGTAAG TATCCTTATT TNNTTTTAA AAGAGCACAA TGTAGGTGTA 300
 TTTGGGTATT TCCAAGAAAA GANTAAANCC ATTAATGCAG TAAA 344

SEQ ID NO:117

LENGTH:351

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00131

SEQUENCE DESCRIPTION:

GATCTGGGCT CCAAGCCAGG AAAGGTGAAC AGAAACCACA AGTNTCCAGC CCTCGGTGCT 60
 GGAGTGGACG TTAATTGTNA GCCACCAGAC TGTCCCGGCA CCTACAGAGA ATGTTTCACA 120
 GTTCTGGCAT TAAATCCTT TGATAGTGA TGTGCTGCT GTTAGCCTTA GTTTCAGTGC 180
 TTTACAAGTC TCGCTTATNA TCTCATTGGT ATTTAGGTAT ACAAACAGT TGATTATTCA 240
 CCACGCCAAT ATCTGGGTCT CTGTATCTCA TGTAGAACAT AAGAAAATGG GAACTAATAG 300

GGAAATTTAT TTATAGCATG AAAATAAACC TGGTGGCTGG AGTCTGCTAA A 351

SEQ ID NO:118

LENGTH:343

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00132

SEQUENCE DESCRIPTION:

GATCCTAAGG CAATAAAAGA ATAAGGAGAT TTGGAAAACC ATTGTCTGTA ATCTCTGAAG 60
AAAAGTGGAC ATTAGGGGAG TCAGTTGAAA AGCAAAGCTA TCACCATTTT CTAAAGAGGA 120
AAAAGGTGAA CCTCACAAAC TATAGACCAA AAAAATAGGA CATCGAGAGA AAGAATATGA 180
AGCTAGCATA GGTTCACAAA GAATGAGTCA AATCAAACAA CATGCATTTT TTATTTATAA 240
AGCATGACTT GTTCATTGTC AATTCATGTT AGCTTAATCA TTAGGCATTA ATGCCATCAC 300
TGCAATGCAT ATGTCAGCAA TAAATAATCA AGGCCCGGCT TCN 343

SEQ ID NO:119

LENGTH:345

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00133

SEQUENCE DESCRIPTION:

GATCTTCCCA CAACACCACA GGA CTGCAGG GTGCACAAC CCCCTGCCAA GGAAAACCAT 60
GCAGTCCTCC CCTCCCTGGT CTCCTGCTTC AGCTCTGTAC AACGAGGGCA AAGATGCTAA 120
ATCTTGCTTT GCATTCAGTA AAGTGTC AAG TGATTAAGTG TGTATTGTA CCCTAGATGA 180
TATGAACCAG CAGTCTTGTT TTGGCATCAT CCTCATCATG TTGTATTCCA GCTTCTTAAG 240
TGGAAGGAAA AGAGTGCTGA GAAATGGCTC TGTATAATCT ATGGCTATCC GAATTCTCTG 300
AAAAANTANT AAAAGTCCCC TCTNTTATAT GAGCCTGTAC AGAAA 345

SEQ ID NO:120

LENGTH:358

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00134

SEQUENCE DESCRIPTION:

GATCCCCCT CTCGAGGGCG ATGAGGATGC GTCTCGCATG GAAGAAGTCG ATTAGGTTAG 60
GAGTTCATAG TTGGAAAAC TGTGCCCTTG TATAGTGTCC CCATGGGCTC CCACTGCAGC 120
CTCGAGTGCC CCTGTCCAC CTGGCTCCCC CTGCTGGTGT CTAGTGTTTT TNCCCTCTC 180
CTGTCCTTGT GTTGAAGGCA GTAACTAAG GGTGTCAAGC CCCATTCCCT CTCTACTCTT 240
GACAGCAGGA TTGGNTGTTG TGTATTGTGG TTTATTGAA TTNCCTTCAT TTTGTTCTGA 300
AATTAAGT ATGCAANAAT AAAAGAATTA TGCCCNNTTT TNATAAANA NNAANAAA 358

SEQ ID NO:121

LENGTH:350

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00135

SEQUENCE DESCRIPTION:

GATCTTCATG CCCTGGGTC TGCCCGNACG GACCCNCATC TCTGTGACTT CCTGGAGACT 60
 CACTTCCTAG ATGAGGAAAGT GAAGCTTNTC AAGAAGATGG GTGACCACCT GACCAACCTC 120
 CACAGGCTGG GTGGCCCGGA GCTGGGCTGG GCGAGTATCT CTTCGAAAGG CTCACTCTCA 180
 AGCAGGACTA AGAGCCTTCT GAGCCCANCG ACTTCTGAAG GGCCCNNTGC AAAGTAATAG 240
 GGCTTCTGNC TAAGGCTCTG CCTNCAGNCA ATAGGNANGC TTTTAAACN ATCCTAACAN 300
 GGNTTGGGAC CAAATGGNAA TAAAGNTTGG TNGATGCAGG AGATATGAAA 350

SEQ ID NO:122

LENGTH:338

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00136

SEQUENCE DESCRIPTION:

GATCTGAGCT GAATTTGAAG ACTATTAATA AGTTATGTTT GGAAGTTTTA ACTTCAATGA 60
 AGTAATTATT TGCTGTGAAA GAAACAAACA TTGAATTACT AAACAAAGAT GGTGCAATAT 120
 CTTTGTTTTT TTTTATGAG GCTCCTGAGA ATCAACCCAA CTGAAGCATT TCAATTCACT 180
 TGAATGAGAA ACGTGTGTTAG TATCAAAAGA GCCCAAGAAG ACGTGGTGT GAAAGGTACA 240
 NTCTCAGAGG TTGGTCAATT ACCGTGGCAC ANTTCTGGT CACTTTGTAC AATGTAGATT 300
 TGAAGTACAG TGGTGAAAAC ATTAATGTG ACATTGNN 338

SEQ ID NO:123

LENGTH:337

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00137

SEQUENCE DESCRIPTION:

GATCAAAAAA CATGAGGNAG AAGAAGCCAA AGCTGAGCGT GAGAAGAAGA NAAAAAGAAC 60
 AGAAAGAAAA GGATAAATAG AATCAGAGAT TTTATTACTC ATTTGGGGCA CCATTTCACT 120
 GTAAAAGCAG TCCTACTCTT CCACACTAGG AAGGCTTTAC TTTTNNAACT TGGTGCACTG 180
 GGAAAATAGG ACATTACATA CTGAATTGGG TCCTTGTCAT TTCTGTCCAA TTGAATACTT 240
 TATTGTAACG ATGATGGTTA CCCTTCATGG ACGTCTTAAT CTCCACACA CATCCCTTT 300
 TTTTGAATA AAATTTGAA AATGGAAATN AAGGAAA 337

SEQ ID NO:124

LENGTH:336

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00138

SEQUENCE DESCRIPTION:

GATCACCATT TGAGATACGC GGCTTAACGC ACATGTGAGT GTAGCTTGCT ACATGAAAAT 60
 GCTAGGCTCT AGGGCATGTA AAACATGAAT ACAGAATACT AGATTGTCT AAGTAATGTC 120
 ATTCGGTTT GTGANTTTGA TTTTCCCTT CATTTCATGT CATATTGNAA ATGCAAACAA 180
 ACTGCTCTCA AGAACACCCA GAAGCTATCT GTGTTACCAG ATGTGTTGTG NACACTCTAC 240

TNTTTTTCAT AGGTGCTACC TGGNAATATA TGTCCATTGT AGTGGTGGNG NGGGNCTNGA 300
 CTCNTCAGG CTCTNTCTN GCCAGNTGNC TNCNGN 336

SEQ ID NO:125

LENGTH:338

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00139

SEQUENCE DESCRIPTION:

GATCTGGGCT GCAGGAGCTG GGGCCACCCA CAGCCCCCCT ACCGACCTGG TGTGGAAGGC 60
 ACAGAACACC TGGGGCTGCG GGAACAGCCT GCGTACGGCT CTCATCAACT CCACTGGGGA 120
 AGAAGTGGCC ATGCGCAAGT TGGTGCGCTC AGTGACTGTG GTTGAGGACG ACGAGGATGA 180
 GGATGGAGAT GACCTGTCTC ATCACCACCA CGTGAGTGTA AGCCGCCGTT GAGGCCGAGC 240
 CTGCACTGGG GCCACCNAGC CAGGCCTGGG GGNAGCNTTT CCCNAGNNTN CNNGTGCCAA 300
 AANTTTTTTN ATTAAGAAGT TGTTTTGGGA ACTTTAAA 338

SEQ ID NO:126

LENGTH:347

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00140

SEQUENCE DESCRIPTION:

GATCAAGCAG ATTCCACGAA TCCTNCGGAC CAGGTTTAAA TANGGCAGGA AAGTTCCTT 60
 CCCTGCTCAC ACACAACGAA AACATGGTGG CCAAAGTGGA TGAGGTGAAG TCCACAATCA 120
 AGTTCCAAAT NAAGAAGGTG TTATGTCTGG CTGTAGCTGT TGGTCACGTG AAGATGNCAG 180
 ACGATGAGCT TGTGTATAAC ATTCACTGG CTGTCAACTT CTTGGTGTC TGTCTAAGG 240
 AAANCTGGCA GANTGTCCGG GCCTTATATA TCANNGNGCA CCATGGGCAA NGCCCCAGCG 300
 GCTTATATT AAGGCACATT TTNATAAAT TCTATTNACC CGGTAAA 347

SEQ ID NO:127

LENGTH:335

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00141

SEQUENCE DESCRIPTION:

GATCAGTTGT AATCAGAATA CAACTGNGTC TTGTAGTTGT AATATGTTCT ATCTTAACCA 60
 CCACTTTCGT ACCAGGAACC TGCTCAGGTT TGTTCTCTAG AAGCTCCCAA CATAGATAGT 120
 CTACATTCA GACTACTAAG TTATTAACAA ACCCTTTGGG CCCATGTTCA CTTAGGGTT 180
 GAGCATAGTG TGAGGAGATG TAAATTAAAT TATAATCCTA TATGTGTGTG TAATAAATAT 240
 TAAAGTGTAT AAATTAAACA GCAGATTCTA AGTATCCAAC AAGAGTCAAA TAAATGATAC 300
 AAAGTCACCA AATAAATAAT ATTAAATCTC ATCTN 335

SEQ ID NO:128

LENGTH:356

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00142

SEQUENCE DESCRIPTION:

GATCTAGTTA AAGTTATTCA ACAGGAGTCT TACACATATA AAGACCCAAT TACAGAATTT 60
GTTGAATGTT TATATGTTAA CTTTGACTTT GATGGGGCTC AGAAAAAGCT GAGGGAATGT 120
GAATCAGTGC TTGTGAATGA CTTCTTCTTG GTGGCTTGTC TTGAGGNNNN CATTGAAAAT 180
GCCCCTCTCT TCATATTTGA GACTTTCTGT CGCATCCACC AGTGTATCAG CATTAAACATG 240
TTGGCAGATA AATTGAACAT GACTCCAGAA GAAGCTGAAA GGTGGATTGT AAATTTGATT 300
AGAAATGCAA GACTGGATGC CAAGATTGAT TCTAAATTNA GGTGATGTGG TTATGN 356

SEQ ID NO:129

LENGTH:333

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00143

SEQUENCE DESCRIPTION:

GATCAAAGNA CTCTGACTGC AGAACTGCCG CTCTCAGTGG ACAGGGCATC TNTNACCCTG 60
AGACCTGTGG CAGACACGTC TTGTTTTCAT TTNATTTTGG TTAAGAGTGC AGTATTGCAG 120
AGTCTAGAGG AATTTTNNNT TCCTTGATTA ACATGCTTTT CCTGGTTGTN ACATCCAGGG 180
CATGGCAGTG GCCTCAGCCT TAAACTTTTG TNCCTACTCC CACCCTCAGC GAACTGGGCA 240
GCACGGGGAG GGTTTGGCTA CCCNTGCCCA TCCNTGAGCC AGGTACCACC ATTGTAAGGA 300
AACACTTNCA GAANTTCAGC TGGTTCCTCC AAA 333

SEQ ID NO:130

LENGTH:332

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00144

SEQUENCE DESCRIPTION:

GATCTCTGTA GATATTCTGT TTTATTTTGG TCATCTTTAG AAGTTATCAG GAATGTGTTT 60
AAAACAAGAA GAGAACTTTT CTAAGGAATG ATACATAGAA AAGATTTTAT TTAAAAATGA 120
GTTGTAAAGC TTGTTTTTCT TTGTTGCTGC AANTATCTGC CCAAGTTAAT GCAAATGGAC 180
ACATTTTTTA TGTCAGAAAA ACACACACAC ACACACACAC ACACACACAC ACACACNCGC 240
GNNACACAGN GANAAAAGTG CTTGNGCTN NNCTCNCTNC CCCTTGCGNT CTGTTGTGTG 300
CGCAGCCTGT TTATNTCTCT NNTATTGTGT CN 332

SEQ ID NO:131

LENGTH:332

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00145

SEQUENCE DESCRIPTION:

GATCTGTGAC CTTACCCCA AACCTGTNCT CTCTGAAACA TGTGCTGTGT CCACTCAGGG 60
TTAAATGGAT TAAGGGCGGT GCAAGATGTG CTTTGTTAAA CAGATGCTTG AAGGCAGCAT 120
GCTCCTTAAG AGTCATCACC ACTCCCTAAT CTCAAGTATC CAGGGAGACA AACACTGCGG 180

AAGGCCGCAG GGTCTCTGC CTAGGAAAAC CAGAGACCTT TGTTCACTTG TTTCTTTGTT 240
 CACTTGTTTA TCTGCTGACC TTCCCTCCAC TATTGTCCTA TGACCCTGCC AAATCCCNT 300
 NTGATGAAAA ACACCCAAGN ATATCANTA AA 332

SEQ ID NO:132

LENGTH:333

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00146

SEQUENCE DESCRIPTION:

GATCGAGGTT GTTTGCAACG ACCGTCTGGG GAAGAAGGTC CGCNTTAAAT GCAACACGGA 60
 TGATACCATC GGGGACCTTA AGAAGCTGAT TGCAGCCCAA ACTGGTACCC GTTGGAACAA 120
 GATTGTCTG AAGAAGTGGT ACACGATTTT NAAGGACCAC GTGTCTCTGG GGGACTATGA 180
 AATCCACGAT GGGATGAACC TGGAGCTTTA TTATCAATAG ATGAGAATCC TCATCTTNCT 240
 GCCCCGCTNT CCNCTNCCA TCCTCATCCC CCACANTNGG GATAGATGCT TNGTTTGTA 300
 AACTCANCN NAATAAAGAC TTAGATGTTG AAA 333

SEQ ID NO:133

LENGTH:330

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00147

SEQUENCE DESCRIPTION:

GATCAGGTCT GTAAATGTGT ACTAAAAAA TNAGAGTTTA TTTATAAACA AAATAGTTTA 60
 TTAAAGAGA AGGTCTCTTC CTTATTGATA TCATGGTATG CATTAATTCC ATTTGTTACT 120
 ATTGTGCACA AAAGCCCTGT TCACAGGGGA ATGGTGTAAC CATTTATACT GTTTTGTTC 180
 CTGTATTAG TAGACATAAC TGTGAATAG TTAGTGAATC ATGATGTAAA GAATATGTGA 240
 CCATCTTCAG GTATGGGATT TCTGAACGTT TCAAATTTC ATCAATGAGC ACTGTCAACA 300
 CCCACAGGNG AGAATAAAAT TACCTGTGCN 330

SEQ ID NO:134

LENGTH:326

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00148

SEQUENCE DESCRIPTION:

GATCGAACCA CTGCACTCCA GCCTNGGTGA CAGAGAGAGA CACTGCCTTN GAAAAAAA 60
 GAATCTCACT CACTATCTAG AGAGGATTGT CAGANTATTC ACGATTCAGN TCTTGAACT 120
 TTGATTATGC AAAAGAGGTA TATATAAATA TTTATTATG ATTCAGGTTT TAGGCTTTGC 180
 AGCTTCTATA AGGTGTTCTC AGGTGGCCCT TGTACNCTN AAAGCATCCT TTAGGAAATN 240
 CTTAAGGNG GGCTTTNTAT AAGGAATAGG NGGNTGTTGA ATTTTACAG GGGGGTTTG 300
 GTCATTNAGN CCCCATTNT GTANGN 326

SEQ ID NO:135

LENGTH:325

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00149

SEQUENCE DESCRIPTION:

GATCATGANC TCTGAAAAA AGAGAAACCT TATCTTTNCT TTGTGGTTCC TTAAACACA 60
 CTCACACACA CTTGGTCAGA GATGCTGTGC TTCTTGGAAG CAAGNCTCA AAGGCAAGGT 120
 GCACGCAGAG GGACGTTTGA GTCTGGGATG AAGCATGTNC GTATTATTTA TATGATGGAA 180
 TTTACGTTT TTATGTNAAG CNTGACAACA CCAGGCAGGT ATGAGAGGAA AGCAAGGCC 240
 GTCCATNGCT GTCGTACNC TTACGGNTTG CTTGTNGGAG NCATTTNGGT ATTGTTTGT 300
 GTAANANCCA AAANGGGCTT TGGNN 325

SEQ ID NO:136

LENGTH:326

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00150

SEQUENCE DESCRIPTION:

GATCNACGCT GTGCCTTGGC AGGGCACAAT GACCTTGTCG AAATCCACCT GTCAGGACGC 60
 CTAGGGGTCT GTACCGGGCT GGCCTGTGCC TATNACCTCT NATGCACACC TCCCACCCC 120
 TGTATTTCCA CCCCTGGACT GGTGGCCCT GCCTTGGGA AGGTCTCCC ATGTGCCTGC 180
 ACCAGGAGAC AGACAGAGAA GGCAGCAGGC GGCCTTGTG GCTCAGCAAG GGGCTCTGCC 240
 CTCCTCCTT CTTCTTGCT TCTNATAGCC CCGGTGTGCG GTGCATACAC CCNACCTCC 300
 TGCAATAAAA TAGTAGCATC GGCAA 326

SEQ ID NO:137

LENGTH:324

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00151

SEQUENCE DESCRIPTION:

GATCAAGNNG CCCTGGAGGC GGTGGCGGC ACCGTGGTTC TGGAGTAGCC TCCAGCTCGG 60
 AGGACTTGTN TNCAGGGGTC CTGGCCCCG GNCAAGGTCC CGCCCTCCG TGGTCACTGG 120
 CTCGCCCA GCACAGGCG CCCAGTGGAG CCGTTGGAA GAATTGCCTG CNGCAGGAG 180
 GGGGCCGGAC AGGCGCACAG ACCTACTGTN GCGGGAGGAA GGGCGGCTG CTGCCTGGTG 240
 ACGGCACCG GANGCCACC AGGACGCGC ACCGGTNAAT GTNCTCTNG TGGCTGCTGA 300
 GAAAAATACA CTGTGCAAGT CAAA 324

SEQ ID NO:138

LENGTH:323

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00152

SEQUENCE DESCRIPTION:

GATCTCAGCT TTTGTTTCC CATGATACCA TCTCTAGGG TAGCAGCTGG CTATAATAAC 60
 TAATGTCTGG ATTATCCTAA CTCTTCTGTT TGTNCTTTCA GGTATTAAAC AATGTTGTGA 120

CTAATTGGCT TCCATTATTT CCCTAGAGTA GGTCTGTGA TNACCCTGGA ATATGTTTGT 180
 AATAGAGTGG GCTATTACAA TCATCTAGGA TAAAGATAAT CGTGGCTTGG AATAAGGGTG 240
 GTAGCAATGG AAGTGATGAG AAGTCATTAG ATGCAGAATA TATTTTATAG ATGGANTGTG 300
 ATAAANTAAA AAATAAACTG GGN 323

SEQ ID NO:139

LENGTH:322

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00153

SEQUENCE DESCRIPTION:

GATCCATTCT CGGAATTCAC AGAATTTTNA TAACATCTNA CTCTCAGGGG GCATGAAGTG 60
 CATAATCTTC CCTAGATTAC AAAAAACATA TAGATGACGG GTTTCCTAT NAACTTCAG 120
 TACTACAAGA AACATAAAAT ATTTAAATAT ATGANATTTA AATATATTTA AAATTATTAA 180
 AGTAATATAA ACATTTTNA GTGACTGTGT TATGTTTTTC TGGTTATTTT GTTTTCTACT 240
 AGTATATTTT TCTGTAAAAA TTGTAAACT ATATCAGCAA TTTCTAATGC CAANAANGTA 300
 AAACCTNGTG TGTATAAATG CN 322

SEQ ID NO:140

LENGTH:323

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00154

SEQUENCE DESCRIPTION:

GATCAGAGGC ACAAGTNCAG AGGCTGTGGT CATGCCGAAC ACTCTGTTAT TTAAGATGGC 60
 TATCCAGATA ATCCTGAACA CTGTGTATTT ATTTAATTTA GACTACCAGC AAAGATTAAA 120
 GCATGAAATG TAAACATCT GATAAACTT ACAGCCCCCT ACACCAAGAG TGTATCTGTG 180
 AAAGAGCTCC TACACTTTGA AACTTAAGA NTCCCTTNTC ATGAAGTTTG CCTGTNCTAG 240
 AATTGTAAGA TTGTTAATTT CCNTCAATCT CTAGTGACAA CACTTAATTT CTTNCTAAT 300
 ANAAAAAGCC TNGTNGGTGN AAA 323

SEQ ID NO:141

LENGTH:328

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00155

SEQUENCE DESCRIPTION:

GATCAAGTTT AAATGACTGT GCTGCCCTT TCACATCAA GAACTACTGA CAACGAAGGC 60
 CGCGCCTGCC TTTCCCATCT GTCTATCTAT CTGGCTGGCA GGAAGGAAA GAACTTGCAT 120
 GTTGGTGAAG GAAGAAGTGG GGTGGAAGAA GTGNGTGGG ACGACAGTGA AATCTAGAGT 180
 AAANCCAAGC TGGCCCAAGG TGTCTGCAG GCTGTAATGC AGNTTAATCA GAGTGCCATT 240
 TTTTTTTTG GGTCAAANG NTTTTAATT TTTNGGAAT NGNNCCANTT TTTTNAATT 300
 NGCAANTAAA AANGTTTAAA ANCTTAAA 328

SEQ ID NO:142

LENGTH:369

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00156

SEQUENCE DESCRIPTION:

GATCTCTGGC AGTGGAGGAA GTCTCTTTAA GAAAATAGTT TAAACAATTT GTTAAAAAAT 60
TTNCCGTCTT ATTCATTTC TGTAACAGTT GATATCTGGC TGTCTTTTT ATAATGCAGA 120
GTGAGAACTT TCCCTACCGT GTTTGATAAA TGTNGTCCAG GTTCTATTGC CAAGAATGTG 180
TTGTCCAAAA TGCCTGTTTA GTTTTTAAAG ATGGAACCTC ACCCTTTGCT TGGTTTTAAG 240
TATGTATGGA ATGTTATGAT AGGACATAGT AGTAGCGGTG GTCAGACATG GAAATGGTGG 300
GGAGACAAAA TTATACATGT GAAATAAACC TCAGTATNTT AATAAAGTAG CACGGNTTCT 360
ATTTGNAAA 369

SEQ ID NO:143

LENGTH:324

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00157

SEQUENCE DESCRIPTION:

GATCATGAAG GAACACATAG CACCAAGAGA GGCCATGCTA AATCTCGCCC TGTCAGANNN 60
NTCCACACTT CTCCTTTGGG GAAGNCTTCC CTGTCCCCCT AGACTAAGTT AAATATTTCT 120
GCACAGTGTT CCCATGGCCC CTTGCATTTT CTTCTTAACT CTCTGTTACA CGTCATTGAA 180
ACTACACTTT TTTGGTCTGT TTTTGTGCTA GACTGTAAGT TCCTTGGGGA CAGGGCCTTT 240
GTCTGTCTCA TCTCTGTATT CCCAAATGNC TAACAGTACA GAGCCATGAC TCAATAAATA 300
CATGTTAAAA TGGGATGAAT GAAA 324

SEQ ID NO:144

LENGTH:316

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00158

SEQUENCE DESCRIPTION:

GATCATTGAA CGAGACAGAA AGCGACCATC CTGGTTCACC CAGAATTGAC ACCAAAGATG 60
TTAAAAGGAT AACTTCACAG TAAATCATTT CTCCTGAAAT AGAGGAAGAT TCTTTACGTT 120
GTTGTNCTTG TTTTAAATC ATCAGTATAG TTAAACACAT TCTTTCTAAG CAGTTTTGTG 180
TGGGATAATT TGAAGAATAT ATTATGAGTA ANCTCCGAAA ATTTTGTTTA TCCAAAGGCT 240
CANTGGATTA TGTTCTATT ATNTACAAGG TTTTAAGTAA ACATANNTT TCCNGNCCNG 300
AGNTTANAGN NATTTN 316

SEQ ID NO:145

LENGTH:323

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00159

SEQUENCE DESCRIPTION:

GATCTTCATT TTATTGCATT AGTTCATGTA GATGGGCATC TCTATGAATT AGATGGGCGG 60
 AAGCATTTC AATNAACCAT GGTGAAACTA GTGATGAAAC TTTATNAGAG GATGCCATAG 120
 AAGTTTGCAA GAAGTTTATG GAGCGCGACC CTGATGAACT AAGATTTAAT GCGATTGCTC 180
 TTTCTGCAGC ATAGCTTGTC AATAATGGAA ACACCAAAAA CTGTATTATT TGCAACTAAA 240
 TTTTCTCTGC CATACTAA CTCAAAAATT TTGATATTTT CATTAACCTG ATGATTAAAC 300
 TTTATGTGAG TTAANCTTTG AAA 323

SEQ ID NO:146

LENGTH:319

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00160

SEQUENCE DESCRIPTION:

GATCTTACTG CTTGTNACTT GAATCCCGTG ATTGTNATAC ATCTCTGGTA TAAGCAACAT 60
 TTGATTTTGG AAGTGTGTAG ACCATCTCTT CATATTTTCA AGATGTAATT TTACATTNCT 120
 GCATTTTAA AACAGTTTGG CCATAATCCT AGATGCACGC TTCTAATTCA TGTACCTGCA 180
 CATGTGACCT TTGTGAACAG NAATTTGCAT GNATAATTNG TGTTTACTTG TAACTNTCTG 240
 GTTATATACT GCTTATATCT GTGGATTCAA GTTACTGAAG TGGANTNCCA ATAGAAAGNA 300
 ANCCCTAGGC CATGTTAAA 319

SEQ ID NO:147

LENGTH:316

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00161

SEQUENCE DESCRIPTION:

GATCTCTGAT TACCAGCCTG ACATCAACAA ATCCCCTCAG TTACAACGTA TAGGTAAAC 60
 AAAGCTTTTA AAAGCTCATG TGGTATGACC TCAAGGTTGC TAACCTGGTC ACTCATGGTA 120
 ATNAGAACT CTGATTGGCA GCTTTGTATT TCTTGACTAA AAACCTAAAT AACTGATTA 180
 GGTTTTAGGC GTTCTTTCAA AGAGGTTCTT GAGAAGATTG AGAACTATCC TATTGGTGC 240
 TTAGTGAAAA GATTTTGAAT TACTGTACGT ACCAGTTGTT GCCATTTCTT TATTAAATTC 300
 AGAAGTTTTT TTGCCN 316

SEQ ID NO:148

LENGTH:319

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00162

SEQUENCE DESCRIPTION:

GATCTTGGAC AGCNTGGGTA TCGAGGCGGA CGACGACCGG CTCAACAAGG TTATCAGTGA 60
 GCTGAATGGA AAAACATTG AAGACGTCAT TGCCAGGGT ATTGGCAAGC TTGCCAGTGT 120
 ACCTGCTGGT GGGGCTGTAG CCGTCTCTNC TGCCCGAGGC TCTGCAGCCC CTGCTGCTGG 180
 TTCTGCCCT GCTGCAGCAG AGGAGAAGAA AGATGAGAAG AAGTAGGAGT CTNAAGAGTC 240
 AGNTGNTGNC ATGGGATTTG GCCTTTTTTG GTTAAATTCC TGNTNCNCTG CAAATAAAGG 300
 CTTTTTTTAC AGANGTAAA 319

SEQ ID NO:149

LENGTH:313

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00163

SEQUENCE DESCRIPTION:

GATCAATGCC CTCATTAAAG CAGCCGGTGT AAATATTGAG CCTTTTGGC CTGGCTTGTT 60
TGCANAGGCC CTGGNCAACG TCAACATTGG GAGCCTCATC TGCAATGTAG GGGCCGGTGG 120
ACCTGCTCCA GCAGCTGGTG CTGCACCAGC AGGAGGTCCT GCCCCCTCCA CTGCTGCTGC 180
TCCAGCTGAG GAGAAGAAAG TGGAAGCAAA GAAAGAAGAA TCCGAGGAGT CTGATGATGA 240
CATGGGCTTT GGNCTGTTG ACTAAACCT CTTTATAAC ATNGTNCANT AAAAAGGCTG 300
GAGCTTTAAT AAA 313

SEQ ID NO:150

LENGTH:313

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00164

SEQUENCE DESCRIPTION:

GATCCAGAAT CCACGGGGTC TGGAGCATAA GGTTTATCTC AAGTNTCAAT TGANCTGCCT 60
CCTCTTGTA GGCAGGGACA ACTGGGAGGA TGAGCCCCAA GAGCCTCAAG AACCAACAA 120
GGTGCCCTA GAAGACACAG AGACAGATGA NCTTTGGGCA TCCTTGGAGG CAGCTGCCAA 180
GCGGANAGCT CTCGGGTTTG GAGCAGCCCC AAGGAGCTCT CCAAACGAGA CGGAGAAAGA 240
AGAAGCGGCC TGGGTCCACC AGCCCTGAC GCCCTGTNN CCACTTTGTA AATAAACTTG 300
CTGAACACCC AAA 313

SEQ ID NO:151

LENGTH:313

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00165

SEQUENCE DESCRIPTION:

GATCATCAAC AAAGAAAGTC TGAGAAATTG TCCCGGAATA AAGGGGCCTA AGGAGACATA 60
ACATCTAAAT GTAATGTAGT ATCCTGGATG GACTCCTGCA ACAGAAAAAG AACTTTAAGT 120
AAAAATTAAG GGAATATTAA TAAAGTATGC ATTTTGGTTA ATAATGTATC AATATTGGTT 180
TATTAGTTGT GACAAATGTA CCAGAGGAAT GTAAATGTC AACAATAAAG GAATTGGATG 240
TGGGGTCCAT GAGATGCTGT ACTATTTTGG CACTTTTCTT AAATCTAAAC TCTTATAAAT 300
TTAANCATAA AGN 313

SEQ ID NO:152

LENGTH:317

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00166

SEQUENCE DESCRIPTION:

GATCTGGCCA TCTACGAGCC AAAGACTTTN AAATCTTTGG CTGCCTTGGC CAGTAGGAGG 60
 CGACACGAAG GATTTNCTGC TGCCTTGGGG GATGGGAAGN AACCTGAAGG CATTTTTNCC 120
 AGAGTGGTGC AGTACCACTN AGGACTGTTG CTGTATTGAT TAGGAAAAGA GACAGAGTAA 180
 TTTNCAGTTT GTTTGATTTA TACTTTTGT TATCTACAAC CCAATAACAG ACATGAGGGA 240
 TGGCCCTGTC TCTCTGGGAC AGAGCCTCAA AGATGATGTC CATGTTTTGT GTGAATGAAA 300
 CTCAAACACT CTTCAA 317

SEQ ID NO:153

LENGTH:310

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00167

SEQUENCE DESCRIPTION:

GATCCCTGTC CCCCTGTCCC CTGCCTCTTT TCCCAATTCC CTTCTTATG CTGGACTTTT 60
 AAAGCTTAAA AAAAATCCGA TTGAATATAA ATGCCTAATT TCATTCTTTG TGAATGGTT 120
 GCTTCCTCCT GATTCCCTAA TTGTGCTGTG TTCGTGTCTT GCACTGGAAT TCAACATTCC 180
 CTTCTCCTTT TGTACTGTGT TGTGCTTGCT GTCTCTCCCG GACANCCTA AAGACTGTCT 240
 TTTTAGCAA AAATTCAGT AAAGTGTTTT CTGTAATCTT TTTTAAAAG GTGAGAACTA 300
 ATTATTGTCN 310

SEQ ID NO:154

LENGTH:309

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00168

SEQUENCE DESCRIPTION:

GATCACCAGC GTTTTCAGCC ATGCTCAGAC AGTGGTTCTT TGTGTAGGTT GTTCAACAGT 60
 GTTGTGCCAG CCTACAGGAG GAAAGGCCAG ACTCACAGAA GGGTGTTTAT TTAGAAGAAA 120
 GCAACACTAA TGATTCAAAC AGCTTCCTGA ATTTAATTT TGTGTTGTCT CACAGAAAGC 180
 CTTATCATAA ATTCATAAT TCTAATTAAT TTACCAAGAT AATGTAATTA CATTGGTTT 240
 TGTAAGGTAT ACAGCAGTAA TCTCCTATT TGGTGTCAGT TTTTCAATAA AGTTTGTATT 300
 ATGGGCAAA 309

SEQ ID NO:155

LENGTH:307

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00169

SEQUENCE DESCRIPTION:

GATCACATAC AGGGGAAAAG CCCTATGNAA TGTAACACAT GCAGGAAAAC CTTCTCTCAA 60
 AAGTCAAATC TCATTGTACA TCAGAGAACA CACATAGGAG AAAANCCTA TGANTGATTT 120
 GGATATTAGA AATTNCCAGC CACAAGTCAG CCTCCATAAT GCNTCAGAGT CTTCACTG 180
 TGGAGANGGG CCTGTTGACA TCCTGATTGT TCANTAATA TCCACAACCT CGCCTTATGT 240
 TACTCCANNG TAACAGTAGG GGTAAANCC ATAGNCTACA ACACCTNTNG GNTGGCTTTT 300

NTTAGGN

307

SEQ ID NO:156

LENGTH:307

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00170

SEQUENCE DESCRIPTION:

GATCCACCAA CTTTGGCCTC CCAAAGTGTT CAGATTACAG GTGTGAGCTG CTACCATGCC 60
TAGCCCCAGC TTCTACTGCT TGANGGCTCT CTTTGGCATC TCCACACATC ATCCTTAGCA 120
GCCCAGACTG CATTCTGTGA GCAGCCTCTT CCCTGGTCTC TTCTTTCAGT CTCTCTGCCT 180
CTAATCCAGT GGCTTTAAGA ATTTTTTGGC TGTGACTTCC AGTAAGAAAT ACAATTTACA 240
TTGTGACCTA GTAAATATGT GTGTAAGATT TATTAAGTGA AATAAAAAATG TTATGATTGA 300
ATTTTTN 307

SEQ ID NO:157

LENGTH:306

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00171

SEQUENCE DESCRIPTION:

GATCTGTCCC TGTGGTGGTG TCTAAGAATC GGACACCTTG GTTTTTGTGT TAGATTGAGC 60
TGGGCAGCTG CAATCAGCTA CTTAATATGC AAATTAGGCA CGTCCCCTCT GTGGGTCCCTT 120
GTTGGTGGCT AATGAAGTGA GGGGAGGGAG GGATGTCACC CAAAAGTAG GCCCTCCCAT 180
TGGCTTTGGC CAGGCCAGAC ACTTCACATC GTTTACATGG TTCTGTGTAA TTTAAAGTT 240
TATGTGTATA AAGCGACGGT TTTCTGTGAA CTGTATATTT TGTAATAAAA TATATTGCTA 300
CTTTGN 306

SEQ ID NO:158

LENGTH:310

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00172

SEQUENCE DESCRIPTION:

GATCTTCAGA TAAATCTGC CATTTNATT TCACTTCCTG AAAGTNAGGG TCGGCTTGTN 60
AAAAGTTGTT AAACAACATG CTAAATGTGA AATGTCAACC CTCACTCTAA ACTTCCCTG 120
TTCAGAGCAT CAGATGAAGA CTTCAATGGG TTTTATAGTG GCTTCTGAT TTTNGGTAGT 180
CCATTGAAGA AGGGAGTTTG AAAGTTGTTG TATACTGTGA ACGATTGTCT GCCCATGTCC 240
TGCCTGAAAT ACCATGATTG TNTATGGAAG GTATCTTTAA TAAAGCTGGA TACAGTTTGG 300
CTTGGAGAAA 310

SEQ ID NO:159

LENGTH:306

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00173

SEQUENCE DESCRIPTION:

GATCTACTTT GGAAAAACAA AGGATATCGT CAATGGGCTG AGGTCTGTNC AGACTTTTGC 60
 AGACAAATCA AAACAAGAAG CTCTGAAGAA TGACCTGGTG GAGGCTTTGA AGAGAAAGCA 120
 GCAATGCTAA ACCTCTGTTT CATGCTAACC AGACACGCCG TGCACTCGTT AGATTCCTTT 180
 CTTAGAAAAC TCGTTTTCTG CTCCCTTCCC TCGTCCCTTC CCTCCCCGAC AGGTCACATA 240
 ACAGCTGCAT CATTGACCGC ACAGCGCCAT CTCTCCCTGA GAATAAAGCC GATAGCCACC 300
 NTCAA 306

SEQ ID NO:160

LENGTH:329

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00174

SEQUENCE DESCRIPTION:

GATCTATTGG ACTTTTTTTT GCAGGAAGTG CATTCTCTGG TCCTTCCCTA TTTCTGTTC 60
 TGGATGTCAG TGCAGTGCAC TGCTTACTGT TTTATCCACT TGGCCACAGA CTTTTCTAA 120
 CAGCTGCGTA TTAATTTCTAT ATACTAATTG CATTGGCAGC ATTGTGTCTT TNACCTNGTA 180
 TACTAGCTTG ANATAGTGCT GTCTCTGATT TCTAGGCTAG TTAATTGAGA TATGAATTTN 240
 CCATAGAATA TGCAGTGATA CAACATTACC ATTCTTCTAT GGAAAGAGAA ACTTTTGATG 300
 ATGAAACAAT AAAGNTTTTA AATATCAAA 329

SEQ ID NO:161

LENGTH:303

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00175

SEQUENCE DESCRIPTION:

GATCTGAATA AAGCAAATCT GCATAAATGG TAACCAGTAG CTCTACTTTN ATTTTNNATG 60
 TTGCTTAACT GTTTTATTTG AAGGAAACCT GTGTGATTTA AAAAGTTATA GCTTTTGCAA 120
 CTTTATTACT GGTTATATAC ATTTGGCCAT TATNATGTGC AAGCAATTGG AAAAAAGTC 180
 AAGTAAATGC TTGTTTTTGT AGTAGTTTGT TCTTGTTAAA AATGTTTATA TGATAATGTC 240
 TGTAAACAGC ATCACTTTGA TTACAATAGA TGTAGTGTG TAATAAACTG TTTAATGGGG 300
 AAA 303

SEQ ID NO:162

LENGTH:298

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00176

SEQUENCE DESCRIPTION:

GATCTCTCTA GCTTTGTCAT AGTTATGTGA TTTTCCTTTG TAGCTACTTT TGCAGGATAA 60
 TAATTTTATA GAAAAGGAAC AGTTGCATTT AGCTTCTTTC CCTTAGTGAC TCTTGAAGTA 120
 CTTAACATAC ACGTTAACTG CAGAGTAAAT TGCTCTGTTC CCAGTAGTTA TAAAGTCCTT 180
 GGACTGTTTT GAAAAGTTTC CTAGGATGTC ATGTCTGCTT GTCAAAGAA ATAATCCCTG 240

TAATATTTAG CTGTAACTG AATATAAAGC TTAATAAAAN CAACCTTGCA TGATTAAA 298

SEQ ID NO:163

LENGTH:309

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00177

SEQUENCE DESCRIPTION:

GATCTCCTTC ATCCCTCTCC AGAAGAGGAG AAGAGGAAAC ACAAGAAGAA ACGCCTGGTG 60
 CAGAGCCCCA ATTCCTACTT CATGGATGTN AAATGCCCAG GATGCTATAA AATCACCACG 120
 GTCTTTAGCC ATGCACAAAC GGTAGTTTG TGTGTTGGCT GCTCCACTGT CCTCTGCCAG 180
 CCTACAGGAG GAAAAGCAAG GCTTACAGAA GGATGTTCTT TCAGGAGGGA AGCAGCACCT 240
 AAAAGGCACT CTGAGGTCAA GGATGAGGTG GGGAANCCAT CTCAATTAAC CACCATTTTT 300
 TGGGTAAA 309

SEQ ID NO:164

LENGTH:295

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00178

SEQUENCE DESCRIPTION:

GATCTCGGTA AAAATCTACC ATTCCCTACA TATTTCTCTG ATGGAGATGA AGAGGAACTG 60
 CCAGAAGATT TGTATGATGA AAACGTGTGT CAGCCCGGTG CGCCTTCTAT TACATTTGCC 120
 TAACATCTTT GGACGTGGCA GAACCTTACA TATTCTGTGA GCTTCGATGA GCCAGAGTGA 180
 TATCATAACC ACCAGAAATC ATACTCTCCT TTCTTAGTCA CAACAAAATC ACACATGTCA 240
 TCTTTGTCAA GGGCATAAAT ATATCATTCA TACCCCATTT AAATTTTGTT AGAAA 295

SEQ ID NO:165

LENGTH:289

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00179

SEQUENCE DESCRIPTION:

GATCCCCACC CCATGTGTTT TAAAAAGGCA GTAGCCTTTG CAGGGACCTG TCTGTCCCAA 60
 CTGTTTGAAC AGTGTGCTCC TCAGATTCTG TGTTCAGAAG NCCCCTGNTG CATTGAGACT 120
 TGAAACCTTT GGATAGGGGA AAAAATTATA TATATATATA TNNNTTGTG CTGTTTGCAT 180
 TTCTTAATTT GTGCTTGGA TGTGTTGATG TGCACAGCTA ATGATTCAAT GCGAGACAAG 240
 ATTGGCGTCT GTGTTGTGGA GGTTCAAAT AAAGAGCACT CTTCATAAA 289

SEQ ID NO:166

LENGTH:300

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00180

SEQUENCE DESCRIPTION:

GATCTGTAAA ATGTGATTTT TTA CTTCAC TTATAACT TGTGATTGGG GAGGTTTGTG 60
 GAAATTCAAT TATGATGAAA AACCTATCTT TTTGTAATG TTGGCATACT TGGGGAATTT 120
 AGTGGCAAAT ACATTCCCCA GCAGGCCTTT TGTGGTTGC ACTAACTGCA AGGTTGCTGG 180
 GAAGTAGAGT CCATTGGTT GATGAGCTTT GACTGCGGTT TTGGAACCTT ACCTCTCCTC 240
 CTTAGCCCAA TATGCTGTCT TGGGTCCTAT TCAAATAAAG TTATTTCTCC TGGTCTCAAA 300

SEQ ID NO:167

LENGTH:292

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00181

SEQUENCE DESCRIPTION:

GATCAAAAAA CCATCTCCAC ATTTAAAAGA GATGTAAGGT GTATTCATAG GGATGGTGGC 60
 TCAACAAATC AAGCAAAC TG GAATCAAGGG GAGGGGGAAG GGAATNAAAT GGAAAGGGAG 120
 GCTGATTCCC TTCCCTGAC TTACCACTAA TTTACTAGGC TACCTACTTT NATGAGTAAC 180
 CTCTCACAGC TACCCAGCAC ATGCCACAAT CCTATGCTCT TGCCTTCTTT NATCTGCACT 240
 GTGTGAAGGG ACTCTTTTAA ATAAATNAGC AAGTGTCTTA AGCTATGTCA AA 292

SEQ ID NO:168

LENGTH:292

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00182

SEQUENCE DESCRIPTION:

GATCTTGGCT GTATTTAATG GCATAGGCTG ACTTTTGCAG ATGGAGGAAN TTCTTGATTA 60
 ATGTTGAAAA AAAACCCTTG ATTATACTCT GTTGGACAAA CCGAGTGCAA TGAATGATGC 120
 TTTTNTGAAA ATGAAATATA ACAAGTGGGT GAATGTGGTT ATGGCCGAAA AGGATATGCA 180
 GTATGCTTAA TGGTAGCAAC TGAAAGAAGA CATCCTGAGC AGTGCCAGCT TTCTTCTGTT 240
 GATGCCGTTT CCTGAACATA GGAAATAGA AACTTGCTTA TCAAACTTA AA 292

SEQ ID NO:169

LENGTH:333

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00183

SEQUENCE DESCRIPTION:

GATCCACATG AACGCACGCC TGAGATTGG CCACTCACCT ATGTTTGGG TGGATTGCCT 60
 AGGAAAGCAA GTCATATGGC CATTGATAGT TCTCATGTAA TTAGTTTTC TCACCACTAG 120
 TACAGATGAC CCGTTTACAC GTGGCTTCCC TCGGAAGCCT CCTCAACAGT AGCTGGTGTG 180
 AAAGACTAAA TCAGTAGAGT TGGAAAAGCT TTATAACCGG TGTGTCATAT GCTTGCTATT 240
 TAAAGCTGTG TGTGGTTTT GTTTTCTGC CACATTCACT AGTTTTTTAA TAAATATTTT 300
 CCAAAANTGG AAAAAAANA NNCCNCNCCN CCN 333

SEQ ID NO:170

LENGTH:401

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00184

SEQUENCE DESCRIPTION:

```
GATCTGGANG GGACACGTCA TGCCTTGGGC CTAGAATACC CTGATGNGAA AAGAGAAGAN 60
AAAGGGAGGC CATATCTACA ACACAGCCTC TCGGCACTGC TGCTCCTTAT TTAACTTTG 120
TNTTGCAATTG TCCTGTATTT ATCACAGTTT CTGTTGAACA GCTTTTCAAG TATTGGGGA 180
GTTTATCTTG CCATCCTCCC CTTCTGGTTC TCTGCACCCA CCTGTCCCAC TGCAGTTCCT 240
TCCGTGCTCT GTGACTTTAA GAGAAGAAGG GGGGAGGGGT CCCGGATTTT ATGTTTGT 300
GNTNTTCTC CTTAGCAGTA GGAAGTATA TTTTCAATT TGAAGAAGT AAAAGATGAA 360
TAAACTGGGT TTTTTTGT GTTGNTTTT GNAAATCAA A 401
```

SEQ ID NO:171

LENGTH:305

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00185

SEQUENCE DESCRIPTION:

```
GATCGAGCTC GCCTATNAGC AAGTGGCAA CCCCTCAA TAAGCCCCTC CTGGGACTCC 60
CTCAACCCC TCCATTTTCT CCACAAAGGC CCTGGTGGT TCCACATTGC TACCAATGG 120
ACACACTCCA AAATGGCCAG TGGGCAGGA ATCCTGGAGC ACTTGTCCG GGATGGTGTG 180
GTGGAAGAGG GGATGAGGA AAGAAATGGG GGGCCTGGGT CAGATTTT TGTGGGGTG 240
GGATGAGTAG GACAACATAT TTCAGTAATA AAATACAGAA TAAAAATCAA GTGTTTTTAC 300
GCAA 305
```

SEQ ID NO:172

LENGTH:289

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00186

SEQUENCE DESCRIPTION:

```
GATCTGAGGC AAGCTGGACA GGAGAGGTGG ATATTTNTTG ATGGAAGAAT TCAAGTTTAT 60
AATCAATTCC CACTAGCAC CTACTGTGTG CTAGGAAGT GAATGTGTAT GTTGACAAG 120
TCCTGCTTGG CCTGATGGGT GGGAGANGGA ACCTGAGCCT GGCTGAGATG GCTAGGCGGA 180
GGGCTTTGAA GTCCAAGCAG CTGAACTGGC TGGGTGGGT TCTACCTTTG AAAGTCAAG 240
ACTTNTTTG GAGCTCTTAA TTACAATATC TGATATTTT ACAGTCTGN 289
```

SEQ ID NO:173

LENGTH:286

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00187

SEQUENCE DESCRIPTION:

```
GATCCCTACC CTNCCGTTG GTCTCTNTCG CTGACTCGAG GCACCTAACA TCCATTCACA 60
CCCAACACAG GCCAGCGACT TCTGGGGCTC AGCCACAGAC ATGGTTTGTN ACTNTTGAGC 120
```

TTCTGTTCCCT AGAGAATCCT AGAGGCTTGA TTGGCCCAGG CTGCTGTNTG TNCTGGAGGC 180
 AAAGAATCCC TACCTCCTAG GGGTGAAAGG AAATNAAAAT GGAAAGTTCT TGTAGCGCAA 240
 GGCCTGACAT GGGTAGCTGC TCAATAAATG CTAGTNTGTT ATTCN 286

SEQ ID NO:174

LENGTH:290

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00188

SEQUENCE DESCRIPTION:

GATCGGGTTC TAAAGGAAAG GGTGGAGAGA TTCAACCAGT TAGCGTGAAA GTTGGAGATA 60
 AAGTTCTTCT CCCAGAATAT GGAGGCACCA AAGTAGTTCT AGATGACAAG NATTATTTCC 120
 TATTAGAGA TGGTGACATT CTTGGAAAGT ACGTAGACTG AAATAAGTCA CTATTGAAAT 180
 GGCATCAACA TGATGCTGCC CATTCCACTG AAGTTCTGAA ATCTTTCGTC ATGTAAATAA 240
 TTTCCATATT TCNCTTTNAT AATAAACTAA TGATAACTAA TGNCATCAAA 290

SEQ ID NO:175

LENGTH:284

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00189

SEQUENCE DESCRIPTION:

GATCAAGGCG CGGACGTATC TACGACCACA TCAACGAGGG GAAGCTGTGG AAACACATCA 60
 NGCACAANTA TGACAACAAG TAGTTCCTTG GNGGCCCTAT CCAGGCCAGA AGGCCANNGC 120
 CACCCAGCAG CTGTTTGCCA GAGCTGGAGC TCAGTTGAAG ATGATGCTCA AGGTACTCTT 180
 CATGGCCACC ATTCGTGTG GAAGAACGNT TTACTIONNA CAGCTCTTTA CCTTCTGTGT 240
 GTTTNAGNTG TTAGNAGATN TCAGGAATAA TGTGATTGCC TTGN 284

SEQ ID NO:176

LENGTH:282

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00190

SEQUENCE DESCRIPTION:

GATCAGAACA TGAAATGCCC TCCTAAATGT CAGCTGTTGT CACACAGTAG CTCCAACACT 60
 TTGAGCATTT TTAAGGGAGT GGCCTCATTT CACTAGAGAC AAATCTTTAA GAATAGTTCT 120
 AAAATTGGGC TTGTGATTTT CATTTCTGAT GTCTCCAGAT TGGCACCCCT TTCTAGTTCA 180
 ATGCCTCACG AGATTTTGCC AGGGGCATCC AAGGCAAACA ATCCCAATCT TTCTATATAA 240
 ANTGTATTCA AGCAAACATC AAATAANTTT CTGGGATATT TN 282

SEQ ID NO:177

LENGTH:278

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00191

SEQUENCE DESCRIPTION:

GATCAGAGTT TGAAATGAAA TGTTCGTCAG GGTGTTGGAA AAATTTTGGT GAGTCTGCA 60
 CATTTCCTT GGTTCAGGCT GGGCATGGAC CAGCCTTCAG ATGGCAGAAG TGGAAGATGA 120
 GCCTACTTGT GAGCGATGTG ACTTTAAGGA AATGAAGACT GGGGAAGAAT AATTAGTGTT 180
 TATAAGACAT TTAAGAGGCC CTTTTTCATA TACTGACTCA CTGATGAATC AGCATTNGCA 240
 TTNTATGGAA NAATATAAAT CCAAAGAAAT AATTTAAA 278

SEQ ID NO:178

LENGTH:281

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00192

SEQUENCE DESCRIPTION:

GATCAAAATA ACCCTCGTAA AAATATATGT ANGGGGTACA CAAAGTAAGC CTCITTATGA 60
 AACAATTGAG GATAATNATG TGAAAGGTTT TAATGATGAT GTTCTACTTC ANATAGTTCA 120
 CTTTCTACTG AATAGACCAA AAGAAGAAAA ATCACAGCTG TTGGAAAACT GAAAAAGCAT 180
 ATTTNATTGA GAACTGTGGG AATATTTAAA TTTTACTGAA GGACCAATAA TGATGAGATT 240
 TGTAAGTGTC AACTATTAAA TACATTGATT TTTGAGACAA A 281

SEQ ID NO:179

LENGTH:278

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00193

SEQUENCE DESCRIPTION:

GATCAGGCCC AGGAAGGGCA CAGGGGCTGA GCACTACAGA AGTCACATGG GTTCTCAGGG 60
 TATGCCAGGG GCAGAAACAG TACCGGCTCT CTGTCACTCA CCTTGAGAGT AGAGCAGACC 120
 CTGTTCTGCT CTGGGCTGTG AAGGGGTGGA GCAGGCAGTG GCCAGCTTTG CCCTTCCTGC 180
 TGTCTCTGTT TCTAGCTCCA TGGTTGGCCT GGTGGGGGTG GAGTCCCTC CCAAACACCA 240
 GACCACACAG TCCTCCAAAA ATAAACATT TATATAGN 278

SEQ ID NO:180

LENGTH:278

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00194

SEQUENCE DESCRIPTION:

GATCTACATT AATATCAAGT CTTGACTCCC TACTTCCCGT CATTCCTCAC AGGACAGAAG 60
 CAGAGTGGGT GGTGGTTATG TTTGACAGAA GGCATTAGGT TGACAACTTG TCATGATTTT 120
 GACGGTAAGC CACCATGATT GTGTTCTCTG CCTCTGGTTG ACCTCNACAA AAACCATTGG 180
 AACTGTGACT TTNAAGGTG CTCTTGCTAA GCTTATATGT GCCTGTTAAT GAAAGTGCCT 240
 GAAAGACCTT CCTTAATAAA GAAGGTTCTA AGCTGAAA 278

SEQ ID NO:181

LENGTH:277

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00195

SEQUENCE DESCRIPTION:

```
GATCTCTCCC CCGTGAAGGA GTTGAGCACA TTAGCAACAA TGTACATTAA TTTTGGATTT 60
TCATTTTCAT GTTTTATTTT GTAAATATTA TCTGATGTTT GGAGCTTGAG TATACAGACT 120
GTAAATATAG TTCTTGTATT TGTACTAATT CTGATTCTTT TGCTNNCNGG CCTTAGATGT 180
GCAATGCAGA CACTATCTAA CTGTGTGTGG TAACCTTGCG TCACGGAGCT GTTAGTGAAC 240
GAGGTAAAAA TAATAAAGGT ACAGCCAGTG CATCAA 277
```

SEQ ID NO:182

LENGTH:282

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00196

SEQUENCE DESCRIPTION:

```
GATCAAAACN GATTACGGT GGGGGAGGAA TNTGAGCTGG AGACAATNAC AGGGGAGAAA 60
GTCAAGACAG TGGTTCAGTT GGAAGGTGAC AATAAACTGG TGACAACTTT CAAAAACATC 120
AAGTCTGTGA CCGAACTCAA CGGCGACATA ATCACCAATA CCATGACATT NGGTGACATT 180
GTCTTCAAGA GAATCAGCAA GAGAATTAA ACAAGTCTGC ATTCATATT ATTTTAGTGT 240
GTAAAAATTA AATGTAATTA AAAGTGANCT TTNGTTTTTA AA 282
```

SEQ ID NO:183

LENGTH:277

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00197

SEQUENCE DESCRIPTION:

```
GATCCAGATG ACCGTGGTNG TTGGGGTATA TCTCCTCGAG GAGCTGGTTA CACCTTTGGG 60
CAAGATATTT CTGAGACATT TAATCATGCC AATGGNCTCA CGTTGGTGTC TAGAGCTCAC 120
CAGCTAGTGA TGGAGGCATA TAACTGGTGN CNNGGCCCGG AATGTAGTAA CGATTTTCAG 180
TGCTCAAAC TTTGTTATCG TTGTGGTAAC CAAGCTGCAA TCATNGANCT TTGCGATAC 240
TCTAAAATAC TCTNTCTTGC AGTTTCACCN AGNNNNN 277
```

SEQ ID NO:184

LENGTH:277

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00198

SEQUENCE DESCRIPTION:

```
GATCTGAGAT TTCCGTGTTT GGCTGAACCT GGGAGACCAG CTGGGCCTCC AAGTAGGATA 60
ACCCCTCACT GAGCACCACA TTCTCTAGCT TCTTGTGAG GCTGGAACGT TTTCTTTAAA 120
ATCCCTTAAT TTTCCATCT CAAAATTATA TCTGTACCTG GGTATCCAG CTCCTTCTTG 180
GGTGTGGGGA AATGAGTTTT CTTTGATAGT TTCTGCCTCA CTCATCCCTC CTGTACCCTG 240
GCCAGAACAT CTCACGATA CTCGAATTCT TTTGGCN 277
```

SEQ ID NO:185

LENGTH:277

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00199

SEQUENCE DESCRIPTION:

GATCGGTTTT TGTTCCTGCG TTACCATATG ATTGTAAATT GTTTTATGTA TTAATCAGTT 60
 AATGCTAATT AATTTTGGCT GATGTCATAT GTTAAAGAGC TATAAATCC AACAACCAAC 120
 TGGTGTGTAA AAATAATTTA AAATTCCTT TACTGAAAGG TATTCCCAT TTTGTGGGG 180
 AAAAGAGCCA AATTTATTAC TTTGTGTTGG GGTTTTAAA ATATTAAGAA ATGTCTAAGT 240
 TATTGTTTGC AACATAAAT ATGATTTTAA ATTCTCN 277

SEQ ID NO:186

LENGTH:276

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00200

SEQUENCE DESCRIPTION:

GATCCTGACA CTGACATGAA GGCAAGCCTT GATTCGTAT GAACGTTGCT GAAGTGGTAA 60
 TTGAGGAAAA CAGTTCCTCA GATTGTTAAG AGTTCCTGA AGATATTGAC ACAATTTNNA 120
 AAAATCAGTA AAGGAATGTA TATAATATTG CNCTCGTGT TTACAGTAAG ATTTGTTGCT 180
 CTCAGACTGT GTAAAACAAA ATTNATNGNT GTTTCTGCA TNTAAAAAA TCTTATTGTA 240
 CCANCTGGTA ANCTATTAAN TGCCTATAAN NCTAAA 276

SEQ ID NO:187

LENGTH:275

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00201

SEQUENCE DESCRIPTION:

GATCAAGGAN GAAAGANTGA CTTCAAATAT GCCTTGTTAG TGTAAATGTG ACTTNTNGAA 60
 CTGTATGAGT ATTTTAAGAT TATTNGAGTA AAGTAAGTTT TAAAAAGCAG TCCCTAATCA 120
 TCAAAAGTAA AAAACTCTTG ATGTAGTCAT ATAACCACAC TAAGAACTCT TCCAGGTGAC 180
 TTCAAAACAT AGGACAGTAC ATCTCTAGTA GANTNTGCCC TGAGAATGAA AAGAATGTAA 240
 CAGTGTTAGT ATTTTGAATA AACATGTTAT TACTN 275

SEQ ID NO:188

LENGTH:273

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00202

SEQUENCE DESCRIPTION:

GATCACTTTT TTTAGAGTGA AGAAAGAACA ANCTTGTTTT TTGTGTTTTT TAAAGGAATA 60
 TAAAATAATG AAGGATGTAT AATTGATGCC AAATAAGCTT GTNCTTTAGT CACACCGACG 120

TCTTATTTT CCCTTTAGGC CAGTTCTGTT TTTAAGGTGT ACATGGNCAA TGTTACAGTG 180
 TAAGAACTC CATATCCATA TGTNCCATT CGCATTTTGT ATTGGTTCAT GTATACCATT 240
 TTTNCAAAAN ANANGGAANA ANNGGNAGTN CTN 273

SEQ ID NO:189

LENGTH:271

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00203

SEQUENCE DESCRIPTION:

GATCTGAAAA GCTCACTTTA AACTCATACT ACATTCGTNA CGAGTATTTN ACGTTAACAT 60
 AATTGAAAAG TACAAGGTCC AAGCTGGCTT TCAAATNATG TCTAAACAGA AATGGGACAA 120
 ATAGACTTGA AAATAGAAGG GATTTATTCC ACCCCTGCAA GGGTAAGAGT CAGGTGAGAG 180
 TCCCTTGGTG AGTCATTTGT ACATCAGTGT CATTCTTCT TAACCTCTGA AGAAAGATGG 240
 GCATCAGAAA TAAAGACAAA GCACTATCAA A 271

SEQ ID NO:190

LENGTH:270

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00204

SEQUENCE DESCRIPTION:

GATCTGCCAC GAGGGCAGCA GCCAAGAGGA CTTGCTCTCT CCATGTGAAT GTACAGGGAC 60
 CTTGGGGACA ATTCATCGGA GCTGCCTGGA GCACTGGCTG TCATCCTCAA ACACCAGCTA 120
 CTGTGAACTC TGCCACTTCA GGTTCGAGT CGAGCGAAAA CCCAGGCCGT TAGTGGAGTG 180
 CCTGGGAAAC CTTGGCCCCC AGATTGGGAG GGGNCTTTT TTTGGNGANA TGGTNNNTT 240
 TGGGTTNTAA ATCNCNCGG NNCCATNTNN 270

SEQ ID NO:191

LENGTH:166

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00205

SEQUENCE DESCRIPTION:

GATCTCTGAG CTGCCCAGCA TAGTCCAAGA CCTAGCCAAT GGCAACATCA CATGGGCTGA 60
 TGTGGAGGCC AGGTATCCTC TGTTTGAAGG GCAAGAGACT GGTAAAAAAG AGACAATCGA 120
 GGAATGAGGA CAATTTTGAC AACTTTTGAC CACTTGGCT AATAAA 166

SEQ ID NO:192

LENGTH:276

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00206

SEQUENCE DESCRIPTION:

GATCTACATG AGAAGTATAG TGGCTCTACC CCCTGAAAGA GGGTGGATGC AGCTGCTTGT 60

GTTTCTGGG GTGACTGTCA TTGGTAATAC GGACACAGTG ACCCATCCTC CATCCTATTT 120
ATAGTGAAG GGCCTTCAAT TGTATCAGTA CTTNTTTTA AGCTCTGGCA CATTGACCTC 180
TATGTGTTAC CAGTCATTAA TGAGCTGCTG CAGAGGTGAC TATTTGTTT ACTTTCTTGG 240
ATGTTAACAT TACACTACTC ACTACTCAAT CTCAAA 276

SEQ ID NO:193

LENGTH:273

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00207

SEQUENCE DESCRIPTION:

GATCTGACAT TTGACATGAA CACAAAGTTG CTAGATGCTC TTGTTGACTT CCAGCAGATG 60
GGATGGGGGA AACACAGCAG TTCTTGGTAA AGTCCTTTGT AATAATAGTT TGATTTTTTT 120
ATTTGAGAG AATCTTTCAT TTTCTATGT ATGCTTTTNN CCTTTTTTGC CCAGTTTCCT 180
TATCACTTGC TGTAGATGGC TTATNTNGCA TTCATGCAGA CTATGTTGCA AGTCTGTTTC 240
ATCTAGTAAA CTGAAAATNA TTGCTTAATC AAA 273

SEQ ID NO:194

LENGTH:267

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00209

SEQUENCE DESCRIPTION:

GATCCCAGAG AGGGAAGAGA ACCAGGGGCC CTTTCTCTT TNAGAATTTN CTTTAAATCA 60
GCCCACCTT TGAATCCCG CCCGCCCAA TCCATTATNT TTTCTGCCT TCCGGGTCCC 120
ATCCTTAGAG CTCGAGTCGT TCCTCCCTT CCTGGATTCC GGGTAGCAGA GGCAGCGCCG 180
CAGGAGGCGG GTGCCGTTT GTCCAGGNC TGGCGTGGT GGAGNNAGGG GTGCTGGAAC 240
AATAAACGGC ACNNNNCAAA TGTCAAA 267

SEQ ID NO:195

LENGTH:384

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00210

SEQUENCE DESCRIPTION:

GATCCAAAAC ACTACTCAGC TCTCTGCAC TGAGGAAATT TTTCCCCTA CATTGACTCC 60
TGGCCTACAT CAGCCAACT TAACCTTGGT GGGGTTTGA TTTGATAGCC AATTAGTTCT 120
GTGCTGGTTG CAAAGAATTG ATATTTAGAT GGTTTTAAAT ACTCAGCAGA TTGTCTTCCT 180
TTATATTGTG TCTTTTTTAT GTNGCATGN GCTTTTGTTA TCAGCCTGAT TTTTGCTCA 240
GTATATGATA GTNCTGCTGA TGTTTTGTT ATTGGGCAGA CATATCTCA TTAAGAGTTT 300
TTGGAACACT CATCAAAATC GATGAATACA TTTCTTCAT AACCCATTG GAATTATTCC 360
TAATAAATG ATAAATACG TAAA 384

SEQ ID NO:196

LENGTH:277

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00211

SEQUENCE DESCRIPTION:

```
GATCTAAAAA AATTCAGAAG AAATATGATG AAAGGAAAAA GAATGCCAAA ATCAGCAGTC 60
TCCTGGAGGA GCAGTTCCAG CAGGGCAAGC TTCTTGCGTG CATCGCTTCA AGGCCGGGAC 120
AGTGTGGCCG AGCAGATGGC TATGTGCTAG AGGGCAAAGA GTTGGAGTTC TATCTTAGGA 180
AAATCAAGGC CCGCAAAGGC AAATAAATCC TTGTTTGTG TTCACCCATG TAATAAAGGT 240
GTTTATTGTT TTGTTCCAC ATTTATGTTG CCTGAAA 277
```

SEQ ID NO:197

LENGTH:271

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00212

SEQUENCE DESCRIPTION:

```
GATCGGGCGG GCGCAGNAAC CGCTCCTACA GCAAGCTGCT GTGCGGCCTG CTGGCCGAGG 60
CGCCTGCGCA TCAGCCCGGA CAGGGTCTAC ATCAACTATT ACGACATGAA CGCGGCCAAT 120
GTGGGCTGGA ACAACTCCAC CTTCGCCTAA GAGCCGCAGG ACCCAGCTG TCTGCGCTGG 180
CTCCACCCGG GAACCCGCCG CACGCTGTGT TCTAGGCCCG NCCACCCCAA CCTTCTGGTG 240
GGGAGAAATA AACGGTTAG AGACTAGGAA A 271
```

SEQ ID NO:198

LENGTH:264

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00213

SEQUENCE DESCRIPTION:

```
GATCCTGTAG TGTTCTGGA GAAGCTAGAG CCTGATTGTA GGCTACTACT CATCAATTAA 60
CTTCTACAGT GGAGACTACT TCTGGGACTG GAATATAAAA AAGAATCAAA GGTCTGATT 120
TTNAGTTGCA ATAAAGGGAA AGACCATGCT CATAGCAGTG CCAACATCTG AAGTGTGGAG 180
CCTTACCCAT TTCATCACCT ACAACGGAAG TAGTTAACTG GAAGAGATTA CCAAGAGAAT 240
AAAAAGAGAC TCATTCACTG GAAA 264
```

SEQ ID NO:199

LENGTH:257

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00215

SEQUENCE DESCRIPTION:

```
GATCTGCCTT AAAGAAAAGA AAATTTTGA AAGAAATATT GTTGCTCAGT GTTGTTAATA 60
TAGCTCAAGA ATTGAGTTTA TATTTGCAGT ATGCTATAAA TGATACCCCC CTACCACACC 120
CACACACACA GTTTTTGTCT AATGAAAATG TTGCTGTGAT TATTATAAT TGGTAGTATT 180
TCTTCCAGAA GAAGCTAAAA TAAGACTGGC ACTTACCCTG AAGTGCATTA ATAAAACCAC 240
ACTTTAAAT TAANAAA 257
```

SEQ ID NO:200

LENGTH:374

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00216

SEQUENCE DESCRIPTION:

```
GATCAACCTG AGCNTGGAGA ATGCCTGGGG CATTTAACGC TCGTCATTG ACATCTGCAT 60
GAAGCTGGAG GAGGGCAAAT ACCTCATCCT CAAGGACCCC AACAAAGCAGG TCATCCGTNT 120
CTACAGCCTC CCTGATGGCA CCTTCAGCTC TGATGAAGAT GAGGAGGAAG AGGAGGAGGA 180
AGAAGNGGAA GAAGATGNGG ANGAACTTA AACCAGTGAT GTGGAGCTGG AGTTTNTCCT 240
TCCACCGAGA CTACGNGGGC CTTTATGCT TAGTGGAATG TNTGTCTAAC TTTGCTCTCT 300
TGACATTTA GCAGTTGAAA TTAAATTATA TANTCTGTTT TNNGTCTTTT NAAATAAANA 360
AAANNANATT NTGN 374
```

SEQ ID NO:201

LENGTH:256

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00217

SEQUENCE DESCRIPTION:

```
GATCTGAACT ATTTGCTTTC TCTTCAAGAT AAGTTGTATT TTACCATGGA AAAATACAGT 60
ATCTAACATT ACCATTCACG TTAAATGAAG TTTCCTCATA ACATTATCT TTAGTTTTAT 120
GAAGTCATCG TGACCAATGT TACAGTAATT TCTGTTAGCT GATTGTGGTA AACAATGTTT 180
AATGNGAAAA GAAATTAAAA CTTTCTTCAT CTGTTGTAGA ATATTCTCT TCTTTAAAT 240
GGCTTCTATT CATAAA 256
```

SEQ ID NO:202

LENGTH:256

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00218

SEQUENCE DESCRIPTION:

```
GATCCCCACT GGAGCAGCCT CTGCAAAAGG GAGCCCATGT AGTGGCCAGG GGCTGTCCAA 60
ACTCCAGCTT CTTCCCTGG GAAAAACCC AAAGAACCAA AAACAAACCA CCCCAAGGAT 120
AATAATAGCT AACTGCTAG CTTCTCAAGT TCTTGTGAAA AACAATTTAC ATAATGACAC 180
AGTAGATGTG GAACACCTAG CCAGTGCCTG GGCAGGTCCC TATTATCATA AATGAACATA 240
AAGTGTCTTA AAAACN 256
```

SEQ ID NO:203

LENGTH:265

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00219

SEQUENCE DESCRIPTION:

GATCCAAATC AGGAAAAGAC GGCGCCACTA CAATGGAGAA GCATATNAGG ATGATGAACA 60
 TCATCCCAGA GGTGGTGTTC AGTGCAGAC CTCTTAATGG GCCAGTGAAT AACACTCACT 120
 GCTGGCATT TATGTGCAGT AGTGAATGAG TGAAGGACTG TAATCATAAT ATGCTCACTA 180
 CTTGCTCTTG TTTTGTGTTT AATAAACTAT AGTAGTGTTA TAANNNGTTA AATGAAGAAT 240
 AAACGCAAAT ATAANAGCTC TGAAA 265

SEQ ID NO:204

LENGTH:253

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00220

SEQUENCE DESCRIPTION:

GATCTAAAGA GACACTTAGA GACTCTTGGG GACCTCAGAT TTCCACCNCT CCACAGCATT 60
 CTGCCTACAC AGTTCCCTC ATTTNCCTA GTTACTCGGA AGAGCGCTGG ACTTGAAATC 120
 AAAATAATTG CGTTATGTCT TTGGTTATGT CGCTTCATCA TAGCACTTTC TAAAACTATT 180
 TGACAAACAT GTATTGCATA CCTACNGCAT TCCAGTTCTN GTACANGTAA TTAAATGCTC 240
 GACTAACGNN AAA 253

SEQ ID NO:205

LENGTH:253

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00221

SEQUENCE DESCRIPTION:

GATCTGGAAT TGGACATTTC TCTGTCAGAG CACAGAGGAG GCTCATATCA CCTCTTCCCT 60
 CTCCTACTTG GCCCAGCTGC TTGGAGGACC GACCCCATGG CTGAGAATAT NACGGCAAGA 120
 GGAACAGAGN TTGCTCCAAG TGGGAAAGGG TCCCAAGCAG TCCAGAGAAG ATGTCTGTGT 180
 GGCTTTCCT CCCTGCCTCC CCCAGCTCCC AACTGGCCT TTGTAAATAA ATGGCGTGGT 240
 CTTTGTGTG AAA 253

SEQ ID NO:206

LENGTH:253

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00222

SEQUENCE DESCRIPTION:

GATCTGCCGT CTGTCACCTC TCTCCAAGTT GAGACAGGGG CCTGGATTTC AGCCCTTCCT 60
 GCCGAGAAAT CTTNTAAATT TCAACCTACC TTTAAAAATA AAGTCTCCCT ACTTAAATC 120
 CAGTAGATAT CATGGCACTA ATGCTAACAC CCCTTCCCC AAATTAATAA AACAAAAATA 180
 AAAAAAGAA AAAANTGCAG GCATGCAAGC TTGGCGTANT CATGGNNTNA GCTGTTTCCC 240
 NGTCACGGCG TGN 253

SEQ ID NO:207

LENGTH:251

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00223

SEQUENCE DESCRIPTION:

GATCGAGACA CGTGATGGGA AGCTGGTGTC TGAGTCCATN ACGTCCTNCC AAGTGAACAG 60
 CTGCGGCAGC CCTCCCAGCC TACCCCTCCT GCGCTGACCC AGAGCCTGGG AAGGAGGCCG 120
 CTATGAGGGT AGCACTGGGA ACAGGAGACC CACCTNAGNC TCAGCCTNGC CTCAGTNTAC 180
 TGGGGAGTTT ACTACCTGGG GCCCANTGA CATGCTCCAG CTACANACAN TTANTTGCTT 240
 TTTTNTTGGN N 251

SEQ ID NO:208

LENGTH:243

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00224

SEQUENCE DESCRIPTION:

GATCGATTCT TGTATATTNA TTTTATCTCT TTCTGTATCT ATAGGTAAAT CTCAAGGGTA 60
 AAATGTTAGG TGTGACATT GAGAACCCTG AAACCCCAT TCCCTGCTCAG AGGAACAGTG 120
 TGAAAAAAA TCTCTTGAGA GATTTAGAAT ATCTTTTCTT TTGCTCATCT TAGACCACAG 180
 ACTGACTTTG AAATTATGTT AAGTGAAATA TCAATGAAAA TAAAGTTTAC TATAAATAAT 240
 AAA 243

SEQ ID NO:209

LENGTH:249

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00225

SEQUENCE DESCRIPTION:

GATCACANTT AATGATTGAG TATAATGTTT GAGGCCAGAC AAGATATATA TTGTGCCTCT 60
 TACAGCCTTT GGNNCNNTTG TTTCATTTT TTAAATATCT TCTATATCCA TATAGTATTC 120
 AAATNATTAA TGCTCATGTA CCAAGGTTTT GCTATAAAAG TTTTGNCTGT ATGAATAATG 180
 TGGCTTTAGT AAATAATCAT TTTTCAACTG TAAACTTATT CTGAAATAAA GTAAAATTCT 240
 AATTGTTTN 249

SEQ ID NO:210

LENGTH:248

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00226

SEQUENCE DESCRIPTION:

GATCATAGAA ATATATGTAA AGTATTCAAT TTTCAATCAT TTTCAAATNA CTGTTATAAA 60
 TTGTTTTTGC TGAGTTGTAA TACTTTTNAG ATACAATGTA TTCCTTGAC TGAAAGAATG 120
 AAAAAGGACT TTTTCAGCAT TTGAGGTAAG TNCTTTAAG TTTTATTAAA ANCATTTTTT 180
 ACAAATATTT TGTACATGCA CTTGCAGTAT TGAGGTTAAT CATTTTAATA AATNCGGAAA 240
 TTAAAAACN 248

SEQ ID NO:211

LENGTH:247

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00227

SEQUENCE DESCRIPTION:

GATCTCAGCN TTGCAACAC ANTTNCTACA TAGATAGTAC TAGGTATNNT TTAGATATGT 60
AAAGAAAGAA ATCACACCAT TAATAATGGT AAGATTGGTT TATGTGATTT TAGTGGTATT 120
TTTGGCACCC TTATATATGT TTTCCAACT TTCAGCAGTG ATATTATTTT CATAACTTAA 180
AAAGTGAGTT TGA AAAAGAA AATCTCCAGC AAGCATCTCA TTAAATAAA GGTTTGTCAT 240
CTTTAAA 247

SEQ ID NO:212

LENGTH:256

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00228

SEQUENCE DESCRIPTION:

GATCAAAACA AACAAATCCAG ATGTATAAGT ACTAGGCAGA AGCCAATTTT AAAATTCCT 60
TGAATAATCC ATGAAAGGAA TAATTCAAAT ACAGATAAAC AGAGTTGGCA GTATATTATA 120
GTGATAATT TGTATTTTCA CAAAAAAAAA NGTTAACTC TTCTTTTCTT TTTATTATAA 180
TGNCAGCTT TNGGTATTTT ATTGTTACCA NGTTCTATTT TTNGANTAA ATTGTTCTCC 240
TTCTAAANGT TTAAA 256

SEQ ID NO:213

LENGTH:244

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00230

SEQUENCE DESCRIPTION:

GATCGGCAAG CCCCACTG TCCCTTGCA GCAAGGCCA CCTTTNATGC CATTTCTAAG 60
ACCTACAGCT ACCTGACCCC CGACCTCTGG AAGGAGACTG TATTCACCAA GTNTCCCTAT 120
CAGGAGTTCA CTGACCACCT NGTCAAGACC CACACCAGAG TCTCCGTGCA GCGGACTCAG 180
GCTCCAGCTG TGGCTACAAC ATAGGGTTT TATACAAGAA AAATAAAGTG AATTAAGCGT 240
GAAA 244

SEQ ID NO:214

LENGTH:243

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00231

SEQUENCE DESCRIPTION:

GATCAGATTG GGTCTGCTC CTCTCAACCT TGAAGTCCCC ACGTATGAGT TCACCAGTGA 60
CGATATGGTG ATTGTTGGTT AAGAGACTTG GACTCAAGTC ATAGGCTTCT TTCAGTCTTT 120
ATGTCACCTC AGGAGACTTA TTTGAGAGGA AGCCTTCTGT ACTTGAAGTT GATTTGAAAT 180

ATGTAAGANT TGATGATGTA TTGGCAAACA TTAATGTGAA GTAAATNGAA TTNAATGTNG 240
AAA 243

SEQ ID NO:215

LENGTH:243

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00232

SEQUENCE DESCRIPTION:

GATCGCCAGT GGAAGAAGAT TAGTGCAATC ATTGAGAAGA GGAAGAAGAT GGAAGCTGAT 60
GGGGTTGAAG TCAAAAGACC AAAATACTAA TCACTAGTTA CAACCAGAGA TGCTCCACAA 120
GGATATGCTC CCCACGGTTT TCTTTCTACA ATTTCCAAAG GTTGCAAGAT GTTTTTTTGT 180
GGATGAATAT AAAATTTTAT TGTGTAATTA CTTGGTTCCA TTAATTTGG TTAAGTTGCT 240
AAA 243

SEQ ID NO:216

LENGTH:243

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00233

SEQUENCE DESCRIPTION:

GATCGTAGAT GTTAACCAAA TCTACAAAAT CCACTACTCC CCCGTTATCA ACGGGATACG 60
TTCCAAGACC CCCAGTGGAT GCCTGAAACT GGCTAATGCT GAACCCTACA TATACTATGT 120
TTTNCTGTA CATATATATG ATAAAGTTTA AATNATAAAT NAGGTACAGT AACAACAATA 180
ACAGTAAAC AACAGTTATA ACAATATACT GTAATAAAG TCATGTGAAT GTGGTGTTC 240
TCN 243

SEQ ID NO:217

LENGTH:242

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00234

SEQUENCE DESCRIPTION:

GATCTTCTCC AGATTGGCAG AAAGTTGATA TAGGTGGACT TTTTACAGG TCAGTTGAGG 60
CAAAAACTA TGGGTTTTT CAGGTGAACC TCCCCATT AAATACTCAG AAGATAAGGT 120
GTGAATGTAT GTATTATTAG AGTCCTAAAG TATTTATAA GTACTGGTT CACCACGCTT 180
TGTGGGAGAG AAATCATTCA AATCATTTTT TTTGTCCGTA CAATAAAGTT TACTAAAAAC 240
CN 242

SEQ ID NO:218

LENGTH:238

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00235

SEQUENCE DESCRIPTION:

GATCTTCGTG ATACTGTACA TAGCTGTTG AAATGCCAGA ATGACTTCTG ACATNCCAAG 60
TTTTTCACAA AATATATTN ATCTGTGATT AGCCATTGA CTAATAATAC TGGCTAACAG 120
ATGTTGAAAA AAATTGTCTG TTTTCTCATT AATTTTGGTC TAAAACATGT TTGCACTTGT 180
NTTGGACTTG TGTTTTATTA ACATTGATTG GCATATTAAA AGTCACTCNG AGCTTAAA 238

SEQ ID NO:219

LENGTH:239

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00236

SEQUENCE DESCRIPTION:

GATCCAAANN ATGACTTCAG AAAAACTTG AAAGTAACAG CAGTGCCTAC ACTACTTAAG 60
TATGGAACAC CTCAAAAACT GGTAGAATCT GAGTGTCTTC AGGCCAACCT GGTGGAAATN 120
TTGTTCTCTG AAGATTAAGA TNGGTAGGAT GGCAATCATG TCTTGATGTC CTGATTTGTT 180
CTAGTATCAA TAAACTGTAT ACTTGCTTTG AATTCATGTT AGCAATAAAT GATGTAAA 239

SEQ ID NO:220

LENGTH:250

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00237

SEQUENCE DESCRIPTION:

GATCAGAGGT GAAGGGACAG AGAGAGGAGA GGAGGAAGAT TGAGCTGGGG GCAACAGCCA 60
AGCTCACCTG GGCAGGTCTC TGCCACCTCC TTGCTCTGTG AGCTGTCAGT CTAGGTTATT 120
CTCTTTTTTT GTGGCTATTT TTAATTGCTT TGGATTTGTT AAATGTTTTT TGTCTTCTGT 180
TAAGTGTGTT TTCTCTGGAG ATAGAATGTA AACCATATTA AAAGGAAAAA GTTTCAGACA 240
AGCAATTAAA 250

SEQ ID NO:221

LENGTH:237

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00238

SEQUENCE DESCRIPTION:

GATCAGCTTT GTCCTGAAA TTGCATCCGA AGAAGAAAGA AAGGGGATGG TGGCTGCGTG 60
GTCCCAGAGG CTGCAGACCA TCTGGAAGGA AGAGCCCATC CCCTGCACAG CCCACTGGCA 120
CTTCGGGCAA TAACTCTGTG GCACGTGGGC ATCACGTAAG CAGCACACTA CGAGGCCAG 180
GCGCAGGCAA AGAGAAGATG GTGCTGTCAT GAAATAAAAT TACAACATAG CTACAAA 237

SEQ ID NO:222

LENGTH:243

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00239

SEQUENCE DESCRIPTION:

GATCAGTGTA GAACTGGTCA TAGAGGAAGA GCTAGAAATC CAGTAGCATG ATTTTAAAT 60
 AACCTGTCCT TGTTTTTGAT GTTAAACAGT AAATGCCAGT AGTGACCAAG AACACAGTGA 120
 TTATATACAC TATACTGGAG GGATTTCATT TTTAATTCAT CTTTATGANG ATTTAGAACT 180
 CATTCTTGT GTTTAAAGGG AATGTTAAT TGAGAAATAA ACATTGTGT ACAAATGCT 240
 AAA 243

SEQ ID NO:223

LENGTH:232

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00240

SEQUENCE DESCRIPTION:

GATCTAATAA CAGGTTGACA TAAGAAATAT TTGTCTCAA AATCAATGTA TTTAATAGTT 60
 GACAGTTACA AATCTCATCA TTGAAAGATT TAATTTAGT TACCTTTTGT TGATTANNN 120
 NNNATTGCAT TTGTATATTG CTAAGTATA AGACAAATTG AGTTATTGAG CTATTAANTG 180
 CACATTTTAA TATAANTGCA GAAATCCCAA ATAAATGCT AACATACTGA AA 232

SEQ ID NO:224

LENGTH:237

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00241

SEQUENCE DESCRIPTION:

GATCACCGTG ACATCCGAGG TGCCTTCTC CAAAAGGTAT TTGAAATATC TCACCAAAAA 60
 ATATTGAAG AAGAATAATC TACGTGACTG GTTGC GCGTA GTTGCTAACA GCAAAGAGAG 120
 TTACGAATTA CGTTACTTCC AGATTAACCA GGACGAAGAA GAGGAGGAAG ACGAGGATTA 180
 AATTCATTT ATCTGGAAAA TTTTGTATGA GTTCTTGAAT AAACTTGGG AACCAAA 237

SEQ ID NO:225

LENGTH:236

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00242

SEQUENCE DESCRIPTION:

GATCTTCACT TAANCTAAGT CTGTGAATTA CTTTATATT ATTTGAAAN ACTCCTTGCA 60
 GTATATTGGC ATGATACAGT AAAAGCANTT TCCACAGATT GTTATCACCT TCTTTAAAAG 120
 AAGTCAAAAT TTAATAAATA CAATAGCAGC TTGTGGTGT CATATTCAAT AACATTTCCA 180
 ATGCTACATA TAATTTTATA GACATAATAA AGAAGGTATT GAAAAAATA AATAAA 236

SEQ ID NO:226

LENGTH:227

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00243

SEQUENCE DESCRIPTION:

GATCGCCACC TACCGCCGCC TGCTGGAAGA TGGCGAGGAC TTTAATCTTG GTGATGCCTT 60
GGACAGCAGC AACTCCATGC AAACCATCCA AAAGACCACC ACCCGCCGGA TAGTGGATGG 120
CAAAGTGGTG TCTGAGACCA ATGACACCAA AGTTCTGAGG CATTAGCCA GCAGAAGCAG 180
GGTACCCTTT GGGGAGCAGG AGGCCAATAA AAAGTTCAGA GTTCAAA 227

SEQ ID NO:227

LENGTH:205

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00244

SEQUENCE DESCRIPTION:

GATCAGCAAG CAGGAGTATG ACGAGTCCGG CCCCTCCATC GTCCACCGCA AATNCTTCTA 60
GGCGGACTAT GACTTAGTTG CGTTACACCC TTTCTTGACA AAACCTAACT TCGCGAGAAA 120
ACAAGATGAG ATTGGCATGG CTTTATTTGT TTTTTTTGTT TTGTTTTGGT TTTTTTTTTT 180
TTTTTGGGTT NNCCCCNGGT TTAAG 205

SEQ ID NO:228

LENGTH:226

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00245

SEQUENCE DESCRIPTION:

GATCTGCCCA AAGAGGTGTT GGCTGAGCTT NAGGCCCTGG AGAGACGTGT GCACAAAATG 60
TNACCTGAGG CCCTAGTCTA GCAAGAGGAC ATAGCACCTT CATCTGGGAA TAGGGAAGGC 120
ACCTTGACGA AATATGAGC AATTTGATAT TAACTAACAT CTTCAATGTG CCATAGACCT 180
TCCCACAAAG ACTGTCCAAT AATAAGAGAT GCTTATCTAT TTTAAA 226

SEQ ID NO:229

LENGTH:228

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00246

SEQUENCE DESCRIPTION:

GATCAGCCCC AGATTTGACG TGCAACTCAA AGACCTGGAA AAATGGCAGA ATAATCTGCT 60
TCCATCCCGC CAGTTTGGTT TCATTGTACT GACAACCTCA GCTGGCATCA TGGACCATGA 120
AGAAGCAAGA CGAAAACACA CAGGAGGGAA AATCCTGGGA TTCTTTTCT AGGGATGTAA 180
TACATATATT TNCAAATAAA ATGCCTCATG GACTCTGGTG CTTCCAAA 228

SEQ ID NO:230

LENGTH:308

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00247

SEQUENCE DESCRIPTION:

GATCTGCGAC CATTTCTGTA CAACACAAGC TGGCCTTGGC AGTTTCGGTG CATAGAAAAT 60

CAGGTGCTAC AGCTCGAGAG GGCAGAGCCA CAGTCCCTGG ACGGCGTGGA CTGAGGCCGG 120
 TTCCTTCCTG GAGGCCTCCT GTCCTCGGGG ACCCCAGCAC CTCATCATCA GCATTGCTGG 180
 AGCCAAGGGT AGGAGCCCTA CACTAGGAGC CCAGGATGGG ACGGNGNATN AGCCGAGAGG 240
 NAGGGAACCT TTNAGTNAAA TTCCTCAAAA AGAGGNTTAG AATAAANCCT TNGGCTTAAA 300
 AAGAGAAA 308

SEQ ID NO:231

LENGTH:230

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00248

SEQUENCE DESCRIPTION:

GATCCAAAGA CAGACCACAG ACTGGGAAAA GTTGAAGAT GAACACTTGA GGAATTCAGC 60
 TTCTCACCTA CTTAGTACAG TTGGGAACCA TACACTTCTG GCATGTTTGG AAATCAAAAT 120
 GTCACATTCT CGGGGGAGGA AGCCCAGAAA ATTGGGTATG TTCTAGAGAT TTACCACCAT 180
 TGCTTATTGC TTTNCTCTT TAATAAAGTT TAGGAAAGTA GAATTTTAAA 230

SEQ ID NO:232

LENGTH:228

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00249

SEQUENCE DESCRIPTION:

GATCTAAAGA TTTCTCTATC CAATGAATCT AACAAAGTCA ATGGAAATTG AACTCTAGAA 60
 TTGTCTCTAG AAAACATAGC TTCTTACTGA ACTTGAACAT TTTTACAACA TTCCTGGTT 120
 TTTGTTTTGT TAGCTAATAA TCTATAATAG TTGAGTATCT CTGGGAATGG GGAGGGAAAT 180
 TATATGTAAT AGAGCTTAAA AATAAAGTGT CAATTTCCTAA GGNCTAAA 228

SEQ ID NO:233

LENGTH:221

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00250

SEQUENCE DESCRIPTION:

GATCAATAAG CATGTCAGAC TGATTAATGT CTAAGTGAA AATTGGTAG TAAATTTNCA 60
 TTTGATATTA GATATAAATA TCTGAATATA AATAATTTNA ATATACTAGT CATGATGTGT 120
 GTTGATTTN AAAAATTATC TGCAACCTTA ATTCAGCTGA AGTNCTTTAT ATTCAAAAG 180
 AATGAATAAC ATGATAATA AAATCGCTAC TTTAAGGGAA A 221

SEQ ID NO:234

LENGTH:219

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00251

SEQUENCE DESCRIPTION:

GATCTCTATG AATGTCAGAG CCCTAACTTT CAGGCTTTGC ATTTTGTATA TGGGAAGAAA 60
 TATGACAATC CTAGGTAATT AAACCATAGA CCCAAAGCCC TTACGTTTGA TGCAATTTAT 120
 TTTTAAAATA GGCCTTGTTT TTCAGCTTCA TCTGCAGTTC TATGTGAAGA TTGATAAATC 180
 AGTTTTTACT TGTTTTATTA ATAAAACGTA ATTNGGAAA 219

SEQ ID NO:235

LENGTH:287

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00252

SEQUENCE DESCRIPTION:

GATCTCCGTT CCGCTCCCAG CGGCTCCAGT GTAAATCCC CTCCCCCTG GGGAAATGCA 60
 CTACCTTGTT TTGGGGGGTT TAGGGGTGTT TTTGTTTTTC AGTTGTTTTG TTTTTTTGTT 120
 TTTTTTTTN CCTTGCCCTT TTNCCCTTT NATTTGGNGG GAATGGGAGG AAGTGGGANC 180
 AGGGAGGTGG GAGGTGGATT TTGTTNATTT TTAAAGCTCA TTTCCAGGGG TGGGANTTTT 240
 TTTTNAANAT GNGNCATGAA NAAAGTTGT TTTTGAAANT AACCAAA 287

SEQ ID NO:236

LENGTH:222

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00253

SEQUENCE DESCRIPTION:

GATCAGAATT GGCAGCACAA AGAAAACGCC CTCTCCTGAC TTGTATTGTG GCAGTCTGAA 60
 CGNCCCAGA AAATTGTGCC AAAGAGTTTA GAAAAATAAA TATACAATAA AAGTAAACAC 120
 ATACACAAA AACAGCAAAC TTCAGGTAAC TATTTTGGAT TGCAAACAGG ATAAATTAAA 180
 TGTTCAAACA ATCTGATAAA ATAACCATTG GGGNCTTGNA AA 222

SEQ ID NO:237

LENGTH:221

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00254

SEQUENCE DESCRIPTION:

GATCATCTTT CCTNTCCAG AGAAGTGGGC TGGATGTCTC CATCTCTGTC TCAACTTTAC 60
 GTGTACTGAG CTGCAACNTC TTACTTCCCT ACTGAAAATA AGAATCTGAA TATAAATTG 120
 TTTTCTCAA TATTTGCTAT GAGAGGTGA TGGATTAATT AAATAAGTCA ATTCCTGGAA 180
 GTTGAGAGAG CAAATAANGT CCTGAGAACC TTCCAGACAA A 221

SEQ ID NO:238

LENGTH:217

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00255

SEQUENCE DESCRIPTION:

GATCAGACGT TTTACAAATN CATGAAGCGA ATTGCTGCTT GTAAGGAGCA GATTTTAAGG 60
 TATTCCTGGA GTGGAGAGCC ACTCTTTTA ACCTGCCCTA CATCAGANGT CACCGAGCTC 120
 CCAGCCTGCA GCCAGTNTGG AGGCCAAAGG ATATTNNATT TTCANCTTAT GCCAGCNCCTG 180
 GTCAGCATGC TCAANAGTGC TANTTTAGGT CTTNCTN 217

SEQ ID NO:239

LENGTH:217

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00256

SEQUENCE DESCRIPTION:

GATCTCTCTG AGTCTTGGCA ACATCCAGCA AAATACTGC TTATTCTCCA AAGAATATTG 60
 GGAGCTCTCA ATCCTCGGTG ATATGGGAAA GAGAACTGAG TATTGGCCCT ATGACTGAGC 120
 TTTCTATAGG AATTTTATTA AAGAATGTTT AATTNGTTG TCCTNCTNAA TGTTCCTCAGT 180
 CAAATAAATG AGTGAGCTGG TTTCGGCTGC TCTTGGN 217

SEQ ID NO:240

LENGTH:216

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00257

SEQUENCE DESCRIPTION:

GATCCCATGG ACATTTGGGG AAAGGGCTCC TTGGGCTGCT GGTGAACTTC TGTGGCCACC 60
 ACCTCCTGCT CTTGACCTCC CTGGGAGGTG CTATCAGTCT GTCTGGCCT TTCAGTTTAA 120
 TAAGTNGNTT CCAGCCCCAG TGTCTGACT TCTNCTGCAN AATAGGAGGG AGGCCTCCTT 180
 TTNGGANGGN NGTACTTTGG GNGATAGTGN GGCCTN 216

SEQ ID NO:241

LENGTH:220

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00258

SEQUENCE DESCRIPTION:

GATCTTTTAA GTTCTCTTCC CTACCCAGTC CCCATTTTCT GGTAAGGTTT CTAGGAGGTC 60
 TGTTAGGTGT ACATCCTGCA GCTTATTGGC TTAAAATGTA CTCTCCTTTT ATNTGGTCTC 120
 TTTGGGGCCG ATTNGGNGAA AGCGAAATCA NTAGTGCAAC TGTTTTGATA CTGAATATTG 180
 ACAAGTGTCT NTTNAAATA AAGACCCANT CCCTTCCAAA 220

SEQ ID NO:242

LENGTH:223

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00259

SEQUENCE DESCRIPTION:

GATCACTAAT CAATAATCTG ATATTTAACA AAATATGGAC AGGCCACTTA TGCTCAGTTT 60

TACCTTAGTT ATTCTTGGT ATCCACAGGC CCAAGTCCCT TTAAATAAAA TACCCTCATA 120
 TTTCATATA ATCTACATAC ATTCTCCCAT ATACTTTAAA TCATCTCTAG ATTACTNATA 180
 ATGTCTAATN CAAAATAAAT GCTATGTAAA TGTAATTATT AAA 223

SEQ ID NO:243

LENGTH:216

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00260

SEQUENCE DESCRIPTION:

GATCAACTTA ATTCTTTTC TTTATCTTCC NTCCCTCACT TCCCTTTTCT CCCACCCTCT 60
 TTTCGAAGCT GTTTCGCTTT GCAATATATT ACTGNNTAAT NAGTTGCAGG ATAATGCAGT 120
 CATAACTTGT TTTCTCCNAA GTATTTGAGT TCAAAACGCC NGTATCTAAA GAAATACGGT 180
 TGGGGTCATT AATAAAGAAA ATCTTTCTAT CTAAA 216

SEQ ID NO:244

LENGTH:212

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00261

SEQUENCE DESCRIPTION:

GATCTCAGAA CAATCAGATG CAAAGCTGAA AGAGATTGTA ACAAATTTCT NTGGCTGGAT 60
 TTGAAGCTTA AACTCCTGTG GATTCACATC ANATACCAGT TCAGTTTGT CATTGTTCTA 120
 GTAAATTAGT TCCATTTGTA AAAGGGTTAC TCTCATACTC CTTATGTACA GAAATCACAT 180
 GAAAAATAAA GGTTCCATAA TGCATAGTTA AA 212

SEQ ID NO:245

LENGTH:221

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00262

SEQUENCE DESCRIPTION:

GATCCATCTG CCTTTGTGGC TGCTGCCCCT GTGGCTGCTG CCACCAACAG CTGCTCCTGC 60
 TGCTGCTGCA GCCCAGCTAA GGTGGAAGCC AAGAAAGAGT CGGAGGAGTC GGACGAGGAT 120
 ATGGGATTG GTCTCTTTGA CTAATCACCA AAAAGCAACC AACTTAGCCA GTTTTATTG 180
 CAAAACAAGG AAATAAAGGC TTACTTCTTT AAAAAGTCAA A 221

SEQ ID NO:246

LENGTH:214

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00263

SEQUENCE DESCRIPTION:

GATCCCATTG GAAGGAATGC TCTACCTCAC AGAACTCTGA ACCCTACAGA AATATGGGCC 60
 TGCTGCCATT TCCTGAAGAC CGGGGCATCG GGGTGGGGTG ATAAAGGATA CAACCTGCAC 120

AGGGGGAAGT TATTAAAGAG GCTGCAAAGT CCAGCCACCC TGAAGATACT CCCCAGTGCT 180
 CCCCTCCTGC TAAAGAACCA GTTACCCAG GAAA 214

SEQ ID NO:247

LENGTH:208

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00264

SEQUENCE DESCRIPTION:

GATCCTCAAC TATTGGAAT NATGGACTGG TGGCCCTGGT ACAGAACCAT GACTGGCTGC 60
 TGAATTCTGA AAACCAGGAC TTGGTTCAAC ATTTAAATTT GATAGTTGCC CTGATTCCCA 120
 TTTTGGGTTT GTGAAAAGTG TATGTATTTA AATTTGCTGT AAAACATAAT CACTAATAAT 180
 ATGCAATAAA TATTCCTTG AAGGGAAA 208

SEQ ID NO:248

LENGTH:208

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00265

SEQUENCE DESCRIPTION:

GATCTGTGGG AGGAATGGCA AGAGAAGCAA CCGGACCCTG AGAGAAGAGT GTTAAGGAAC 60
 CTGCGCATGT GGTAGCTTG ACCTTTCTGT TGGGCATGAC ATGGGGTTTT GCATTCTTG 120
 CCTGGGGACC NTTAAATATC CCCTTCATGT ACCTCTTCTC CATCTCCAN TTCATTACAA 180
 GGTAAGATAA ATGTACATG AATAGTCN 208

SEQ ID NO:249

LENGTH:201

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00266

SEQUENCE DESCRIPTION:

GATCAAATAT CACTAAATAC TTAAATTGT TTTACTTAAG AGTCTAATCT GGGAAGTTTT 60
 CAAATCATAC TATTAATGTG TAATCTAAGC TCTTCAGATG TATCCATGAA TAATCCTGGA 120
 ACAATATTGC TTGTATTCCT GTCATAGAAC AGGTTTTGTA ATCTTTAAAA GAAATGAAAA 180
 TTTATATAAT AAAGTTTCAA A 201

SEQ ID NO:250

LENGTH:211

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00267

SEQUENCE DESCRIPTION:

GATCACCTTG GTGTTCTTG TTTGGAAGAT TATTCCTCT GAATTTCTGG GCTTGGTCTT 60
 CCAGTTGGCA TTGCGTGAA GTTGATTGA AACAATTAN TGAAAAATATT AAATATTTGG 120
 TTTCAAAAGG CAGATTTATC TTCTCCAAC ATTCTGTTAT TTCTGATACT TTTGAAAAAC 180

TAATAAAAAAT TAATAAAAGA CATGAACTAA A

211

SEQ ID NO:251

LENGTH:208

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00268

SEQUENCE DESCRIPTION:

GATCCAAGAA AACGCCTCAC TGCCTTAACC TTAAGTGTTC TTCCTGGCGC TAAAAAGAGC 60
 TGTATTTTTT AAAGTGCTGG GGCAAACAAA GNANCCCCAA AAGAGTTGAT GTGTGTTTAA 120
 AAAGNAAAAA CCCAATGAGG AACAATTGGA GATTTTATG CAGAACTAA ATAATCCTTA 180
 ATAAATAAAT CTCTATTTTG GAATCAAA 208

SEQ ID NO:252

LENGTH:205

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00269

SEQUENCE DESCRIPTION:

GATCTTCTAA AAAAGGAACA GAAAATGGTG TGAATGGAAC ATTAAGTCA AATGTAGCAG 60
 ACTCTCCCG GAATAAAAAA GAGAAATCTT CATAATGAAT TATAAGTCA TTGATTAATG 120
 TCCCCAAGA AATCTGCTTT CTACTATATC TTTCAGCATT AGAGATTTTC CTGTTCTNGA 180
 AAATNCAGTC TGTGCTCTTT GATTN 205

SEQ ID NO:253

LENGTH:212

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00270

SEQUENCE DESCRIPTION:

GATCTAGGCA AAGAAGAATA CAAATNAAAC CCCNTTCTTT CTCGTTTCCN GTCCAACAAC 60
 TCTGTAGAGC TCTCTGCACC CGTTACCCCT TTCCACCTTT TGTATTTAAT TTTAAAGTCA 120
 NGTGTACNTG CAAGGAATGC TGGATGCAAG ATAGATACTA TATTAACTG TACTGTTATT 180
 TAAGATGTAA TAAAGCAGTT TGACATGAGA AA 212

SEQ ID NO:254

LENGTH:209

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00271

SEQUENCE DESCRIPTION:

GATCTAAGAT GATTATTTTG TAAAGACTT TCTAGTGTAC AAGACACCAT TGTGTCCAAC 60
 TGTATATAGC TGCCAATTAG TTTTCTTTGT TTTTACTTTG TCCTTTGCTA TCTGTGTTAT 120
 GACTCAATGT GGATTGTTT ATACACATTT TATTGTATC ATTCATGTT AAACCTCAAA 180
 TAAATGCTTC CTTATGTGAA AAAAAACAA 209

SEQ ID NO:255

LENGTH:197

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00272

SEQUENCE DESCRIPTION:

GATCTGCCAG CAGTGTCTT GCAATATGAG GAAGACAGTT ACAGCCACAT TATGGCTCTC 60
ATTGAACAGT ACGCAGCACC CCTGCCCCCA GCCGTCTTTC TGGGGCTTGC GCGCAAAATC 120
TACAAGCGGA GAAAGTGACC TAGAGATTGC AAGGGCGGGG AGAGGAGGCT CTCAATAAAT 180
AATCGTGTA CTTAAA 197

SEQ ID NO:256

LENGTH:196

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00273

SEQUENCE DESCRIPTION:

GATCTATCAC CTGTAATCAT AACTGGCTTC TGCTTGTAAT CCACACAACA CCAGGACTTA 60
AGACAAATGG GACTNATGTC ATCTTGAGCT CTTCAATTTAT NTAACTGTA ATTTATTTGG 120
AGTGGAGGCA TTGTTTNA GAAAAACATG TCATGTAGGT TGTCTAAAAA TAAATGCAT 180
TTAACTCAT TTGAAA 196

SEQ ID NO:257

LENGTH:196

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00274

SEQUENCE DESCRIPTION:

GATCTCACCA GGAGAAATGA ATATGTGAGG TGATGGATGT AACTAGCTTG ATTGTGGTAA 60
TCAATTTGCG AATGTGTACA TATATCAAAA CATCACATTG TACAAAATAC ATACAGTTTT 120
TGTCATTTA AAGATATCAG AATTCTAGAA TATGATAAAG TTGTGTTTTC AAGCAAGTAA 180
AGATAGNTTA CTAAA 196

SEQ ID NO:258

LENGTH:197

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00275

SEQUENCE DESCRIPTION:

GATCAGATTT TNCATTTTN AATGTTCCGT GTTTTCTTAA GTAGCATGTA TGACATTTAT 60
AATNTTAAAA AATNTTTTAA AATATGTGTA TGATACATAT TTTNATTGT CTTAGGGCAG 120
GCTTTTGAAA ATNTCAGCCT GTAGCCAAAT GCAAGATTTT CTCCATCCTT TAATAAAAAG 180
CACACTGAGA AATCCTN 197

SEQ ID NO:259

LENGTH:199

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00276

SEQUENCE DESCRIPTION:

GATCTCTGTC TTGAGTTTCT CCTTCCCAT CAGCTGAAGC ACTCTTCAGA GACTACGTCC 60
ACAGACACTG ATGCTGAGGC CTCCCTGGAG GAAGGAGGGT TAGGGGTGCC TATCCTCAAG 120
TATTGGAAGA GCAGAATTGA GGGAGAGACC TTTCTTCCTT GTTGAGGGTG AAAAATAAAT 180
ANGAATTACA TGTCTAAA 199

SEQ ID NO:260

LENGTH:197

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00277

SEQUENCE DESCRIPTION:

GATCAAGAAG GCTGGAACGG AACTGGTTAA CTTCTTGAGC TATTCGTGG AACTTGAAC 60
ACAGCCTGCC ACCCAGTGAA GTGTCCAGAC CATTGTCTTC CAACCCAGC TGGCCTCTAG 120
AACACCCACT GGCCAGTCCT AGAGCTCCTG TCCCTACCCA CTCTTGCTA CAATAAATGC 180
TGAATGAATC CNNNAAA 197

SEQ ID NO:261

LENGTH:195

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00278

SEQUENCE DESCRIPTION:

GATCTGAGTC AGTCGGAATT TGTGAAACAG GGTAGCAAAC AAGATATTTT ACTTCCATGT 60
ATACAATAAT TTTTTTAAAN NNTGCAATTT GCGTTGCAGC AATCAGTGTT AAATCATTG 120
CATAAGATTT AACAGCATTT TTTATAATGA ATGTAAACAT TTAACTTAA TGGTACTTAA 180
AATAATTAA AAGGN 195

SEQ ID NO:262

LENGTH:193

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00279

SEQUENCE DESCRIPTION:

GATCTAGTGT AATGGAAGAC CTTTGAGAAC CTGGGTGTAT TAACTTTGTG TATATAGTGT 60
AAATATCCCC ACTGTACTGT TAGAGGCCAA CAATTCTAGT ATGGCTTGTT GGCAAAGAGT 120
GCTACACCGT TTCAATGAAA CAATGTATGT TTGTTTAAAC TGAATAAAA TAAATACATG 180
CTTAATCCTG AAA 193

SEQ ID NO:263

LENGTH:196

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00280

SEQUENCE DESCRIPTION:

GATCCCTGGG ACCAACC GCA TCCTCAGCTT CTCCTCCGAG AAATGCTGGA GCAGGCTGTT 60
CAGACCGACG TTGCCATCAA AACACATACA CCCAGAAAGA AACAACAGAA ACCAAAATC 120
ACAAGGCGCA TGATTACTTG TTTTATATTT CATGTTGGGT TTTCCCTCCC ACTATTAAAC 180
AGTCTGTTTC CGTAAA 196

SEQ ID NO:264

LENGTH:192

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00281

SEQUENCE DESCRIPTION:

GATCTGTAA AAAAGAAATC TGTTTCAACA GATGACCGTG TACAATACCG TGTGGTGAAA 60
ATGAATTCAG ACTTATTAAT TGATGAACCT GTTAAATCTN CTCAGTGTCT ATTTATCAGC 120
ACAATACACA CAGGAGANCT GTTGATGGCA TATTGAATAG ATTTNCCTGA ATAANTTGCT 180
CTGGAAACCA AA 192

SEQ ID NO:265

LENGTH:189

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00282

SEQUENCE DESCRIPTION:

GATCCTCGTC TTACAGCGAA TGGTTTCAAG ATAAAATTGA TACCAGGAGT TTCAATTACT 60
GAAAATTACT TGGAAATAGA AGGAATGGCT AATTGTNTCC CATTCTATGG AGTAGCAGAT 120
TTAAAGAAA TNCTTAATGC TATATTAANC AGAAATGCAA AGGNNGTTTA TGANTGTNGA 180
CCTCGCANN 189

SEQ ID NO:266

LENGTH:188

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00283

SEQUENCE DESCRIPTION:

GATCTTTTGT ACTTTAGGAC ATTAATTTGT ACAACTTTTG TATATATAAA AGCTTAGGAA 60
CTTTCTGTTT AGCAGGAAGG CAACACATTC CTACACTTTT AATGTATATG TTTGTTATAA 120
TGTCCATGTA AACATGCCCT ATGTTGTGTC CTTTAATTA GTTGTCTCA ATAAACAAAA 180
TGTAGAGN 188

SEQ ID NO:267

LENGTH:206

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00284

SEQUENCE DESCRIPTION:

GATCCTGAGA ACTTGAATT CCTTGTAAGT GGAGCTCGGA GCTGCACCGA GGGCAACCAG 60
GACAGCTGTG TGTGCAGACC TCATGTGTTG GGTTCCTCTCC CCTCCTTCCT GTTCCTCTTA 120
TATACCAGTT TATCCCCATT CTTTTTTTTT TCTTACTCCA AAATAAATCA NGGCTGCAAT 180
GCAGCTGGTG CTGTTCAGAT TCTAAA 206

SEQ ID NO:268

LENGTH:190

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00285

SEQUENCE DESCRIPTION:

GATCAGAAAA AGAAAGAAGC CAAAGAGAAA GGTACCTGGG TTCAACTAAA GCGCCANCCT 60
GCTCCACCCA GAGAAGCACA CTTTGTGAGA ACCAATGGGA AGGAGCCTGA GCTGCTGGAA 120
CCTATTCCCT ATGAATTCAT GGCATAATAG GTGTAAAAA AAAAANTAAA GGGCCCTCTG 180
GGGCTACAAA 190

SEQ ID NO:269

LENGTH:189

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00286

SEQUENCE DESCRIPTION:

GATCAAGATA TTAAATNTC GGATTATCT TTCCCATAT CCAAGTACCA ATNCTGTTGT 60
AAACAACGTG TATAGTGCCT AAAATTGTAT GAAAATCCTT TTAACCATT TAACCTAGAT 120
GTTTAAACAA TCTAATCTCT TATTCTAATA AATATACTAT GAAATAAAAA AAANNGNTTG 180
AAAGCTAAA 189

SEQ ID NO:270

LENGTH:189

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00287

SEQUENCE DESCRIPTION:

GATCTTGTGT ATTGAGCTTA TTGTTGAAAG GGATTTTGA AGGACAGAAC AATTACTGCA 60
TGATGAATCT TCCTNTCTCT GCCTTCTGAG CACCGNCTTT AATTTCCATA TCTTCAAGTC 120
TTGAAGAAGT TGATGTTAAT TGAAGAATTC ACTTGTCTGG TTGAAATAAA GCCTGTTTCT 180
GTTGTGAAA 189

SEQ ID NO:271

LENGTH:186

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00288

SEQUENCE DESCRIPTION:

GATCTGATTT GCTAGTTCTT CCTTGTGAGA GTTATAAACT GAGAGTGACG TCACTTCAGC 60
CAGAACATAT TCTCCATACT CTGCATATAA TTTGTGGCTG CAGAATATTG TAATTTGTTG 120
CACACTATGT AACAAAACAA CTGAAGATAT GTTAAATAAA TATTGTACTT ATTGGAAGTA 180
ATATCN 186

SEQ ID NO:272

LENGTH:185

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00289

SEQUENCE DESCRIPTION:

GATCTAAAAT GTCAGCATCA TGCAAAGTGC ACGATATATA GTGAATTNG CTCTAAAAGA 60
GCATGAACAA GTCTTTCTAA TGTTTTGTAC AGTGCCTGGC ACTCTGTGGG TGCTCAATAA 120
ATGGATAGGA GTTTTCATTT GAAGGATATT TGAATTTTAA AAATAAAGTG TTTTATTCCC 180
NTAAA 185

SEQ ID NO:273

LENGTH:184

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00290

SEQUENCE DESCRIPTION:

GATCTGGTCA CTGTGGTTCC TGCATGAAGA CAGTGGCTGG CGGTGCCTGG ACGTACAATA 60
CCACTTCCGC TGTCACGGTA AAGTCCGCCA TCAGAAGACT GAAGGAGTTG AAAGACCACT 120
AGACGCTCCT CTACTCTTTG AGACATCACT GGCCTATAAT AAATGGGTAA ATTTATGTAA 180
CAAA 184

SEQ ID NO:274

LENGTH:185

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00291

SEQUENCE DESCRIPTION:

GATCTGATTT GCTAGTTCTT CCTTGTAGAG TTATAAATGG AAANATTACA CTATCTGATT 60
AATAGTTTCT TNATACTCTG CATATAATTT NTGGCTGCAG AATATTGTAA TTTGTTGCAC 120
ACTATGTAAC AAAACAACCTG AAGATATGTT TAATNNATAT TGTACTTATT GGAAGTAATA 180
TCAAA 185

SEQ ID NO:275

LENGTH:188

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00292

SEQUENCE DESCRIPTION:

GATCAAAGAC ATCCTCATCC AGTATGACCG GACCCTGCTG GTAGCTGACC CTCGTCGCTG 60
CGAGTCCAAA AAGTTTGGAG GCCCTGGTGC CCGCGCTCGC TACCAGAAAT CCTACCGATA 120
AGCCCATCGT GACTCAAAAC TCACTTGTAT AATAAACAGT TTTTGAGGGA TTTTAAAGTT 180
TCAAGAAA 188

SEQ ID NO:276

LENGTH:182

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00293

SEQUENCE DESCRIPTION:

GATCGGGNTA CTACAAAGTT CTGGGAAAGG GAAAGCTCCC AAAGCAGCCT NGTCATCGTG 60
AAGGCCAAAT NCTTCAGCAG AAGAGCTGAG GAGAAGATTA AGAGTGTTGG GGGGGCCTGT 120
NTCCTGGTGG CTTGAAGCCA CATGGAGGGN GTTTCATTAA ATGCTAACTA CTTTNCCTA 180
AA 182

SEQ ID NO:277

LENGTH:195

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00294

SEQUENCE DESCRIPTION:

GATCCAGCCA GAGGATGCCA CGCCAGCCCA GCGCTACCAG GCTGCCCAAG GGGGGCGGGC 60
CTGGGAAGAG CCCTACACGG GGCAGCACCT AGGATGGGGC AGAGACTTGT TGCATCTTTG 120
TCCCCAGCAA AGGCTACATG TTACCTCCTT CAATTGATAA TAAACCTTC TGAGATGCAG 180
AGGGTCCAGG TCAAA 195

SEQ ID NO:278

LENGTH:327

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00295

SEQUENCE DESCRIPTION:

GATCCCATTA ACTCGATGCT GAGTATCTAC ATGGATACAT TAAATATATT TATGCGAGTT 60
GCAACTATGC TGGCAACTGG AGGCAACAGA AAGAAATNAA GTGACTCAGC TTCTGGCTTC 120
TCTGCTACAT CAAATATCTT GTTTAATGGG GCAGATATGC ATTAAATAGT TTGTACAAGC 180
AGCTTTCGTT GAAGTTTAGA AGATAAGAAA CATGTCATCA TATTTAAATG TTCCGGTAAT 240
GTGATGCCCT AGNTCTGCCT TTTTCTCTGG AGAATAAATG CAGTAATCCT CTCCCAAAAA 300
AAAAAAAAAN NNNTNNNTNN NNNTNNN 327

SEQ ID NO:279

LENGTH:183

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00296

SEQUENCE DESCRIPTION:

GATCCAAATC CTCATCTTAC TTTCCCGACC TTAAGGATGT AGCTGCTGCT TGTCTGTTC 60
AAGTTGCTGG AGCAGGGGTC ATGTGAGGCC AGGCCTGTAG CTCCTACCTG GGGCCTATTT 120
CTACTTTCAT TTTGTATTTC TGGTCTGTGA AAATGATTGA ATAAAGGGAA CTGACTTTGG 180
AAA 183

SEQ ID NO:280

LENGTH:180

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00297

SEQUENCE DESCRIPTION:

GATCAAAGTG GCTGCAGCAG AGTTAGCTGT CTAGCGCCTA GCAAGGTGCC TTTGTACCTC 60
AGGTGTTTTA GGTGTGAGAT GTTTCAGTGA ACCAAAGTTC TGATACCTTG TTTACATGTT 120
TGTTTTTATG GCATTTCTAT CTATTGTGGC TTTACCAAAA AATAAAATGT CCCTACCAGN 180

SEQ ID NO:281

LENGTH:180

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00298

SEQUENCE DESCRIPTION:

GATCACATGA TTTTGTCTCT CAGTTCCTATT AATGTTCTTG GATTCTGTTC AATGTTCTGT 60
TCACATTGCA GAAAAAGCAT TTGACAAAAA AATTCAGTA GCTGCTGAAA AAGCATTGTA 120
TAAAAATCAG CATACCTTTA TGATACAAAA AACCTTCAAT AAAGTGGGTA TATATGNACN 180

SEQ ID NO:282

LENGTH:178

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00299

SEQUENCE DESCRIPTION:

GATCTTGAAT TATTTATAAA CTGGAAAGTG GTTTGATTAT TGTGAGTCAA AACTCTAAGT 60
GGTTAAAAAT TAGTATGAAT TTTTAGCTT CTTAATGAAT ATGGATTAA AACTCTCCAG 120
TTCTTATTTT ATGAAATGAC TTGCCTTTCT GGTAATACAA TGCTGATTTT TTAGTAAA 178

SEQ ID NO:283

LENGTH:182

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00300

SEQUENCE DESCRIPTION:

GATCCCAAAT ATGAAGTCAT CGAAAAACCC CAGGCCTGAA GAAATAAAGT AAAAATNAAT 60

CTGGTAATTT GTCACGGATT AGTTGTACAA CTAGTTAGAA GTTTCAGAAT AAACATGCAT 120
TTCATAACTG TCAAATGTTC TTTAATTCT GAGTCCAAAT AAATTATTG GTGATGTTGA 180
AA 182

SEQ ID NO:284

LENGTH:179

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00301

SEQUENCE DESCRIPTION:

GATCTCTGAG TGAGAGGGAA ANAGGTCAGA TTTATACAAC TGAGCGCCAG AGGGGAAAAT 60
GCACCTTGTT GGAGTGAGAA ATGTTCTGAA ACTGAATTAC TTCTGTACA GCTGAGATAG 120
CTTCTTCTGA ACTATTATTA AATAAGTGAA TACAAAGGCC CTATGATGGG AAATCCAGN 179

SEQ ID NO:285

LENGTH:201

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00302

SEQUENCE DESCRIPTION:

GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG CTGTGGACCG GGATGCAGTN 60
TCAGGCATGG GAGTCATTGT CCACATCATC GAGAAGGACA AAATCACCAC CAGGACACTG 120
AAGGCCCGAA TGGACTAACC CTGTTCCCAG AGNCCACTTT TTTTCTNTT TTTGANATAA 180
AATAGCCTGT CTTTCAANAA A 201

SEQ ID NO:286

LENGTH:176

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00303

SEQUENCE DESCRIPTION:

GATCGGAGAT GCTTTGTAAT CTA CTGTGTTCA GCTGGAAACA GCTCATGTTA CGCGGAAAAA 60
ACTACAAGTA ATGTTCAAAT CTATTTTGGG TCATTTTAT GTACCTTTGG GTTCAGGCAT 120
TATTTGGGGG GTTTTGTTC CAAAGGAACT AAATAAAGTC ATATTGCTTA TAGAAA 176

SEQ ID NO:287

LENGTH:176

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00304

SEQUENCE DESCRIPTION:

GATCTTTGCT GGGAAACAGC TGTGAAGATG GACGCACCCT GTCTGACTAC AACATCCAGA 60
AAGAGTCCAC TCTGCACTTG GTCCTGCGCT TGAGGGGGGG TGTCTAAGTT TCCCCTTTTA 120
AGGTTTCAAC AAATTCATT GCACTTTCCT TTCAATAAAG TTGTTGCATT CCCAAA 176

SEQ ID NO:288

LENGTH:176

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00305

SEQUENCE DESCRIPTION:

GATCCGCAAG ACCAAGTACC GCCCCGACCT GCGCATGGCA GCCATCCGCA GGCCAGCNTC 60
ATCCTGCGCA NCAGAAGCCT GTAATNGTGA AGAGGAAGCG GACCCGACCC ACCAAGAGCT 120
CCTGAGCCCC CTGCCCCCAG AGCAATAAAG TCAGCTGGCT TTCTNACCTG AAGAAA 176

SEQ ID NO:289

LENGTH:175

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00306

SEQUENCE DESCRIPTION:

GATCTCAAAA CACAGTGAGA GGTCTGAAGG CTGGCTTCTG AAGAATCCCT GATGTCTTAT 60
TGGAACAACC ACTGAGCTAC GGAGAGCTCT GCTGTGATGG GCTAGGCACT TTATATCTGT 120
GTGAATACAG ATTTATAAAA CAGGTTAATA AACTTATCCA AGGTCACATT TCAAA 175

SEQ ID NO:290

LENGTH:165

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00307

SEQUENCE DESCRIPTION:

GATCTGAATT CTTTATGTAT ATTTGTAGCT ATATTTATA CAAAGTGCTT TAAGTGTTGA 60
GAGTCAATTA AACACCTTTA CTCTTAGAAA TACGGATTCTG GCAGCCTTCA GTGAATATTG 120
GTTTCTCTTT GGTATGTCAA TAAAAGTTTA TCCGTATGTC AGAAA 165

SEQ ID NO:291

LENGTH:186

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00308

SEQUENCE DESCRIPTION:

GATCATTCTT TCTGTAGCTC AGGAGAGCAC CCCTCCACCC CATTGCTCG CAGTATCCTA 60
GAATCTTTGT GCTCTCGCTG CAGTTCCCTT TGGGTTCAT GTTTCTCTTG TTCCCTNCCA 120
TGCCTAGCTG GNTTGCAGAG TTAAGTTTAT GATTATGAAA TAAAAAATA ACTGACAATT 180
NTCAAA 186

SEQ ID NO:292

LENGTH:175

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00309

SEQUENCE DESCRIPTION:

GATCTTGTAG AAAATTTTGA TGAGGCATCA AAGAATGAAG CTAATAAAA GTTGGTTTT 60
 TGGGAAGCTGG CATGGACTAG ATTTAACAAA TCAGCTATGT GGTCCAAAG TTTACAGAC 120
 ATGGAGAACA TCACCTGTTA CTAGTTCAGT AATATAAATA TTTGTATAT TAATN 175

SEQ ID NO:293

LENGTH:406

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00310

SEQUENCE DESCRIPTION:

GATCAGATTA CCAGGAACAT CAGGAGTGGA TTCCTGCCCC AACCAAACCG CATTCTGTG 60
 GATTTTTTTA TTCAACTTAA TTGGCTATTC CAAAGATTTT TTTTTCCTA TTTTGACGA 120
 TTGGNGCCCT TAAGATGCAC GATGGAATTG TGTTTNCGT TTTNNGTAA AAGGAGCAA 180
 GCGNGGNCCT GGAGATAAC GCTGGAGCAA TCTCCTTGGA AGGATTCAGC ACGAGTAGAT 240
 GGTAAACATT TAAAGGGGAA AGGGGGGTTT GTTTAAAATA GTAAATCAGT AAGTCACTTC 300
 TAAATTTAAA GAAACCAAAA TTGGGAGTTG AAGAATAAGT AGGGTTTCCA ATTGGGCTAT 360
 TGCCGNTTN CTTTGNAAAA ATTAAACCAT TTTTAAAAA CCTAAA 406

SEQ ID NO:294

LENGTH:218

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00311

SEQUENCE DESCRIPTION:

GATCCCATAG ACCAGAGCCC ACCTTTTNA TAACTTAGT AAAGTCTTNG AGACTAGAAG 60
 CAAGATAGTT TGTGACACAT AAGCTTCCCA AAAACTNGAA TAGATTTTNA CTGAATAGTG 120
 GTCTATCTGA TGGTATATGT TTCTTAAAGG TCCAANTGTA ATAAAAAANA TTGAAAAANA 180
 GGTCTCAGTG TTTTNAATGC ACTNCATATT TGTNTGCN 218

SEQ ID NO:295

LENGTH:176

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00312

SEQUENCE DESCRIPTION:

GATCCACCAA GCACGCCTAT NAATACAAAG TAACTATNA TTTNATTGT GAAATTTTCA 60
 TAGATGGAAT ATTGAATATN CTGTCCATTT CATTTTACAA TNATCTACC ACTTATTTT 120
 GTACCATGTA TTTCAATTGC CTGTTTAGTG AAAAATAAAA ATTAATAAAA CCTAAA 176

SEQ ID NO:296

LENGTH:172

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00313

SEQUENCE DESCRIPTION:

GATCCCAGCA AGATAATGTC CTGTCTTCTA AGATGTGCAT CAAGCCTGGT ACATACTGAA 60
 AACCTATAA GGCCTGGAT AATTTTGTG TGATTATTCA TTGAAGAAAC ATTTATTTTC 120
 CAATTGTGTG AAGTTTTTGA CTGTTAATAA AAGAATCTGT CAACCATCTA AA 172

SEQ ID NO:297

LENGTH:173

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00314

SEQUENCE DESCRIPTION:

GATCGGTGAC ATCGTCAAGA TGGGCGAGTG CCGGCCTCTG AGCAAGACAG TCGCCTTCAA 60
 CGTGCTCAAG GTCACCAAGG CTGCCGGCAC CAAGAAGCAG TTCCAGAAGT TCTGAGGCTG 120
 GACATCGGCC CGTCCCCAC AATGAAATAA AGTTATTTTC TCATTCCAG AAA 173

SEQ ID NO:298

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00315

SEQUENCE DESCRIPTION:

GATCGTTTCC AGATGAGAAT TCACAAGCGA CTCATTGACT TGCACAGTCC TTCTGAGATN 60
 TGTTAAGCAG ATTACTTCCA TCAGTATTGA GCCAGGAGTT GAGGTGGAAG TCACCATTGC 120
 AGATGCTTAA GTCAACTATT TTAATAAATT GATGACCAGT TGTAAA 167

SEQ ID NO:299

LENGTH:171

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00316

SEQUENCE DESCRIPTION:

GATCTGGTGG TGGAAGTGGT GGATATGGTA GCAGAAGGTT CTA AAAACAG CAGAAAAGGG 60
 TTGAATGAGA ACCCTACTTG CCTAAATNAG GAATGTCTTT CCTACCATCT AAAATACGAA 120
 GGTTCCTGGC TGGGTAAGGT TTGTAGTTGA CAGTAAAACC TGATGACACC N 171

SEQ ID NO:300

LENGTH:176

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00317

SEQUENCE DESCRIPTION:

GATCCGAGTG TGATTGGAAT TCTGTGATAT TTTCACACTG GTAAATGTGA CCTCTATTTT 60
 ACTTACTGCT ATAAATAGGT TTATATTATT GATTCACCTA CTGACTTTGC ATTTTCGTTT 120
 TTAAAAGGAT GTATAAATTT TTACCTGTTT AAATAAAATT TAATTCAAAA TGTA AA 176

SEQ ID NO:301

LENGTH:169

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00320

SEQUENCE DESCRIPTION:

GATCTTTGTT TTGTGTTTAA CCATAATGGT TGTGTACTGA ACCACTTCAT ATTTGTAATA 60
TATAATATAT ATATATNNGN TNCCCTNAAG ACTCAGCCTC CTGGTTTACC CCCCCGGCCT 120
GGGCATCTNA CCTCCCCAC CCCAGTGTGA TTAAACATCC NGGNACTGN 169

SEQ ID NO:302

LENGTH:174

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00322

SEQUENCE DESCRIPTION:

GATCTAGCTC TGAATGTATG TTTCTGACG TTTTACATTT CCACTTTCCT ATTCCATTCA 60
TTAAGCTAGC CAACAATCCA CCATCCTTTA AAGATTGTTT TCATAACTGA AAAAAACCA 120
CATAATCTAA ATAGAGCAAA GCTACAAGAA ATAAATTTAT TTAACGCAA GAAA 174

SEQ ID NO:303

LENGTH:177

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00323

SEQUENCE DESCRIPTION:

GATCCTAGCA TATGTTAAAA TTCAAATTAA TGTAACACAG ATTAACAACA ACAAAGAAAC 60
TGTCTATTG AGTGAAGTCA TGCTTCTAT TATAATAACT TGGCTTCGGT TATCCATCA 120
ATGCACACNN ATACTGTTAT CTGATTGTTT ATAATAAAGA ATACTGTACC TNNTAAA 177

SEQ ID NO:304

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00325

SEQUENCE DESCRIPTION:

GATCAGATGG TTTTAGTATT GTGGCAGAAG CGAGAAAAC TGTGTTATTG AAAAAAAAG 60
AAAAAGAAAG CAAGAAAAA AGATACTATG GGTCAAGTG TAACTCCATG GAAATGCCAC 120
GTCTGCTCTT CAGTGAAGAA GCTGGTTTAG AGTCTCACAG AAAACTN 167

SEQ ID NO:305

LENGTH:170

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00327

SEQUENCE DESCRIPTION:

GATCGCTCAC AATNTTTCCT CCAAGAACCG CAAAGCCATC GTGGAAAGAG CTGCCCAACT 60
GGCCATCANA GTCACCAACC CCAATNCCAG GCTGCGCAGT GAAGAAAATA AGTAGGCAGC 120
TCATGTGCAC ATTTTCTGTT TAAATAAATG TAAAACTGC CATCTGGAAA 170

SEQ ID NO:306

LENGTH:171

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00328

SEQUENCE DESCRIPTION:

GATCGGGAAT GGTCTGTGTG TTATCAGCTG CGACTGGTTC ACTGCGNCTT AGACAAGCCT 60
CATGGGGACT GGGGATTCTG GCCAGTGTA TTTCTGTCAA CCACGGACGT TTGCCTTCAT 120
GTGTAGAATT TACTGTTGTT ATGCAAATTA TATTTTCAAT TATAAATGAA A 171

SEQ ID NO:307

LENGTH:164

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00329

SEQUENCE DESCRIPTION:

GATCAGACAG AATAATATTT NCTAGTTATT ATGTGTAAGA TGAGTTGCTA TTTTCCTAAT 60
GCTCATTCTG ATACAACTAT TTTCCGTGTC AAATATCTAC TGTGCCCAAA TGTACTCAAT 120
TTAAATCATT ACTCTGTAAA ATAAATAAGC AGATGATTCT TAAA 164

SEQ ID NO:308

LENGTH:261

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00330

SEQUENCE DESCRIPTION:

GATCCCCGCC CTGGGGTCTG GTCCTCGCCC ATCCTGCAGG GATTGCCAC CGTCTTCCAG 60
ACACCCACC TGAGGGGGGC ACCAGGTTA GTGCTGCTGC TTCACTGNT GCACCCGCGC 120
CCTCGGCCGG CCCCCGAGC AGCCTTTGTA CTCTGCTTGC GGAGGGCTGG GAGACCCTCC 180
AGGACATTCC CACNNTCNCC CATGCTGCCA AGTTNNNNCT ATAGCTACAA ATAAAAAAA 240
ACCTTGTTTT CAAGAAATAA A 261

SEQ ID NO:309

LENGTH:163

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00331

SEQUENCE DESCRIPTION:

GATCGAGTCA AGATGAGTTA GTGGAGCTGG GCTTGGCCAG GGAGTCTGGG GACAAGGAAG 60

CAGATTTTCC TGATTCTGGC TCTAGCTTCC CTGCCAAGAT TTTGGTTTTN ATTTTTTTAT 120
 TTGAACTTTA GTCGTGTAAT AAACCTACCA GTGGCAAACC AAA 163

SEQ ID NO:310

LENGTH:165

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00332

SEQUENCE DESCRIPTION:

GATCATGCTG CTGTGATACT GAGTTTTCTA AACAGCATAA GGAAGACTTG CTCCCCTGTC 60
 CTATGAAAGA GTATAGTTTT GGAGGGGAGA AGTGGGACAA AAAAGATGCA GTTTCCTTT 120
 GTATTGGGAA ATGTGAAAAT AAAATTNTCA ACTCTTTCAG TTAAA 165

SEQ ID NO:311

LENGTH:164

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00333

SEQUENCE DESCRIPTION:

GATCTCAGTT TCCTGGCTTT TCCTCCCTCA GCCCCTTCTC ACCCCTTTGC TGTCTGTGT 60
 AGTGATTGG TGAGAAATCG TTGCTGCACC CTTCCCCCAG CACCATTAT GAGTCTCAAG 120
 TTTTATTATT GCAATAAAAG TGCTTTATGC CGGCTTTTCT CAAA 164

SEQ ID NO:312

LENGTH:337

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00334

SEQUENCE DESCRIPTION:

GATCATTGAA TGTGAGACCC TTCTAACATG ATTTGAGAAG CTGTACAAGT ATAGGCAGAG 60
 TTATTTTCTT GTTTACATTT TTTTTTTGTT TTGGGGAAAA AATTGGTAGG TGTCTAATNA 120
 CTGTTTACTT CATTGTTATA TTGCAGTAAA AGTTTAAAN CANCCATTGC ATGTTNGCTT 180
 TTGATGTATC CCTTTGNGAA ATTAGCACTT TTGGGGCCAN TGGNGAAATG CAGCATTAC 240
 TCTCCCTGTC TTTTCCCCTT CCCTCAGCAG AAACGTGTTT ATCAGCANGT CGTGAGTCAA 300
 ACTGCTGCCT TTTAAAAANC CCACAAANTT GNTNNGN 337

SEQ ID NO:313

LENGTH:176

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00335

SEQUENCE DESCRIPTION:

GATCCGCCGT CACTGGGGTG GCAATGTCCT GGGTCCTAAG TCTGTGGCTC GTATCGCCAA 60
 GCTCGAAAAG GCAAAGGCTA AAGAACTGC CACTAACTG GGTAAATGT AACTGTGTA 120
 GTTTTCTGTA CATAAAAATA ATTGAAATAA TACAAATTTT CCTTCAGCCA GTGAAA 176

SEQ ID NO:314

LENGTH:176

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00336

SEQUENCE DESCRIPTION:

GATCACCTCT GAGACCCACC TTGCTCATAA ACAAATGCC CATGTTGGTC CTCTGCCCTG 60
GACCTGTGAC ATTCTGGACT ATTNNTGTGT TTATTGTGG CCGAGTGTA CAACCATATA 120
ATAAATCACC TCTCCGCTG TTTAGCTGA AGNATTANGN CATCTTGTCT ATTAAT 176

SEQ ID NO:315

LENGTH:258

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00337

SEQUENCE DESCRIPTION:

GATCATATTT AATGAATTAT AGTATAATGC TTGCAGGCCC AGTACAAGCA TATATATNGT 60
GCCTCTTACA GCCTTTGGAA TACATTGTTT CCATTTTTA AATATCTTCT ATATCCNNNT 120
AGTATTCAAA TTATTAATGC TCATGTACCA AGGTNTTGCT ATAAAAGTTT TGTCTGTATG 180
AATAATGTGG CTTTAGTAAA TAATCATTTN TCAACTGTAA ACTNATTCTG AAATAAAGTA 240
AAATNCTAAT TGTTTAAA 258

SEQ ID NO:316

LENGTH:153

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00338

SEQUENCE DESCRIPTION:

GATCTTGGAC ACTTACAGAT TGAGCTGTAT GAATTCAGCG GGTCTCACTC CAGAGGGTCA 60
GAACGTTTGC TTTAGTTTTT TCATCTGTTT TGTCCTTGA GTCAGTGCTG TTGATGATGA 120
GTTGTCTTGA ATAAATNATG TGTTCTTTGC AAA 153

SEQ ID NO:317

LENGTH:157

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00339

SEQUENCE DESCRIPTION:

GATCAAAGCT AGAAAATGNA GATTCCTTAG CCTGGATTTC CTCTAACAT GTTATCAAAT 60
CTGGGTATCT TTCCAGGCTT CCCTGACTTG CTTAGTTTT TAAGATTGT GTTTNCTNT 120
NTCCACAAGG AATAAATGAG AGGGAATCGA CTGTAAA 157

SEQ ID NO:318

LENGTH:161

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00340

SEQUENCE DESCRIPTION:

GATCTCCTTA TATAGCAGCC AAAATCAATG AAGCTAAAGA TTTACTAGAA GGTCAAGCTA 60
 AAAAATGAAG TAAATGTATG ATGAATTTTA AGTTCGTATT AGTTTATGTA TATGAGTACT 120
 AAGNNTTTTA TAATAAAATG CCTCAGAGCT ACAATTTTAA A 161

SEQ ID NO:319

LENGTH:313

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00341

SEQUENCE DESCRIPTION:

GATCTGAAAA CATGTAGAGA AGATGAGTTG AGGACAGCTT TTCTAAGGCA ATGTNATGTC 60
 TTTCCTTTCT NATTTCTNNT TCTCTGCGTT GTTAGTTTNN AAGAGTGGAG GAGCTAGGGG 120
 CTCCAGAAAG AATCTTACAC ATGTTTGTAA GACATTGATG TCATAGGGAG CGGGGAGCTG 180
 CATTCCCTTC TGGGCTGTGA CTGCTAAATC TCAGTATGAA CAGACCAGGC GGAAAGCTTG 240
 GTGGCCAAGC AGTCTGTGTG CTTCCCCGCT GATGGAGAAC GTTGCCTTGT TCACAATAGG 300
 GCCTCATGGG TGN 313

SEQ ID NO:320

LENGTH:161

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00342

SEQUENCE DESCRIPTION:

GATCTTGTTT ACAAGTAATC TGTGACAGT GCCAATAAAT NATAAAAAAA AAATTAACAT 60
 GTCACAATGT AACGGATGAC CATATGCACA ATTCCATGAA TTAAATCTGT TTCCTGTGTT 120
 AGTCAGTATT CTAAATAAAA ATTTATAATT GAAACATGAA A 161

SEQ ID NO:321

LENGTH:163

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00343

SEQUENCE DESCRIPTION:

GATCTATTGA NAGCCCTCTC TCNCATTCTG TAATGAGTAC AGCAGAGACC TTCCTGCTTT 60
 TAACTGGGGA CTCCAGATTT TCCCCAACT TGCTTCTGTT GAGATTTTTC CCTCACCTTG 120
 CCTCTCAGGC ACAATAAATA TAGTTATACC ACTGCCCATC AAA 163

SEQ ID NO:322

LENGTH:156

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00344

SEQUENCE DESCRIPTION:

GATCATCCTA ACAATGTGGG GCTGTTAGGT TTTACCTTTG ANCTTTCATA GCACTGCAGA 60
 AACCTTTAAA AAAAAAATGN TNNATGAATT TTTCTTTCC TACAGTTGGG TAGGGTAGGG 120
 GAAGGNGGNT AAGCTTTTTT TTTNAAATG ACTGAN 156

SEQ ID NO:323

LENGTH:255

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00346

SEQUENCE DESCRIPTION:

GATCATGCTG CCCTGGGACC CAACTGGTAA GATTGGCCCT AAGAAGCCCC TGCCTGACCA 60
 CGTGAGCATT GTGGAACCCA AAGATGAGAT ACTGCCACC ACCCCCATCT CAGAACAGAA 120
 GGGTGGGAAG CCAGAGCCGN CTGCCATGCC CCAGCCAGTC CCCACAGCAT AACAGGGTCT 180
 CCTTGGCAGC TGTATTCTGG AGTCTGGATG TTGCTCTCTA AAGACCTTTA ATAAAATTTT 240
 GTACAAAGGC ACAA 255

SEQ ID NO:324

LENGTH:154

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00347

SEQUENCE DESCRIPTION:

GATCTCTAGT ATAACACTCA GGCTACTGAG GTATTTTAGA GCAACAAGCT GGGTTACTTT 60
 CAGAGCAACC AGCTTGACTG GAACTGAGAG TAAATTGGGA ATGTATGACC AATCTTAGAC 120
 CCTGAAAAAT GGCAGAAAAT ACATGGAAAT TTGN 154

SEQ ID NO:325

LENGTH:153

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00348

SEQUENCE DESCRIPTION:

GATCTAGGGA AGACAACGTA GTCACCTCG GTGCTTCCTC TGTCTCCTCT TTCTCCCTGG 60
 CCTGTGGTTG TCCCCAGCC TCTGCCACCC TCCACCTCCT CGGTCAGCCC CAGCCCCAGG 120
 TTGATAAATC TATTGATTGA TTGTGATAGT AAA 153

SEQ ID NO:326

LENGTH:154

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00349

SEQUENCE DESCRIPTION:

GATCTCTAAT ATTTTAAAGC CCAAGCCCCT TGGACACTGC AGCTCTTTTC AGTTTTTGCT 60

TATACACAAT TCATTCTTTG CAGCTAATTA AGCCGAAGAA GCCTGGGAAT CAAGTTTGAA 120
ACAAAGATTA ATAAAGTTCT TTGCCTAGTA TAAA 154

SEQ ID NO:327

LENGTH:158

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00350

SEQUENCE DESCRIPTION:

GATCAAATTC TAATGGAATT GAGCCGGTTT CTTATCCTAA ATGTTTCCTC CCTTTTACA 60
ATCTCTGTCC AGCACCTCTT GGTAAATAA TGTATGCTGT GAGACATGNA ATTAAACAG 120
GCCTATGGAA TAAATTATT TAAACCAGN AGGTTAAA 158

SEQ ID NO:328

LENGTH:155

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00351

SEQUENCE DESCRIPTION:

GATCTTAAAG CAGAATGCCN TTTNCTTTT TTGCTTCAGT TGTAAGAAG AGGGAATACA 60
TGATAAGTA ACTGGTTTGA TTTCTCGTTC ATTGTACACT GCCTCTGAAC ANCTAATTGT 120
TTTtagTTGT CTAAATAAAA TGCCTCTAAA ACAA 155

SEQ ID NO:329

LENGTH:165

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00352

SEQUENCE DESCRIPTION:

GATCCAAGAG GAAGAATCCA GCTGCCTATG AAAATAACAA ATNAGCAACG CATCCGGATG 60
ACGGTTCCCT GTCTCTGAAA GACCTTCTC TGGAAGAGGA GTCTGCATTG TAGTGTCTCA 120
AAGACACAAT AAACCTCCTA TGGTCTGCAC TGTGTGATA TAAA 165

SEQ ID NO:330

LENGTH:149

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00353

SEQUENCE DESCRIPTION:

GATCTACTTT GTTTGAGCAA AACAGCATT TTTGTTATGT TAATNATGGT TAATTTCCAT 60
TTTATTGGTT TTATGTTTAT TTTAATTTGT AAATGTTTGA GCATTTATNA TTGTATGTNA 120
NCTATATTN CCTATTTNAT GTTGATAAA 149

SEQ ID NO:331

LENGTH:151

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00354

SEQUENCE DESCRIPTION:

GATCAAAATG CTAAACATG ATGATTAAGT GCACACCGTG TGCCATAGAA TGGCACATGT 60
CATTGCCCAC TTCTGTGTAG ACATGGTTCT GGTTTAACTA ATATTTGTCT GTGTGCTACT 120
AACAGATTAT AATAAATTGT CATCAGTGAA A 151

SEQ ID NO:332

LENGTH:147

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00355

SEQUENCE DESCRIPTION:

GATCTTTGTT CTAGGCAGCT GGGAAATAGAC ATGGTACTTA CCTTAGAGTT TTCCAATTTA 60
TCTCAATTTT ATATGGCTTG TGATTCATTT NCTTAATCCA AATATATATA ANCGTGTGTG 120
GTCTNATTCT NCCCCCGCA ANANNAN 147

SEQ ID NO:333

LENGTH:151

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00356

SEQUENCE DESCRIPTION:

GATCCTTACG GAAAAGGAAC AGATTGTNCC TAAACCAGAN GAGGAGGTTG CCCAGANGAA 60
AAAGATATCC CAGANGAAAC TGAAGAAACA AAAACTTATG GCACGGGAGT AAATTCAGCA 120
TTAAAATAAA TGTAATTAAGGAAAAGAA A 151

SEQ ID NO:334

LENGTH:204

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00357

SEQUENCE DESCRIPTION:

GATCTTTGCA GTAATTTCTA GGAGCTGTTT ATGTTTGGAG GTAATTGGTC CTTTGTCCAT 60
ATATATGAGA TGTAAGTNTT ATTTCCAGT TTATCTTTT GCTTATTTT TTTGACTTTT 120
TATTGTAAAA TAAACATCA AACTGCACAG AACAGTTGAA TAGCTTAATG AATAACTACA 180
GTAAAAGCTA TGGTAACCAC TAAA 204

SEQ ID NO:335

LENGTH:146

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00358

SEQUENCE DESCRIPTION:

2153480

GATCCAATTA ACATGTGGGG TTCTTGGTNT GGGTCTGGGG AGCTGAAGGA TTTNATGGAG 60
CTGGTGCTTT GGAGGAATCT TAAGGGAAAG NAGTAGAAGC TCAGGCCTTT AAAGGATTC 120
ANCTCCTCCT CTCTGTAATT NNTNCN 146

SEQ ID NO:336

LENGTH:146

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00359

SEQUENCE DESCRIPTION:

GATCGCATCT NTTAAACAGG TACAAGTTGA CATGAGGTTA GTTTAATTGT ACACCATGAT 60
ATTGGTGTA TTTATGCTGT TAAGTCCAAA CCTTTATCTG TCTGTNATTC TTAATGTTGA 120
ATAANCTTG ANTTTTTCC TTAAA 146

SEQ ID NO:337

LENGTH:147

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00360

SEQUENCE DESCRIPTION:

GATCAGTGTT GAAGAAAGTG CAAAAGGAAC TTTTATATAT TTAACAGTGT AGGAAATTGT 60
CTATTCCTGA TATAATTACT GTAGTACTCT TGCTTAAGGC AAGNGTTTCA NATTTACNGT 120
TGAAATAAAC CCAACTCTTC NTGNAAC 147

SEQ ID NO:338

LENGTH:147

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00361

SEQUENCE DESCRIPTION:

GATCTNGAAA ATNATCATTG AACATATTAA TGGTTATTC TTTTCTTGG ATTTCCAGAA 60
AAGCCTCTTA ATTTTATGCT TTCTCATCGA AGTAATGTAC CCTTTTTTC TGAAACTGAA 120
TTAAATACTC ATTNATCNN NTGNAAC 147

SEQ ID NO:339

LENGTH:140

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00362

SEQUENCE DESCRIPTION:

GATCAGTTTT TTCACCTGGA AGCATTGTGTT TCTACTTTGA TATGACTGTT TTTCGGACAG 60
TTTATTGTT GAGAGTGTGA CAAAAGTTA CATGTTTGCA CCTTTCTAGT TGAAAATAAA 120
GTGTATATTT TTCCTATAAA 140

SEQ ID NO:340

00382

LENGTH:144

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00363

SEQUENCE DESCRIPTION:

GATCTGAACT TTTCATCTGC AGAGGCAAGA AAAATATTTA ACATTGTGAC TTGACTGTGG 60
AAGATGATGG TTGCATGTTT CTAGTTTGTA TATGTTTCCA TCTTTGTAAT AAGATGATTT 120
AATAAATCTC TTAAATACT TAAA 144

SEQ ID NO:341

LENGTH:291

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00364

SEQUENCE DESCRIPTION:

GATCAAAAGC TTATTCATCT GTTTTNCCTT TTCGTTGGTG TAAAGCCAAC ACCCTGTCTA 60
AAAAACATAA ATTTCTTTAA TCATTTTGCC TCTTTTCTCT GTGCTTCAAT TAATAAAAAA 120
TGGAAAGAAT CTAATAGAGT GGTACAGCAC TGTTATTTT CAAAGATGTG TTGCTATCCT 180
GAAAATTCTG TAGGTTCTGT GGAAGTTCCA GTGTTCTCTC TTATTCCACT TCGGTAGAGG 240
ATTCTAGTT TCTGTGGGC TAATTAAATA AATCATTAACT ACTCTTCTAA A 291

SEQ ID NO:342

LENGTH:139

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00365

SEQUENCE DESCRIPTION:

GATCTTAAAC CTATGATTCA GTAAGTCTT ACCATATAAA AACGATAATT GCTTTATTTG 60
GAAAAGAATT TAGGAATACT AAGGACAATT ATTTTATAG ACAAAGTAAA AAGACAGATA 120
TTTAAGAGGC ATAACCAAA 139

SEQ ID NO:343

LENGTH:143

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00366

SEQUENCE DESCRIPTION:

GATCCGTGGC AGGGCTGCTG AGGCCTGTGG GTGGGACACC ANNTGCGAAA CCCTCATCCA 60
GTTTCTCTC CATCTCTTTT CTTGTACAA TCCCATTTCC TATTACCATT CTNTGCAATA 120
AACTCAAATC ACATGTCTGC AAA 143

SEQ ID NO:344

LENGTH:139

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00367

SEQUENCE DESCRIPTION:

GATCCAGTGA CATTGTGAGT GAAGACGCAA ACAGGTTTTG ACTCCTGCAT GGCCGATGAC 60
 CTTTTCTGTA GGCTTACCAG AAAAGTACAT NCAACAGTTC TTTGAGGTTT AACTAGAGCA 120
 GCAAATAAAG CAAAAGTTN 139

SEQ ID NO:345

LENGTH:140

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00368

SEQUENCE DESCRIPTION:

GATCAAGAAT CTTTTGTGAA ATTATAGAAA TTTACTATGT AAATGCTTGA TGGAATTTT 60
 TCCTGCTAGT GTAGCTTCTG AAAGGTGCTT TCTCCATTTA TTAAAACTA CCCATGCAAT 120
 TAAAAGGTAC AATGCAGAAA 140

SEQ ID NO:346

LENGTH:142

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00369

SEQUENCE DESCRIPTION:

GATCCAGCTT GCCAGGGACT TAGGTTTATC CTGTTTTGTT TGCTACTGGT TACAAATTCT 60
 ATTTTCTGTA CAATTAGTCA GACTAAAGTT TTCCTGTGT TTGTTTGGCA AAACAAATTA 120
 AACAAAAAGT AAGGTTTTTA AA 142

SEQ ID NO:347

LENGTH:156

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00370

SEQUENCE DESCRIPTION:

GATCTCCGTN AAACACATTT TTNTTCTTAG TCTATCTCTT GTACAAACGA TGTGCTTTGA 60
 AGATGTTAGT GTATAACAAT TGATGTTTGT TTTCTNTTTG ATTTTAAACA GAGAAAAAAT 120
 AAAAGGGGGT AATAGCTCCT TTTTCTTCT TTCAA 156

SEQ ID NO:348

LENGTH:135

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00372

SEQUENCE DESCRIPTION:

GATCTACAAT NGGAGTTGTG AGTNGCAATC TTACATGGCT ACGNCTTTCG TTTGATAGCC 60
 AGTCATGGTN ACCACATGAG AACCATATGC TGAGATGCAA TAAAGTAAGA GAATGTTTTC 120
 TGACAAAAAA ATCTN 135

SEQ ID NO:349

LENGTH:133

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00373

SEQUENCE DESCRIPTION:

GATCTTAAGC GTGTCTTGAG TTCCATGCAA ATTCAATTCT GTTGATAATG TGTCCATAAT 60
CAAATCATCA TCTTGCAATG CAAGGGCTAC CCCATAATTA TCAGACATTA AAATAGTTTA 120
TTTCTTTTTC AAA 133

SEQ ID NO:350

LENGTH:137

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00374

SEQUENCE DESCRIPTION:

GATCTCGTTC CGCCGGTTCC CCTTGGCCGC CAGTTCCGTT CTCCTCACGG GCCGAACGGA 60
ACAAGGGGTC CAGCTTGCGG GGGACCCTCC CCAGCCCATT CCTGCTGTCA AACAAACAAA 120
ACCTTGCAAA GCGCAAA 137

SEQ ID NO:351

LENGTH:132

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00375

SEQUENCE DESCRIPTION:

GATCAAGCGT GCTTTCCTTA TCCGAGGAGC AGAAAATCGT TGTGAAAGTG TTGAAGGCAC 60
AAGCACAGAG TCAGAAAGCT AAATAAAAAA ATGAAACTTT TTTGAGTAAT AAAAATGAAA 120
AGACGCTGTA AA 132

SEQ ID NO:352

LENGTH:142

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00376

SEQUENCE DESCRIPTION:

GATCAAGTTC CCGCTGCCCC ACCGGGTNCT GCGCCGTCAG CACAAGCCAC GNTTACCAC 60
CAAGAGGCCC AACACCTTCT TCTAGGTGCA GGGCCCTCTT CCGNGTTTTG CCCCATAA 120
ACTCANGAAC GNCCCGGTAA AA 142

SEQ ID NO:353

LENGTH:142

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00377

SEQUENCE DESCRIPTION:

GATCAAGGAT ATTTGAAATC ACTACTGTGT TTNCTGCGT ATCTGGGGCG GGGGCAGGTT 60
 GGGGGGCACA AAGTTAACAT ATTCTTGGTT AACCATGGTT AAATATGCTA TTTTAATAAA 120
 AATATTGAAA CTCACCAGTA AA 142

SEQ ID NO:354

LENGTH:134

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00378

SEQUENCE DESCRIPTION:

GATCTCTAAT GAAAAAGGGA TGTCTTTTG TTTATAGTCA TGTGGCAAGA TGAGAGTAAA 60
 ACCAGAGAGC AAACCTCTAT AAGTNTTGAG TATATGTATA CATTTGAAAT AAACCAGAAA 120
 TTTGTTACCT TAAA 134

SEQ ID NO:355

LENGTH:132

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00379

SEQUENCE DESCRIPTION:

GATCAGCTCT GAGGTGCACT TCTTCACATA CTGTACATAC CTGTGACCAC TCTTGGGAGT 60
 GCTGCAGTCT TTAATCATGC TGTTTAAACT GTTGTGGCAC AAGTTCTCTT GTCCAAATAA 120
 AATTTATTAA TN 132

SEQ ID NO:356

LENGTH:143

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00380

SEQUENCE DESCRIPTION:

GATCNGGGCT GGATTGACGG ATGTCACCCC CNATCCCCTC GTGACATGCA CGTCNGCAGG 60
 AATGGGGGGT CTGCNGTGGT CGCCNGTCGT GTGAACAAGA TTCCGTCAA AATATTTCTG 120
 TTAATAAATT GCCTTCATGT AAA 143

SEQ ID NO:357

LENGTH:136

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00381

SEQUENCE DESCRIPTION:

GATCTAGAAG ATGATGTTCA AACTATGAAA CTGCTTGTA ATTGTGAAAT GACTTTGTTC 60
 TTTGCTTGT TTTTNAATT TCCTATAATG NACATACTAA CTTTAAAAA ATAAAGGTTA 120
 TTTTAAAAGC CTGAAA 136

SEQ ID NO:358

LENGTH:133

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00382

SEQUENCE DESCRIPTION:

GATCTTCTAT GTAACAGTTG AAATNTGGAA GTGACGTCAC TTACCTGTCT AACGTGGTGT 60
GGGNGAGAAT TTACAAGTCC TTTATTGNAA GAATAATTGT TGCAAAATAT ATTGCTTCTA 120
CTTTGCCTGG AAA 133

SEQ ID NO:359

LENGTH:130

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00383

SEQUENCE DESCRIPTION:

GATCAAGAAT TTGGGTGGGA GAAAAGAAAG TGGGTATCA AGGGTGATNN GAAATTTTCT 60
GCAGCATTAA AGCTGGCGCT TAATAAGAAT AAGTAATAAT AAAGAAATT CTAACATTCC 120
ATGTCAGAAA 130

SEQ ID NO:360

LENGTH:157

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00384

SEQUENCE DESCRIPTION:

GATCTGAAAC TAATAGTAGG AGTTCCCCA GAAGTCATTT TCAGCCTTAA TTCTCATCAT 60
GTATAATTA CCATAAATNA TGCATGNTG TTTACTTTAG TGACGTTCCA CAGAATAAAA 120
GGAAACAAGT TTGCCATCTT GGTGTTGCAA TATGAAA 157

SEQ ID NO:361

LENGTH:132

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00385

SEQUENCE DESCRIPTION:

GATCTGAAAA GCGTCTNCA CTGCTTTATC TCATGATGCT TGCTTGTAAG ACTTGATTN 60
AGTTTTTCAT NNCTCAAATA GGAATACTAC CTTTGAATTC AATAAAATTC ACTGCAGGAT 120
AGACCAGTTA AA 132

SEQ ID NO:362

LENGTH:197

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00386

SEQUENCE DESCRIPTION:

GATCTGCCAG GNTGGGTGGT TCTACTGCTT TCTCAATTC TAAGAACCTT TTTTTTTCT 60
NAAAGAGTTC TGCTGAATTA TTTGACAATA TTTGNAAGTA CCATGTTTCC TNGNGGGGTA 120
TGCTCTGTNC TGGTTTCTGT TTTNAAATCA AATGCCTGTT TGGGAGGAGA TGAACGNATT 180
NAGTCTATTA GATTGN 197

SEQ ID NO:363

LENGTH:128

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00387

SEQUENCE DESCRIPTION:

GATCACAGTG TCAGAGACGC GTCCTCTTTC TTGGGGAAGT TGAGGAGTGC CCTTCAGAGC 60
CAGTAGCAGG CAGGGGTGGG TAGGCACCCT CCTTCCTGTT TTTATCTAAT AAAATGCTAA 120
CCTGCAAA 128

SEQ ID NO:364

LENGTH:127

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00388

SEQUENCE DESCRIPTION:

GATCCCAGGA GACACCAGGG CCAGAGTGAC CACAGCAGGG CAGGCATCAT CGTGTGTGTG 60
TGTGTGTGGA TGTGTGTGTG TGGGTTTTNT AAAGAATTCT TGACCAATAA AAGCAAAAC 120
TGCAAA 127

SEQ ID NO:365

LENGTH:129

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00389

SEQUENCE DESCRIPTION:

GATCTACAAA TGGGAAGCTT GTGAGTGGCC CATCTTTGTT GGCCTACGAA CTTTGGTTTG 60
ATGCCAGTCA GGTGCCACAT GAGAACCTTT GCTGAGATGC AAATAAAGTA AGAGAATGTT 120
TTCCTGAAA 129

SEQ ID NO:366

LENGTH:125

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00390

SEQUENCE DESCRIPTION:

GATCAGCTAT TAAATTTATA TAAACATAG GCATGTTTGT ACTAATGAAA CGTACTGTCA 60
ACCTCTATCA CATTGTAAAA TTAACACTTT TGGTGGTAAC TCAATAAAAT TGAGAAAATT 120

GGAAA

125

SEQ ID NO:367

LENGTH:246

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00391

SEQUENCE DESCRIPTION:

GATCTTTTTA ATTATAATTT TGTTGTATTT GTTTCCTAGG AGCAAGTGTT CCTGCTGCCA 60
GTTCTTTCCT CTTTAGGCGT GGTGAGAAA AAGCAGAAAC TTTACATAAA GCTGTATTTT 120
TTAATCATCT TTAATTTGAA ACTTAAGNAA ATGAATTTAT TCTGTNATAT TTATGTAAC 180
NATTTCTGG NAGTNATATC TACTAGTNTT GNTTGATAAT AATAAAATTN GGCTATACCT 240
TGNAAA 246

SEQ ID NO:368

LENGTH:132

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00392

SEQUENCE DESCRIPTION:

GATCTAAAT TTATTGGGT GATGTTTGCA TAACAGTGCA AATATACTGA AAACCACTGA 60
ATTTTACACT TTAAATCAGT GGCTTCTGTG GTATGTTATC AATATTTCTC AATAAACTT 120
CAAAAAATA AA 132

SEQ ID NO:369

LENGTH:131

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00393

SEQUENCE DESCRIPTION:

GATCTGGTAT TAGGAAATTA CTTTCACAGT AAATATCAAA GAAAAAGAT TAAGGGTCTC 60
TTTGCCATGC TTTTCATCAT ATGCACCAA TGTAATTTT GTACAATAAA ATTTTATTTT 120
CTAAGTAGAA A 131

SEQ ID NO:370

LENGTH:123

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00394

SEQUENCE DESCRIPTION:

GATCTGAAAA AGAACACTGT GCGAGATTGT ATTCCTGCTT ATCCTTTCCA AGTTAGTAGG 60
CAGATTGGAA CTATAGAATT TATCCGTGAT AATAATAAAG TCCGCATAAC TTTTGTCTG 120
AAA 123

SEQ ID NO:371

LENGTH:123

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00395

SEQUENCE DESCRIPTION:

GATCTAAAGA GAACTGTAG ATTGTTTTCC TGACAGCAAA AGACTAATGT GACAAAATGA 60
AGTCATTGTA AAGAAGCGAT GCAACTTGTC AAATATTTAA TAAAGAATTA TGGAAGCTGG 120
AAA 123

SEQ ID NO:372

LENGTH:124

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00396

SEQUENCE DESCRIPTION:

GATCACAAC T GNAAGATAAC AAGAGATTTA AGTTTTAAGG GCATTTAATC AGGAGGAAAG 60
GTTTGGAAAA CTAATCAGG TGTATTTNTT GTTTAAGCAG AAATAAAGTT TAATTTTNC 120
TTGN 124

SEQ ID NO:373

LENGTH:122

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00397

SEQUENCE DESCRIPTION:

GATCTGTGTT AGAATGAGTG CTTTCCCTTC CTAATGATGT GATTGTGGAT TAGGAATTCG 60
TGACCGAGTG ATTTTGGCC AGTGGTTGGG TTAAATTC TATTAATTTGTTAGTTGG 120
GN 122

SEQ ID NO:374

LENGTH:121

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00398

SEQUENCE DESCRIPTION:

GATCGCCGCC CTGCTGGCCA CCTGCGNTGG NGCTGGCNCT CGTGGTCGTC GCGCTGAGAA 60
AGTTTTCTCC CTCCTGAAGC GAATAAAGGG GCCGCNGCCG GCCGCGGCGC GACTCGGCAA 120
A 121

SEQ ID NO:375

LENGTH:120

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00399

SEQUENCE DESCRIPTION:

GATCAGGCCC GGTGCCTGCA GACCTGGTGC TCCCTCGGGC AGGGCTGGGT GCCGCACCGC 60
CTGCTGGCTT TTCTGGCAGC TCCTCTGTAT CAGAACCAAT AAAGTGCAC TGTCTCGGN 120

SEQ ID NO:376

LENGTH:119

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00400

SEQUENCE DESCRIPTION:

GATCAGGCAG TCCTNAGGA TAGACAGATA TACACACCAC ACACACACAC CACATACACC 60
ACACACACAC GTCCCATCC ACTNACCCAC AACTACACA GNCTGNTNCC TTATAGCTN 119

SEQ ID NO:377

LENGTH:225

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00401

SEQUENCE DESCRIPTION:

GATCTNATTT GTAACCCACT GAGAGGACAG AGAGAAATAA GTGCCCTCTC CCACCCTCTN 60
CCTACTGGTC TCTCTATGCC TCTCTACAGT CTCGTCTCTT NTACCCTGGC CCCTCTCCCT 120
TGGGCTGTGA TGA AAAATTG CTGACTGTAG CTTTGGGAG TTTAGCTCTG AGAACCGTAG 180
ATGGATTNCA GTTCTGGGAA AATAAAACCC GTTGATTACT NAAAA 225

SEQ ID NO:378

LENGTH:125

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00402

SEQUENCE DESCRIPTION:

GATCTTAATA TATTTGAAAA AAACCTTCATT CTCGTGAGTC ATTTAAATGT GTACAATGTA 60
CACACTGGTA CTTAGAGTTT CNGTTTGATT CTTTTTAAT AAACCTACTCT TTGATTAAA 120
GCAAA 125

SEQ ID NO:379

LENGTH:147

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00403

SEQUENCE DESCRIPTION:

GATCTCAGTT CTGCGTTTAT TGTAAGTTGA TAAAAACATC TGGAAGAAAA TAACTAAAAC 60
TGTTTGCATC TTTGTATGTA TTTATTACTT GATGTAATAA AGCTTATTTT CATTAACAAT 120
TTGTATTAAA ATNTGGGTTC CTTGAAA 147

SEQ ID NO:380

LENGTH:116

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00404

SEQUENCE DESCRIPTION:

GATCACCTTT TCAGAAATTT AGATGTGAAC ACCAAAAGAA GCATTTTCTC AACAAAAATT 60
AATAGCTGGT TCTATTTTTT TTAAACCTAG AAAAAATAAA GTTGATTTTT TTCAA 116

SEQ ID NO:381

LENGTH:119

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00405

SEQUENCE DESCRIPTION:

GATCAATAGG GAGAGAAAAT CCACATTCTT GGGCTGAACG CGGGCCTCTG AACTGCTTA 60
CACTGCACTC TGACCTGTA GTACAGCAAT AACCGTCTAA TAAAGAGCCT ACCCCCAA 119

SEQ ID NO:382

LENGTH:115

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00406

SEQUENCE DESCRIPTION:

GATCTTTATT ATGGAANCA TTTCAAGTTT ACTCCTTCTG TTTTAAGTTT TGTCAGCTG 60
TACCCACGCT GGGTATTACN NCCNAAATAA TCTGTNAGTG AAAGTTGCCA TTATN 115

SEQ ID NO:383

LENGTH:115

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00407

SEQUENCE DESCRIPTION:

GATCGANCTG CGCAANTGNG NAAGCTGCAG AGGACATCGC GTACCANCTC TCACGCTCTC 60
GGAACATCAC CTACCTGCCA GCGGGGCAGT CCGTGCTCCT CCAGCTGCCC CAGTN 115

SEQ ID NO:384

LENGTH:113

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00408

SEQUENCE DESCRIPTION:

GATCTCTCAA AAAACAAAGA ATTACATGAG TTAGTACATG AAAAAATTAT GGGAAACTAC 60
ATGAAATATA CTGTTACGTT CAATAAACAT TAGCTTCTGT ATATAATANT AAA 113

SEQ ID NO:385

LENGTH:116

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00409

SEQUENCE DESCRIPTION:

GATCTCTTCC CCCAACTTCC TAACACTTAT TAATTTATGA AACTGTTTT CTCAGCGCAG 60
TTTTGTTTTG TGTGTCCATT GGATTACAAA CTTTATTAAA AAATATAAAA CACAAA 116

SEQ ID NO:386

LENGTH:118

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00410

SEQUENCE DESCRIPTION:

GATCTCTCTC TTCTCGCGCG CGCACTCTCT CTTCAACACT CCCCTGCGTA CCCCGGTTCT 60
AGCAAACACC AATTGATTGA CTGAGAATCT GATAAAGCAA CAAAAGATT GTCCCAA 118

SEQ ID NO:387

LENGTH:247

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00411

SEQUENCE DESCRIPTION:

GATCTATAAA AAGTCAGCAA CTGATGTGTT TGAAAAGCAT CCTGTCTNT ATATCCTAAT 60
GTTTGGATGT GTCTTNCTA AAGTCTCACA AAAATTAGTG GTAGCTCACA TGACCAAAG 120
TGAACATAT CTNCAAGACA CTGTCTNNGG GGGGCCAGGT CTTTGTITT TAGGNCCAGT 180
ACTTNATAA TTTTNTAGAC GGATATGGT GTCCTATGGA TGGCAATGGG TGNTTNTCTC 240
ATTGNN 247

SEQ ID NO:388

LENGTH:112

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00412

SEQUENCE DESCRIPTION:

GATCCTAGGA AGAGAGAACA GAGTGGCTCA CAAGCCCCAA CACAGTNAGC AGCAGATGAC 60
AGGCACNCTN AGACCACACT NTAGGCCACC CATGGGNCCA AAAGGGAACA GN 112

SEQ ID NO:389

LENGTH:111

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00413

SEQUENCE DESCRIPTION:

GATCACCACN TAAGTCAGAA AAATGTATTT TTAAATGTTT CTTGAAGTGC CTTTGAACA 60
TTTTTAAACA GCGGATTTAA ATAATGCATA AANTAAATTG CCATGNTCAA A 111

SEQ ID NO:390

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00414

SEQUENCE DESCRIPTION:

GATCACCTTA GTTTGATTCT ATTTTTCAGC TTGCAAAAAG TGACTTATAT TCCAAAGAAA 60
TTAAAATGTT GAAATCCAAA TCCTAGAAAT AAAATGAGTT AACTTCAA 109

SEQ ID NO:391

LENGTH:111

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00415

SEQUENCE DESCRIPTION:

GATCGTNACG CTCGCATCTA TAGATAACGG CTCTCCAGAC CTGAGCTTTC CGCGTCANAA 60
TG TAGGAATN GTTTTCCTG CAGAGAATAA AAGGACCACG TGNAATACTT N 111

SEQ ID NO:392

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00416

SEQUENCE DESCRIPTION:

GATCTTATTG AAGGACATCT TACAGCTTCC CAATGAGAGG CCAGGAAGTG TGAACATACT 60
GATAGAAAAA GACTATATTT TATCCCTCAT AAAATGTTT AAATGTAAA 109

SEQ ID NO:393

LENGTH:116

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00417

SEQUENCE DESCRIPTION:

GATCACTGAG TGTACAGAAG AGAGAAATTC AAACAAAATA TTGCTGTTCT TCAGTTTGT 60
TTGTGGAATT TAAATNACT CAAATTTAAA ATAAATNACT GGACTGTGGA AATAAA 116

SEQ ID NO:394

LENGTH:115

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00418

SEQUENCE DESCRIPTION:

GATCTCAAGA GTTCACCTGG CTNACAGAAA GAAGATGCCA GATGACACTT AAGACCTACT 60
TGTGATATTT AAATGATGCA ATAAAAGACC TATTGATTG GACCTTCTTC TTAAA 115

SEQ ID NO:395

LENGTH:114

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00419

SEQUENCE DESCRIPTION:

GATCATTCTG AACTGTACAT ATTTATGTNG CGAGAGGCAA AGGGCAAGTT TTGGATTTTC 60
CTTCTTCCAA GTTTGTTTTT AAACGACAAA TAAAAAAGA ACATTTTAAA TAAA 114

SEQ ID NO:396

LENGTH:106

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00420

SEQUENCE DESCRIPTION:

GATCTGAATC TNTGACTTAT TGATTATGGA ACCTGTCAAG TAGTTTTNAA CTCTCCCAGT 60
GAGGATAATT AAACATGCTC AGCCTGAGCC ACCTCTAAGT NTCAAA 106

SEQ ID NO:397

LENGTH:107

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00421

SEQUENCE DESCRIPTION:

GATCGTTCTT CATGGGGGTA AGAAAAGCTG GTCTGGAGTT GCTGAATGTT GCATTAATTG 60
TGCTGTTTGC TTGTAGTTGA ATAAAAATAG AAACCTGAAT GAAGAAA 107

SEQ ID NO:398

LENGTH:112

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00422

SEQUENCE DESCRIPTION:

GATCCCCTCA AAAGGCAGGA NTGCTGCCCT CTNCCATGGT GCCCGTNCCT CTTTGCTGTN 60
TATGTNAACC ACCCATGTAA GGAATAAAC CTGGCACTAG GTCTTAAATA AA 112

SEQ ID NO:399

LENGTH:105

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00423

SEQUENCE DESCRIPTION:

GATCANCTCT AAGGTGCAAC TNCCTCCACA TACTGTACAT ACCTGTNACC ACTCTTGGA 60
GTCTGCAGT CTTTAATCAT NCTGTTTAAAN CTGTTGTGGC ACAAN 105

SEQ ID NO:400

LENGTH:104

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00424

SEQUENCE DESCRIPTION:

GATCTGGAAC TTGAAGATGC CATTACATACA GCCACTTAAC CTAAAGGGAA AGCTTTGAAG 60
GGCAAATGAC AGAGGGTAAC ATAGGAGGTN GGATNCTNAA TNNN 104

SEQ ID NO:401

LENGTH:104

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00425

SEQUENCE DESCRIPTION:

GATCTTTGAT ATATCATAGT CATTAAAAGA CNTTTTCGTA TTTGTATTGA TAATGTATTA 60
AAAGTNGTTT GTNCTTAATA AAAGACTTCT TTAANCATCT NAAA 104

SEQ ID NO:402

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00426

SEQUENCE DESCRIPTION:

GATCCCCGGC CTCAGTCCCT ACTCTGCTTT GGGATAGTGT GAGCTTCATT TTGTACACGT 60
GTGACTTCGT CCAGTTACAA ACCCAATAAA CTCTGTAGAG TGGAACAAA 109

SEQ ID NO:403

LENGTH:110

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00427

SEQUENCE DESCRIPTION:

GATCACCTGC AGCTGGCCAC ACCACAGGCC CCCGNTGCCT GCAGCACTAC TCNGTNCCTN 60
AAACACCTGG CCTGCTAGGA GGCTCCAATA AAGCTAACCC GGACCAGAAA 110

SEQ ID NO:404

LENGTH:157

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00428

SEQUENCE DESCRIPTION:

GATCCTCAGA ACTTCTCTGG GACAATTCA GTTCTAATAA TGTCCTTAAA TTTTATTTCC 60
AGCTCCTGTT CCTTGGAAAA TNTCCATTGT ATGTGCATTT TTAAATGAT GTCTGTACAT 120

AAAGGCAGTT CTGAAATAAA GAAAATTTTA AAATAAA

157

SEQ ID NO:405

LENGTH:103

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00429

SEQUENCE DESCRIPTION:

GATCAGCAAC ATTTGCTGAG CCTGTTTTN AAGCTAATGT GTATTCTNAC TAATNTNCCT 60
ATCAAGAAATG GATTTGTAAT ATATNCTGTC TATTTCTAAT GTN 103

SEQ ID NO:406

LENGTH:105

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00430

SEQUENCE DESCRIPTION:

GATCTGTAAG CACAGTCTTA TTTNCTTTTG TTGTCCAGAA TACTTATAAT TCTTGAGCCT 60
CCCAGAAATT GGAAGCTAAA TAAAGCAACT CAAGTTTCCT TAAA 105

SEQ ID NO:407

LENGTH:104

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00431

SEQUENCE DESCRIPTION:

GATCAGCATC ATTGGAACAT GGGGACGAGT GACGGCAGGA GGACCACGAG GAAATACCCT 60
CAAACTAAC TTGTTTACAA CAAAATAAAG TATTCACTAC CAAA 104

SEQ ID NO:408

LENGTH:105

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00433

SEQUENCE DESCRIPTION:

GATCTATCAC TCTCGTNCTT GTAGCTCCCA GCCGAGGACG TCGGATGTAA TCGTCCTTNC 60
TGCTTTGCCA CCCCATTTCC GTCAATAAAG TGGTTTGAAC CAAA 105

SEQ ID NO:409

LENGTH:105

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00434

SEQUENCE DESCRIPTION:

GATCAAACCT TTCTGGCCTG TTATGATTCT NAACATTGA CTTGAACCAC AAGTGAATCT 60

TTCTCCTGGT GACTCAAATA AAAGTATAAT TTNACCTGC GGAAA

105

SEQ ID NO:410

LENGTH:101

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00435

SEQUENCE DESCRIPTION:

GATCAACACA AAGCACAATG NATTACNCGN AATTCAGTAT TTTCAAATTT ACATATTTAA 60

AGTCATGCAA GCTGTAACTT CCCNGTCAAA ATTACTNGCT N 101

SEQ ID NO:411

LENGTH:100

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00436

SEQUENCE DESCRIPTION:

GATCATAAAG NNCTATCAAG GAGTTCATC AAGGCATCCA TGTCAGTGGT GCTATGCTGG 60

TTACAACCTG AGATTTTGA AATAAAAAAT TTGCATAAA 100

SEQ ID NO:412

LENGTH:103

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00437

SEQUENCE DESCRIPTION:

GATCAACAGG CTTATTAGAA GAATGAACTA AGGTGTCTAC CATGATTATN TTTCTAAGCT 60

GGTTGGTTAA TAAACAGTAC CTGCTCTCAA ATTGAAAAAG AAA 103

SEQ ID NO:413

LENGTH:99

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00438

SEQUENCE DESCRIPTION:

GATCTTGTGC TGTGTCAAAG TAACAGACTA GAACCTTCTT TCAAGTACCT GAATTGAAAT 60

NAAACTCATT TTGAATAATA AAAACTCTAG AAACCTCAA 99

SEQ ID NO:414

LENGTH:99

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00439

SEQUENCE DESCRIPTION:

GATCTGTAAT AGCATATTGT AGATGCACTT TGCAGCAGTT GGAAAAGAAA GTGTTGTGTG 60

ATTTGATTGA AATAAACTA AATGTGTTGT CCTCCTAAA

99

SEQ ID NO:415

LENGTH:96

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00440

SEQUENCE DESCRIPTION:

GATCCCTGTG CCAGGAGCCA ACCTGGTCTT CCCGAGGGTC AGTGCCCCAG TGAAGACAGA 60
AGCGAGAGAA TAAAGTCCC TGTAGGTCCT CTGTCN 96

SEQ ID NO:416

LENGTH:97

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00441

SEQUENCE DESCRIPTION:

GATCCTCCCA TCCGTGTTGT GAGCACAGGC ATTTGTGTNT GGNCTGTCCT CCCTGTTGAT 60
TGGTCTGGCA TTTCCGGTAT TAAAATGATA ANATAAA 97

SEQ ID NO:417

LENGTH:93

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00442

SEQUENCE DESCRIPTION:

GATCCTGCAT ATCTCAAGGA CCCTAAAGTT TGTAACATCA GATATCGGGA ATAAATTCTA 60
TCACGTTACC ACTAATAAAC TTATTTTACA GTN 93

SEQ ID NO:418

LENGTH:97

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00443

SEQUENCE DESCRIPTION:

GATCTGTATT TTGCAAATAT TTTCTTCAAT ATGTGGCTTG TCTTTTGGTT CTCTTAACAA 60
GGTCTCTTCC AGAGTATAAN CTGTAAATAT TAAGAAA 97

SEQ ID NO:419

LENGTH:98

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00444

SEQUENCE DESCRIPTION:

GATCTGGACA GAATCGCCGG ACAGGTGGCA GCTGCAACAA GAAGCATTAG AACAAACCAT 60

GCTGGGTAA TAAATTGCCT CATTGTAAT CCTGGAAA

98

SEQ ID NO:420

LENGTH:100

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00445

SEQUENCE DESCRIPTION:

GATCTATTCT GAGTATTTT TAGAGAGTTA ATATTTATAT TTTTAGTAAT TTTCTGGTAG 60

AAGGAAATTG CACAATAAAA TNATTGGTT TGGTTTGAAA 100

SEQ ID NO:421

LENGTH:93

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00446

SEQUENCE DESCRIPTION:

GATCGTTGGC ACCATAGCCT TATGGCCAAC AGGTGGTNTG TGGTGAAAGG GCGTGGAGT 60

TTCAATATCA ATAAACCACC TGATATCAAT AAA 93

SEQ ID NO:422

LENGTH:94

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00447

SEQUENCE DESCRIPTION:

GATCTGTGTT TNCCCTGACG AATGGAATTT ATCCTCACAA ATTGGTGTTT TAAATGTNTT 60

AAGAACCTAA TTAAATAGCT GACTACAAAA CAAA 94

SEQ ID NO:423

LENGTH:206

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00448

SEQUENCE DESCRIPTION:

GATCCCAAAC CTTACGGCCA AGTTTCTTCT AGTATGATGG AAAGTTTCTT TTTCTTTGC 60

TCTGAATAAA ACTGAACTGT GGGTTCTCTA TAAGTGGCAT TTTGGGCTTT CCCTCTTTT 120

TGTAAGCAA TGTCTGCCTA GTTTATTGTC CAGTTAACTT TAGTGACCTT TAAAAGTTG 180

GCATTGTAAT TAAACAACCT TGCAAA 206

SEQ ID NO:424

LENGTH:481

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00450

SEQUENCE DESCRIPTION:

GATCTCACCA CTGCACTCCA GCCTGGGCAA CAGAGCGAGA CTCTGTCTCA ACAACAACAA 60
 CAAAAAGTCC TGAACATGAT TGTGGAAGTG TGTGCTCTT TCAAGTTCTA TCACTTTTGG 120
 TTTGCAAAGT TCAAAGCTGT ATTGTTGGT ACATATACAT GTAGGTTTGC CAAGTCTTTG 180
 TGGTGAATTG ACTCTTCTGT CATTATGTGA TGTCAATTTT TTGCCTTTTA ATAGTCTTGT 240
 CAATACTTTA CCTGATGTTT TCATAGTGAC TCCTGCATAT TTTGATTAAT GTTGCATGG 300
 TTAATATTTC TTCATTTTAT TTTAAAGCTT ACCTGTATCA TTAATTATGA AGTCAGTTTC 360
 TTTGAACAGC ATATACTCAG GCCATGCTTT TTTNATTCA TTCCTGCATA TGGCTCTCCT 420
 TAAATTGGGA ATGGTGGAAA ATGGNTTAC CATTAANAAT AAATTAATTG GTATTTTAA 480
 A 481

SEQ ID NO:425

LENGTH:87

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00451

SEQUENCE DESCRIPTION:

GATCTGGTCC ATGAGGCTGC CCAGAGAAAG CACTGCTTCT NTATGTCTCT TGTGGTATTG 60
 GAACAATAAA CCCGTACAAC CTGCAAA 87

SEQ ID NO:426

LENGTH:93

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00453

SEQUENCE DESCRIPTION:

GATCATACTT GAAAGTGAAC TTTAACATTG AAAAATCGTA CAGTCATTTC AAGAATAAGA 60
 AAATAAAATT TTCTCTTTGT CTGAACCTGC AAA 93

SEQ ID NO:427

LENGTH:85

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00454

SEQUENCE DESCRIPTION:

GATCCCATGT GCTCTCACAC CATGTTTTTG TACAGAACTG ATGGTTGAAT CTTTGTCTC 60
 TTGAAATAAA CAGAAGAAAA TGAAA 85

SEQ ID NO:428

LENGTH:87

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00455

SEQUENCE DESCRIPTION:

GATCTATTAA AGAAGTAATT GGCCTTCTG AGCTGATTTT TCCATCTTTT GTAATTATCT 60

TTATTAAAAA ATTGTACTTG GATTAAA

87

SEQ ID NO:429

LENGTH:91

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00456

SEQUENCE DESCRIPTION:

GATCTCATTG CATGGGAAAA AAAAAATCC TGTCTTNTTC ANAAATTGAC AATGTAAATA 60
AATTNAAATA TGGTTCACGT TTACTCTTAA A 91

SEQ ID NO:430

LENGTH:84

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00457

SEQUENCE DESCRIPTION:

GATCTGAGAA ACAGGTGTGA CAAGAGCATG AACCANAGGT GCACCTGGGG CAGTTCCTTA 60
ATAAACTGG TTTGTACAGT CAAA 84

SEQ ID NO:431

LENGTH:83

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00458

SEQUENCE DESCRIPTION:

GATCATGAGA GTGCCTGTCC CTTGTGAGCA CTATGAAAGT GTTAGCTGTT CTTTACCAGA 60
ATAAATGCAT TTCTATATCT TCN 83

SEQ ID NO:432

LENGTH:84

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00459

SEQUENCE DESCRIPTION:

GATCACCAGC TGAATATATT GTTTTACAAT AGTTCTGTGG GGCTGTTTTT TTGTTATNAA 60
ACAAATAATT TAGATGGTGG TAAA 84

SEQ ID NO:433

LENGTH:80

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00460

SEQUENCE DESCRIPTION:

GATCTTGATG GATTNCATA CGATTGTAAA TGNAGCTATA TTAAAGTCTA TTAAAGGAAG 60

CCCTTCTTGT TTGAGGGAGN

80

SEQ ID NO:434

LENGTH:86

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00461

SEQUENCE DESCRIPTION:

GATCTATGCT TGTGTTTTT TGTAATCCAT ATCATAGTTG CTTTCTTTAA TTGTCCTTC 60

TGAATAAACA GTTATTTTAA GATAAA 86

SEQ ID NO:435

LENGTH:83

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00462

SEQUENCE DESCRIPTION:

GATCCAGTCA CTGACTCTGT CTGGTGTGA CAGAGGATTT ATTAAAGCTA TTATTTTAAT 60

AAAGNACTTT GTACATTTT AAA 83

SEQ ID NO:436

LENGTH:85

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00463

SEQUENCE DESCRIPTION:

GATCTACATA CAAACAAATG CAACCAACTA TCCAAGTCGT TATACCAAGG TAAACCCCC 60

AATAAACCGT TGAACATGTG ACAAA 85

SEQ ID NO:437

LENGTH:86

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00464

SEQUENCE DESCRIPTION:

GATCTGCTTT TACTTTGTAA TTTGTAGTTC TCAAAAGACT TTTTTTTAAA AAAATAAAGN 60

CCATACTTAC ACTTAGGCTT TATAAA 86

SEQ ID NO:438

LENGTH:83

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00465

SEQUENCE DESCRIPTION:

GATCATTCTG AGTGTGCGAG TGTGTGTGCA CATGTTACAA AGGCANCTGC CATGTTAATA 60

AAATATTCAA TTTGAAATCC AAA

83

SEQ ID NO:439

LENGTH:78

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00466

SEQUENCE DESCRIPTION:

GATCCAAACT GTCTTTTTT TGTATCTGTT ATTTAAAGCC CAGTGGATAT TTCAATNAAA 60
AAAAAATCT AAAGATGN 78

SEQ ID NO:440

LENGTH:80

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00467

SEQUENCE DESCRIPTION:

GATCTGACCA CCTCTGCCCT GTCCACCAGG ATAAGTGACA CCTAGGACCC AGGAAATAAA 60
TGCCGATGAT TTGTGTGAAA 80

SEQ ID NO:441

LENGTH:73

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00468

SEQUENCE DESCRIPTION:

GATCTTACAG GGAGAGAGAT TGGGTGCAAT TTGCCTCTTT CTTGAATAA AAAGCTCTTT 60
GCTCACCTC AAA 73

SEQ ID NO:442

LENGTH:197

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00469

SEQUENCE DESCRIPTION:

GATCAAAAGT CTACATAACT AATACTCACA GCTGAGCTAT GTAGTATGCT ATGATTAAAT 60
TTACTTATGT AACTTTTATT GTCTTTGGCA TTAACAGTGT TTCAAAAAAT TTCCTGTGTA 120
TACCCATCAG TGATTCATTC CCAAATCTNC TAGAAGCATA AGTGTCTCAA TATATTAAAA 180
CATATTGAAT AATCAAA 197

SEQ ID NO:443

LENGTH:75

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00470

SEQUENCE DESCRIPTION:

GATCCAGGCG CCAGGCTGGC GGTTCGTGAG TGTCGAGGCA CCACTAAATA TAGCTGTCTG 60
CCGTCCACTC ATAAA 75

SEQ ID NO:444

LENGTH:74

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00471

SEQUENCE DESCRIPTION:

GATCANATTG TAAGCTTTTC TGTTTNATTT CTTTAAAGAA CCTTTGAATA AAAACATCT 60
GAAATTTTAA NAAA 74

SEQ ID NO:445

LENGTH:73

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00473

SEQUENCE DESCRIPTION:

GATCTCTTTG TAGCCATCCT GTTAAATTTG TAAACAATCT AATTAAATGG CATCAGCACT 60
TTAACCAATG AAA 73

SEQ ID NO:446

LENGTH:71

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00474

SEQUENCE DESCRIPTION:

GATCATGTCT GAATTATGTA TGAAAATTAT TCTATGTTTT TATAATAAAA ATAATATATC 60
AGACATCGAA A 71

SEQ ID NO:447

LENGTH:69

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00475

SEQUENCE DESCRIPTION:

GATCTCTACC CACCCCATGC CTCTCCCNAG TCTTGGATAC TAATAAAATG ATAAGCATTC 60
TGTTTCTCN 69

SEQ ID NO:448

LENGTH:68

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00477

SEQUENCE DESCRIPTION:

GATCGTAATG TAAATTCTT TTACCATGTA CAAGAATTAT TAAATACAG GTACTTGACC 60
ACATTCTN 68

SEQ ID NO:449

LENGTH:72

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00478

SEQUENCE DESCRIPTION:

GATCGGGCCC CGGGGGCCTG AGCCTGGGAC CCCACCCNGT GTTAATGAAA AATGAGTTTT 60
GGCAGCGCCA AA 72

SEQ ID NO:450

LENGTH:64

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00479

SEQUENCE DESCRIPTION:

GATCCTTTTG TAATGACTTA CACTGGAAAT GCGAACATTT GCAGTAAAAA AATATATATA 60
TAAA 64

SEQ ID NO:451

LENGTH:66

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00480

SEQUENCE DESCRIPTION:

GATCATGCAT TTAGATTAT ATTTTNCCA NAAAATACAA GGTATAATA AACTAAGAN 60
CTACCN 66

SEQ ID NO:452

LENGTH:70

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00481

SEQUENCE DESCRIPTION:

GATCTCTATT GTAATCTCTA TTGGAGATTA CAATGATTAA ATCAATAAAT AACTGAAACT 60
TGAANATAAA 70

SEQ ID NO:453

LENGTH:65

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00482

SEQUENCE DESCRIPTION:

GATCACTAAT TTTGCATCAG TAAATGAAT TTTTAA CCAATAATC ATCAATTATT 60
AGAAA 65

SEQ ID NO:454

LENGTH:63

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00483

SEQUENCE DESCRIPTION:

GATCAGTT GCGTCATTGT GTATTAAATA CTTGGAATAA ATCAAGCAGG TCTCAACGCC 60
AAA 63

SEQ ID NO:455

LENGTH:68

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00484

SEQUENCE DESCRIPTION:

GATCATTAAT TGTAAGCGC TTGTAAAAT TCACATTAC AAAATAATAA AGTCAGTTCA 60
AACCTAAA 68

SEQ ID NO:456

LENGTH:63

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00485

SEQUENCE DESCRIPTION:

GATCTGTGTC TGAGTCATCT TTGTATCTG CCTAGCACCT ATCAATAAAT ACTTCTTGAA 60
TGN 63

SEQ ID NO:457

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00486

SEQUENCE DESCRIPTION:

GATCATGGGA ATATGCAGAA TTTCCAATGT ATTTTAAAT ACAAATAAAA TTGTAATTAA 60
GN 62

SEQ ID NO:458

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00487

2153480

SEQUENCE DESCRIPTION:

GATCTAACAC TAACTGTATT GTTTTGTTC CATCAAATAA ACATCTTCTG TGGACCAGGA 60
AA 62

SEQ ID NO:459

LENGTH:61

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00488

SEQUENCE DESCRIPTION:

GATCTCGGCT CACTGCAATC TCTGCCTCCC GGGTTTCAAG CTTGTCCAGG NNNATCTCAA 60
A 61

SEQ ID NO:460

LENGTH:61

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00489

SEQUENCE DESCRIPTION:

GATCAACCTG AGTTTAAAA TACCTTTAAT AAATATNAGT NGAAAAAATG TCTACTTNAA 60
A 61

SEQ ID NO:461

LENGTH:61

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00491

SEQUENCE DESCRIPTION:

GATCAAACAC CCCACCCTCA CAAAAATGGC CACGTTGCAA TAAAAATTGT GGCATATTAC 60
N 61

SEQ ID NO:462

LENGTH:86

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00493

SEQUENCE DESCRIPTION:

GATCTTTATT TTCCCTTTGT ATTCATTTTA AGCATCTAAA TAAATTGCTG TATTGTGCTT 60
AATGTAAATA TTGCTTTAT TACAAA 86

SEQ ID NO:463

LENGTH:66

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00494

00408

SEQUENCE DESCRIPTION:

GATCTCTACT ACTGTTGATT TTGCCCTCGG AGCAAAGTGA ATAAAGCAAC AAGATGAAAA 60
CTGAAA 66

SEQ ID NO:464

LENGTH:70

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00495

SEQUENCE DESCRIPTION:

GATCAAACTA GAACTCATAT GCCATACTAG ATATGGTTGT CAATAAACTT ATGACGTGAA 60
AAAAAAGAAA 70

SEQ ID NO:465

LENGTH:57

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00496

SEQUENCE DESCRIPTION:

GATCCAAAA GTGCGCGATG CGAGTAGTCA AGTCGTACTC CGCCATCTTG CCAAAGN 57

SEQ ID NO:466

LENGTH:65

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00497

SEQUENCE DESCRIPTION:

GATCTAAAGC TCTTCGATT TTATACTGAT TAAATCAGTA CTGCAGTATT TGATTAACCA 60
AGAAA 65

SEQ ID NO:467

LENGTH:55

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00498

SEQUENCE DESCRIPTION:

GATCTAAGGC AAGAGTTTCA GATTACTGT TGGAAATAGA CCCAACTCTT CATGN 55

SEQ ID NO:468

LENGTH:56

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00500

SEQUENCE DESCRIPTION:

GATCATAAAT ATTAATGGNG AAAAACTGT AGTAATAAAT TTCNATATGC CAGAAA 56

SEQ ID NO:469

LENGTH:52

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00503

SEQUENCE DESCRIPTION:

GATCTGTTCA GTGTCACCTCT GTACCCTCAA CATATATCCC TTGTGCGATA AA 52

SEQ ID NO:470

LENGTH:54

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00504

SEQUENCE DESCRIPTION:

GATCCCCGGT NGGTTTTGTG CTCAAAATAA AAAGCCTCAG TGACCCATGA GAAA 54

SEQ ID NO:471

LENGTH:57

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00505

SEQUENCE DESCRIPTION:

GATCATCCGG TTATAGAGCA TAATTTGCCA ATAAAGCTTT TGGAAGCGGG AAAGAAA 57

SEQ ID NO:472

LENGTH:60

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00506

SEQUENCE DESCRIPTION:

GATCCAGTGT TGGNATTCTT TGGTGTAAT AAACGTTTGG TTTTATTAT NCAGGTAAA 60

SEQ ID NO:473

LENGTH:51

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00507

SEQUENCE DESCRIPTION:

GATCTCATTT ATTGCCACAG ATGCACAAAA TAAATAACCC AAAATCACAA A 51

SEQ ID NO:474

LENGTH:80

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00510

SEQUENCE DESCRIPTION:

GATCATATAT TTTGACAAAA TATATTTATA ACTACGTATT AAAAGAAAAA AATAAAATGA 60
GTCATTATTT TAAAGGTAAA 80

SEQ ID NO:475

LENGTH:77

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00511

SEQUENCE DESCRIPTION:

GATCCAAAAC TTTAATGTTG CACNTGTATT CCAAATAAAG GGTA AAAACA GAACCAAAGT 60
TATAACTCCA ACACAAA 77

SEQ ID NO:476

LENGTH:669

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00532

SEQUENCE DESCRIPTION:

GATCAAAAAG AAGGCTTAGA ATTCTGCAGT TAAGCTGAGG TTTAACTAA AAANTGTTTC 60
CTTGGGTCAG TGGTTTTNAG GTCCAGTAGC TAGGCTTTTT TCTTTTGTCC TTCCTGTTGG 120
AATGAAAAACA TTTGATTTT CCTTCATCTG TGACTGGTGC CATAGACACA GGTTTATAGT 180
TTAACTTAC AGTATTGTTT GAAATTTACC TGTTTTNTT GTCAAACCTG AGCACTCCTC 240
CTGCTGAAGT TTCTTATTTA ATTCCAGAGT ACTGTCCTCT ACTCTAAGGC ATTACTTTTA 300
AGTGTATTAT GAAGGCAGTT TTCAAAGGAT ATGACCAGTT GGGGGTAATT CAAATTA AAA 360
AGGAAAAGAT TTGTTTGGGA AGTAACTGGG TGTCTCTAAG AGGGAATTT TAGGATGTCC 420
AGTTTGGGAG GCTCTTTCCC CCCTCAAATT GAGANGCTCC TTGGTTAATT CAGAGCTCCC 480
ANGACTAGGC CCTGGGCTAA CCAANCATTN GGGNGGCCAA AGGTAGGGA ACCATTNGNT 540
ACCAAGCTTT TGNANCAGGG GGNTTNTNC CATTGGGTA ATAGGGCCCT TTTCANGCCT 600
TTANGGGTAN GCTTTTTTAN CCCNGAAACC NTTNNTNNT TTGNAATTAA ACCGGAACCT 660
TTGNCAAA 669

SEQ ID NO:477

LENGTH:651

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00533

SEQUENCE DESCRIPTION:

GATCAACCTG GAGCTCTACG CCTCCTACGT TTACCTGTCC ATGTCTTACT ACTTTNACCG 60
CGATGATGTG GCTTTNAAGA ACTTTGCCAA ATACTTTCTT CACCAATCTC ATGAGGAGAG 120
GGAACATGCT GAGAACTGA TGAAGCTGCA GAACCAACGA GGTGGCCGAA TCTTCCTTCA 180
GGATATCAAG AAACCAGACT GTGATGACTG GGAGAGCGGG CTGAATGCAA TGGAGTGTGC 240
ATTACATTTG GAAAAAATG TGAATCAGTC ACTACTGGAA CTGCACAAAC TGGCCACTGA 300
CAAAAATGAC CNCCATTTGT GTGACTTCAT TGAGACACAT TACCTGAATG AGCAGGTGAA 360

AGCCATCAAA GAATTGGGTG ACCACGTGAC CAACTTGCGC AAGATGGGAG CGCCCGANTC 420
 TGGCTTNGGC GGAATATCTC TTTGACAAGC ACACCNTGGG AGACAGTGNT AATGGAAGCT 480
 TAAGCCTTGG GGNTAATTN CCCCATANGC NGTTGGGTG ACTTCNCTGG TCANCAGGGC 540
 AGTTCANTGA ATGTTNGGGG TTNCCTTTAC CTTTNCNTTA GGTNGTCCNA AACAATCCNT 600
 NAAAGTCTTT GNTTTGNACC NTCCGNNA TAANGGATTN GGGCCCGAA A 651

SEQ ID NO:478

LENGTH:617

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00534

SEQUENCE DESCRIPTION:

GATCAAGAAA GTGGGGGGAA AAAAAACAAA CGTTAAAACC TCAATCCTCA GTAGGAAGGT 60
 AGATTACATT AGGTGAAATT ATAGGTAATC TATGTATGTN CTAATGGGGT TGGAAAGAAC 120
 CTTACAGAGC ATATTACCTG ATAACTGGA GTGGGTTTGG GAGAACAAAC TAATAGGATT 180
 ATNGTNTCTC CTAGTTGGTA CCTGGGAGCA ATTGACATGC CCCCTTCAGA ACCTTAACTG 240
 TTAGTAGCAG TGGCTGTAAC AACACAAACC AGTGACCAGA GATAACAGCT TTNGGCCAA 300
 GCTGGCCTGA CGGTATGGCT GCAGGANGTG ACTGAGCAGT AGCGGTACTC AGCCAGACCA 360
 AGACGGAGAG GGGAGAGTCC ACAGCTTTCT GGAGCTAAGG CATTCTGGTG GTAGAAAAGT 420
 GTGCCNAAG CCTTCATNGG CGGGTTATAN GGTCTNAAGA TAAGTCTCCT CTTGTNTGGG 480
 ATNCCATACT NTGCTAAATA ACCNNGGTAT TANCCGGGTT TTCCNTGTAA CNGCCTCTNG 540
 GGAGGAANTG ACTNNGNAAG NTGGCACAGG TNTTTAAGCN TNAATGGAAA GGGNNAAATC 600
 CTNCTCAAAN TAGAACN 617

SEQ ID NO:479

LENGTH:569

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00535

SEQUENCE DESCRIPTION:

GATCTGTCAG CTGCTTAATT AATTGAAACT TCTCTGTCAT TGATGTTGCA TTTCCAAGGA 60
 GATAATCTCC TTCTTGGTGC CTAATTTTCT AGATGATAAT AGGCTAGTTT TGATTCTTG 120
 CTCATTTTCA GAATAACTTT CCAGGAAGAG ATGGCATTTA GAACTTCAGC TTTGGTGCTC 180
 AGGTATAAAG CCAATTAAGG TACAATTGTA CCATAAAGGG AACAATCTGT TTCTGATTGC 240
 ACAGTTTCTA ATTTTAAAA CTGNNGTGGT TTGCATTTC TAAAAGGCAA AGTTTACAGA 300
 NCCATAAACA TTCTCAATTT TCTTTATGCT AGACATATAA ATTTATTTT CCAACTGTA 360
 ATAGGATTTG GGGTAAAAAG NTGTCTCAG GTNCCCTCNC CCANTTTGCC AATGGGGNAA 420
 AAAAAAGGCT TAATTTTTC CATNNTACT TNAATTTTC TAAAACCCNT GGTAACCCCC 480
 CATTGGNACC CCNATTTTTC CANCTTTAAG GGTCTNGCAT NGGCNGGCTT TTTNAATTNN 540
 CCCTGGGGGG GTTTTNCCTG GGAGGGCCN 569

SEQ ID NO:480

LENGTH:556

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00536

SEQUENCE DESCRIPTION:

GATCCTGAGC NTGGTGCTGT GCTGTGGCAT CCGGAACAGC TCCGTGTACT GAGGCCCCGC 60
 AGCTCTGGCC ACAGGGACCT CTGCAGTGCC CCCTAAGTGA CCCGGACACT TCCGAGGGGG 120
 CCATCACC GC CTGNTATAT AACGTTTCCG GTATTACTCT GCTACACGTA GCCTTTTAC 180
 TTTTGGGGTT TTGTTTTTGT TCTGAACTTT CCTGTTACCT TTTCAGGGCT GACGTCACAT 240
 GTAGGTGGCG TGTATGAGTG GAGACGGGCC TGGGTCTTGG GGA CTNGAGG GCAAGGGGTC 300
 CTTCTGCCCT GGGGTCCCAG GGTGCTCTGC CTGCTCAGCC AGGCCTNTCC TGGGAGCCAA 360
 TNGNCCAAGA GACTCAGCTT GGNCAAANTT GGGGGGGNTN TGTNCAACCA NGCCCGCENN 420
 TCCTNTTNGG GTTAAAAAGT TTAACCTTGT TTCCCTTTCT NGCCCCGGTT TTGGAGAACC 480
 CGANTTTTTT GGGGNAATTT TTTGCTTNA ATNAACTTNT NCCTTTTTTA AAAANGTGGG 540
 TTTAAACTN TNAATN 556

SEQ ID NO:481

LENGTH:551

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00537

SEQUENCE DESCRIPTION:

GATCTACTGT CTTTGTTCAA AGGTCAAATA AAAACCTAGT CTCCTTTTAT TCTACTTTCT 60
 ATTCTTAGCT AGAATGAAAC TCAGCATATA TACACTTCTG GACATAATAA TATTGAATAG 120
 TAATTACCTT TACTAGATGA AAGAAATTTT CATTACAAAC TTAAATCATG TAAAACTCAA 180
 CAACTCAGAT TCCTGGACCT GGTGTCCTGG NTGGGTCCAA GGTGATTTTA CAGAAGNAAA 240
 AANCAACTNA AGCATTCTGG TGGCAACATA GAGATTGTAG GCTGCTTCTA AGGAAGTNAT 300
 TAACAATTNG GAAATTCNA AGTAGGATGA GAGTAGTAA CTGGATACGA GTGAAGTTTA 360
 TATCCAAGTT CAGNCTCAAA GGCATNATTA TGATTNGCTT CTCCCATGT CTNCCATGGN 420
 CCTGCTTCTC AAAGTTTTTC TNATCNATCA CACTGCTGCC TAAGTGTCT GAGNATGCAT 480
 GNGGTNTTCA ATTCAGCGTN NTNTNAATCN GGNNTANCTN TGGATTGGGA TGGGGATACG 540
 GACNTTAAGG N 551

SEQ ID NO:482

LENGTH:520

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00538

SEQUENCE DESCRIPTION:

GATCTTAATT TTGAAATTGA CATGAAAGTG TCATATCAGT AATCTGTGAA CCACCAGTCC 60
 TTGGTACCTA TCAGAGGGTC AAAAATCAGC ATTAATATA ACCAAAAAAC TTTATAGTGA 120
 CTGATTCAAA TTTGAATACT GGTTTTAGCT AATGTAGTAG TAATGAACTG GTTTGGGGGT 180
 AAGATTTTCC TGGTATCTTA TTGCTGTAGA AATTTTCCTT TAACAGTTAC AGTGTTTTCT 240
 TCCAATCCT TCACTTCTCT GTCCTGGCTT GTAAAGAAAA CATCTGAGGA CTGAGGGGTC 300
 ATATTTGAAT TGCTCTNTAT AATACCATAG ACTACTCATT GCTTAGACTN TACTAAGCTA 360
 GAAATCACAA GAGCATAAGC NACTCTNAAA ATTNATATNA TGNGAATGTA AAAGGTACCT 420
 GNCTGCAAA ATCTNGANCN TCACTTTGGC TCAAGTNTCN NGTTAACCTG TNNNNTAATA 480
 CNGNNATGTG AATTNGGCCA CCAGGTCCAT GNTTGGCAAA 520

SEQ ID NO:483

LENGTH:517

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00539

SEQUENCE DESCRIPTION:

GATCATGCTT TTNGTGCCTG TCACCAGGTC TCCCAAGTGC ACTCATCCAG GTCAGTGCTC 60
AGATGTGTTT AAGGAGACCC TATATTCAGG GAAGTTGCGT GAACACTGCA GTGGGGAGAA 120
TTGAGAATAG TCAGGCCTAT CAGTCTCACA GAATCACCCC TCTACCTTG ATATTCCACT 180
TAGCTGTAGA GTCCATCTGT TTGTCCATCT GCTGAAATGA GAAAAGAAAA ATTTATGCAC 240
TGATTTAAAA CAAACCAAAA AAAAAGAAAA AAACAAAAAA AAAATCCNT CCTTCTNGC 300
TGACCAAAAN TGTGCAGTTA ATNCTGGGNG CTTGAAANTG CAGTGGTGAA TNTGGACCA 360
GCCTGTCTGT ATATCTGGTA GCTCTTTTCT GGCTTNGTTT TTNCTTACCA GTATTCNGGC 420
CTAACGTTTT GCTTCGGGNN TGGTAATATN NCCTNGNAAG NACANCNGTG GGTGTGGAA 480
ATGGGTTNGG CAAAANGGAA NTTCCNGGGG TTTTGGN 517

SEQ ID NO:484

LENGTH:515

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00540

SEQUENCE DESCRIPTION:

GATCTTCTGG CTCTACCACC ACAAGATATT ATCCTTGCAT CTNATGTGTT CTTTGAACCA 60
GAAGATTTTA AAGACATTTT GGCTACAATA TATTTNTTAA TGCACAAGAA TCCCAAGGTC 120
CAATTGTGGT CTACTTATCA AGTTAGGAGT GCTGACTGGT CACTGAAGC TTTACTCTAC 180
AAATGGGATA TGAATGTGT CCACANNGNT CTTGAGTCTT TTGATGCAGA CAAAGAAGAT 240
ATAGCAGAAT CTACNTTCC AGGAAGACAT ACAGTTGAAA TGCTGGTCAT TTCCTTTGCA 300
AAGNACAGTC TCTGAATNAT ACCNACAACC NGTNCTGGGA CAGTATCAAT ACTGATGAGC 360
AACCNGGCAC ACAAATATG AGCAGACCAC TTCAGCTTGA GGAATGCAGT GGGTCTGAGG 420
ATGGTCAAGT CTGTTTGCCT TAGATTTTGN TGCTCACTTG CCACACTTGA AANCTNNTT 480
GGAACAAAAN TTAAATTCG GGTTCCAAG GTAAA 515

SEQ ID NO:485

LENGTH:510

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00541

SEQUENCE DESCRIPTION:

GATCTGCAGC TCTCAGAGGA CGACTGAGGC AGCCCATCTG GGGGGCCTGT AGGGGCTGCC 60
GGGCTGGTGG CCAGTNTTTC CACCTCCCTG GCAGTCAGGC CTAGAGGCTG GCGTCTGTGC 120
AGTTGGGGGA GGCAGTAGAC ACGGGACAGG CTTTATNATT TATTTTNNAG CATGAAAGAC 180
CAAACGTATC GAGAGCTGGG CTGGGCTGGG CTGGTGTGGC TGCTGAAGCC CCACAGCTGT 240
GGGCTGCTGA AGTCAGCTCC GCGGGGGAGC TGCCCTGACG TCAGCAGACC GAGACCAGTC 300
CCAGTTCCAG GGGGAGGCCT GCAGGCNCTG GCCCTTCCAC CACCTNTGCC CTNCGTCTGC 360

AGANCTTGGT NCATCTGCAC CAGGCTCTGC TTNACTCNNN NANAGTNTTT GGAAATTTGT 420
 TCTNNTCCTN TGAAAGTCAC ATTTGNTTNT AAAAATTTTG TGGNTTGAAT CGGAAACGGG 480
 AAGNAATAAA GCGGTGGGNG GNAGGGCAAA 510

SEQ ID NO:486

LENGTH:507

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00542

SEQUENCE DESCRIPTION:

GATCCTTACA TCTGCCATT CTGTGGTTAG TCAATGGCTT GCAATAAATG TGCAAACCTGC 60
 ATCTATAGGA AACATTTTGG TGATTACGGA ATACTTTAGT TGATTGCTGA AAATATTGAA 120
 AGGTCTTCAT TTTACAGTGA TGAGTACATA TGCATGTTTC GGGGACTTGG CCCTTCTGAT 180
 GAGGGGGCCCT CGGTACTCTG GATAACGAAG CTTGTGCAGA GTGGTAACCA TGCTTACACA 240
 CTAAACTATA ATATAAAGGA AATGAAGCCA TGTTAATCTG AGAGCAGTGT CGCCATAGTT 300
 GTGTTGTTTA CAATACTCTA TAAATGGGGT TCCTGTTGCC CTGTAATTAA CCTGCTGCCC 360
 GTAGAGGCCT TTCCAGTTCC TTTTCTGTCC TTNCCCCTTT CTTAACACAA GCTCAAATTT 420
 TCCTAACTNG GTTTTNNATT TGGAGGNCTT TAAAANGGN CCATTTTCAA TACCATNAAA 480
 ANTAACCAGG GCTTTATAAT ANTAAAA 507

SEQ ID NO:487

LENGTH:155

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00543

SEQUENCE DESCRIPTION:

GATCCACTAC CGGAAGAAGA AACAGCTCAT NAGGCTACGG AAACAGGCCG AGAAGAACGT 60
 NGAGAAGAAA ATTGACAAAT ACACAGAGGT CCTCAAGACC CACGGACTCC TGGTCTTAGC 120
 CCAATAAAGA CTGTTAATTC CTCAAAAAAA NGAAA 155

SEQ ID NO:488

LENGTH:499

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00544

SEQUENCE DESCRIPTION:

GATCTTAAAA ACTAACTTCT AAGATGATTT CATCTTCTCA TAGTATAGAG TTTACTTTGT 60
 ACACGTTTGA AACCAACTAC TGTAGAAGAT GAGGAATCTA TTGTAATTTT TTGCTTTATT 120
 TTCATCTGCC AGTGGACTTA TTTGAAATTT TCACTTTGT CAAATNATTT TTNGTATTAG 180
 TTTTGTATGC AGACATAAAA ATAGCAATCA TTTTAAATNG TCAAAATTTT CAGATTACTG 240
 GTAAAAATTA TTTGAAAACA AACTTATGGG TAATAAAGGC TAGTCAGAAC CNTATACCAT 300
 AAAGTGATGT TACCATACAG ATTAATATGT AGCAAAANTG TATGCTTGAT ATTNCTCACC 360
 NGTGNTAATG TTNCTGCNGT ATTCCAGCNG ACCAAACCAA TATTAAGNAT GCATCTGTAT 420
 AAAATGGGNG CCTATNGGNT AATGGGAATN ATNNGGGTAA TNGGCCTNTA CCNGGNTGGT 480
 NATAATGGNG CCCTNTGGN 499

SEQ ID NO:489

LENGTH:516

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00545

SEQUENCE DESCRIPTION:

GATCTACCCC GGACACGGGA GGCGCTACGC CAGGNCCGAC GGGAAAGGTTT TCCAGTTTCT 60
 TAATGCGAAA TGCGAGTCGG CTTTCCTTTC CAAGAGGAAT CCTCGGCAGA TAAACTGGAC 120
 TGTCCTCTAC AGAAGGAAGC AAAAAAAGGG ACAGTCGGAA GAAATTCAAA AGAAAAGAAC 180
 CCGCCGAGCA GTCAAATTCC AGAGGGCCAT TACTGGTGCA TCTTTTGCTG ATATAATGGC 240
 CAAGAGGAAT CAGAAACCTG AAGTTAGAAA GGCTCAACGA GAACAAGCTA TCAGGGCTGC 300
 TAAGGNAGCA AAANAGGGCT AAGCAAGCAT CTAAGAGGNC TTGCAAATGG CTGCTTGCTA 360
 AGGCACCTTC AAAGGGCAGC ACCTTAGGCN AAAAGGATTT GTNTAAGCCN TGTTGAAAAG 420
 TTTCCAGCTT CCCCCTNTTT TGGTTGGGAA NNGGNTAAAC CTTGGCAGGG TTTTGNTTTT 480
 TTTAATTAAN AGGTTTGGGG TTTTAANCTN TTAAAA 516

SEQ ID NO:490

LENGTH:497

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00546

SEQUENCE DESCRIPTION:

GATCAAGCTG ACAGACCCNN CTCTGCTCTG ACCTGGAGGT CTCCACTCTG GTCAGCAAGT 60
 ATCCAGACAT CAGGGATGAC CACATCGGTG CGCTNCTGGC TGTGCGTGGG GACGCCAGCC 120
 GTGACATGAA GCAGACCATC ATGGAGACCC TGGAGCAGGG CCCAGCACAG GCCAGCCCCA 180
 GCTACGTGCC CCTCTTCAAG GACATTGTGG TGCCCAGCTG AACGTGGCCA AGCTGCTCAA 240
 GTAGCCTCCG CGGNCTGCCT GCTCGCCCTC CACAGCTNNG TCCTGCTTTA GAACGCGGGC 300
 AGTNATTGTC TCTTGGCACA CGTGTCTTTT TAGTGACGGC TGTNTTATAG TGCANTGTNA 360
 TGACNNGGTG TCGTGCAGT GANGTCNGAG GGCACGTGCG GAGGCNGTAN TTTGCTGTAA 420
 AGGCTGTGGG TTCAGNGTTT NCNGACAGCG TTNNTGGGT GTTGTNTTTC AGNGGTGAAG 480
 TGTTNNGGAA AGNGNCN 497

SEQ ID NO:491

LENGTH:494

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00547

SEQUENCE DESCRIPTION:

GATCCAAGAA ACAATTCTG ATAATTGTGT GGTGATTTN TCAAAAACAT CCTGTTCTTA 60
 CTGTACAATG GCAAAAAAGC TTTTCCATGA CATGAATGTT AACTATAAAG TGGTGGAAC 120
 GGACCTGCTT GAATATGGAA ACCAGTTCCA AGATGCTCTT TACAAAATGA CTGGTGAAAG 180
 ANCTGTTCCA AGANTATTTG TCAATGGTAC TTTTATTGGA GGTGCAACTG AACTCATAG 240
 GCTTCACAAA GAAGGAAAAT TGCTCCCACT AGTTCATCAG TGTATTTAA NNNNAAGTAA 300
 GAGGAAAGAA TTTCACTGAT GTTTATACTA ATAAGTTTGC TAGTACAGTG TCAGTTATTT 360

AAAGTGGTAA TGCCCGNTAA TGTCTTTTAA ATGTTTTGAG GGATGTTTTA AAATACATGC 420
NATTGTCTTC ACGGAGGAGG GNTGTAAAAA TTANTGGGCC AATAAATTGC GGGTGGGAAN 480
CCNTNTTCTT NAAA 494

SEQ ID NO:492

LENGTH:489

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00548

SEQUENCE DESCRIPTION:

GATCTTGACG AGGCTGCGGT GTCTGCTGCT ATTCTCCGAG CTTGCAATG CCGCCTAAGG 60
ACGACAAGAA GAAGAAGGAC GCTGGAAAGT CGGCCAAGAA AGACAAAGAC CCAGTGAACA 120
AATCCGGGGG CAAGGCCAAA AAGAAGAAGT GGTCCAAAGG CAAAGTTCGG GACAAGCTCA 180
ATAACTTAGT CTTGTTTGAC AANGNTACCT ATGATAAACT CTTTAAGGAA GTTNCCAAC 240
ATANACTTAT AACCNAGCT GTGGTCTCTG AGAGACTGAA GATTCGAGGC TCCCTGGCCA 300
GGGCAGCCNT TCAGGAGCTC CTTANGTAAA GGNCTTATCA AACTGGTTTC AAAGCACTGA 360
GCTCANGTAA TTTACACCAG AANTACCANG GGTNGAGATG CTCCAGCTTG CTTGTGAAGA 420
TGCATGATTA GGTCCACCAG CTGTACATTT GGAAGAANTA NANCTTNTGT TAAATCAATG 480
GNGTNAAAA 489

SEQ ID NO:493

LENGTH:487

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00549

SEQUENCE DESCRIPTION:

GATCCTCTGN CACGGGATAA ATTTNCAGGN GAAGAGTGAG GTTGTCATGG CCTCAGCTAT 60
GCTTCNNGGC TCTCCCTCAA GAGTGCAACC TTGGCTAGAG AACTCACAGC TCTGGGAAAA 120
AGAGGAGCAG ACAGGGTTCC CTGGGCCCAG TCTCAGCCCA GCCACTGATG CTGGATGACC 180
TTGGCCTGAC CCTGGTCTGG TCTCANAATC ACTTTTCCA TCTGTAAAAT TGAGATGAAT 240
TTTNGTGTG AAAGTNCTC CNNGAGCAGA TGTCTAGAA GGTTTTAGGA ATAGTGACAG 300
AGTCAGGNCA CCCNAAGGGC CATGGGGAGC CAGCTGACCT GCTTNGCCGA AGGATTCTG 360
ACAGACTATC TTTGGGGATG TTTTCAAAGA AGGGATATAG GTTATTGACN TNNGGGCATT 420
TAAAGNAAAT TNTNTCTCGG GGATTAANTT TTTAGGANAA TNAAAGCTTT NGTGTCTANN 480
GGCAAGN 487

SEQ ID NO:494

LENGTH:481

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00551

SEQUENCE DESCRIPTION:

GATCCCCAGC TGCCACTGAA TCTGGCTGCC CTTCAGGCC ACCTGGCCCA GGAGAACCGT 60
GTGGTGGCCT TCTTCAGCCT GGCTCTACTG CTTGCCCCAC TGGTGGAGAC GCTTATTCTA 120
CTGGACCGGC TGCTGTACCT TCAGGAACAG GGTTCATG CTGAGCTCCT GCCCATCTTC 180

AGTCCTGAAC TCTCTCCCAG AAACCTGGTT CTGGTGGCCA CCAAGATGCC CCTGGGTCAG 240
 GCTCTTTNTG TTCTGGAGAC TGAAGACAGC TGATGCAGCC TGAGGAGACA TCTCAGACCC 300
 CATCATCTGA AAGTGNCCAG AGAGCACAGT GGCAGAGTAC ATCTNATCCA GAGAAACAGC 360
 ATCCTGCATC CTCCAGAGTC CTGGTTCCTT CAAGTTTCAT CNCTTTTNTC TCCTTTCCAT 420
 GGGNTTATGT AAATACAATT GTAAAGTTTT AATTAAATTA AAAAATTGGG TTATCTGGAA 480
 A 481

SEQ ID NO:495

LENGTH:472

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00552

SEQUENCE DESCRIPTION:

GATCTAAGCT CCAGGCACGC CTGAAGATGT GTTGCTACTC TNACATCCCG AGTTTCTGTC 60
 CACACATTGC ATGCACAGCG CCCACACAT TGGATACTGT TGTTACGAT AATTTCTCCC 120
 GTTTTCAGA GCATTTAACA TAGCTTGGAG GCGTAAATG GCTCTGTATT TTAATAACAC 180
 AGAAACATTT GAGCATTGTA TTTCTCGCAT CCCTTCTCGT GAGCNCTTAG ACCTTTTNTC 240
 ATTTTAGTCG GATTTTGTGTT TGGAAATTTG CTTTNGTATG AACACTCAGC AGAAAAGTAC 300
 TTACTTCTNG CCAGTTATCT ATTAACCAAA ACCNTTGATT TGTAAGTTTA AAGNTTAACC 360
 GNCAAGTTC TNTNCATAAC TGCCTTGCC AGTNNGGGGT NGTNCCGGIN CTGGTTAATN 420
 GCCTGTGGCN TTTTNGGTGG TTTGTGNTTG GTNTTACNT GNGCANTTAA GN 472

SEQ ID NO:496

LENGTH:461

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00553

SEQUENCE DESCRIPTION:

GATCAACCAA TTTTNTAAA AGTTCAGTCG AAAGCTTTTA AGTATAGCTT CCTCCCTTGA 60
 AAAAAATGT AAACATGAC TGCTGAGTGA TAAACACTG TGGTGTGAAA GTNTCATCTT 120
 CACTGCCAAT CAGGCAAAGA CCGGAAAGAT TTGCATTTTA TTATGTCTGT CITATCATGC 180
 AATGGAAATN ATGCTTTTNG TAAGTATGCA TCTTACCAAT GATGTAACGG TTAATACCN 240
 TTGAATGTTT TAATAACCAA GTNGCTGCTG AACTTATACT AAATCAGGGG CCAAAAAACT 300
 NGCTCTNATC NNCTCAAATN GTATNCNATA TCCATTAATG TATCAGTTAT NCCAAAGCCT 360
 TCAGGTGGAG GGGTTTACCA CCNTCCTAGG TCGTTCAACC AGGTTTTGTG AGGAATGCAT 420
 TCAAAGTGGC TNTATAAAG ANGATTTTCT TTAGCATGAA A 461

SEQ ID NO:497

LENGTH:459

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00554

SEQUENCE DESCRIPTION:

GATCCCAAAA TTCCACTTTT CAACACAGAT GTGGACAACC TAGAAGGGAA GACACCACCA 60
 GTTTTTNCTT CTAAAGGCAA ATACAGGGCT CTGAAATGG ATTTTCCTCT ACCCCCTTCT 120

ACTTACGNCA CCATGGCCAT TCGAGAAGTG CTAAAAATGG ATACCAGTAT CAAGAACCAG 180
 ACGCAGCTGA ATACAACCTG GCTTCGCTGA GCAGTACCTT GTCCACAGAT TAGAAAACGT 240
 ACACAAGTGT TTGCTTCCTG GCTCCCTGTG CATTTTTGTN TTAGTTCAGA CTCATATATG 300
 GATTTCAAAT CTTTGTAAATA AAAATTATTT GTATTTTAA GTNTTTATTA GCTTAAAGAA 360
 ATAATTNGCA ATATTNGTAC ATGTACACAA AATNCNGGAG GTTCTTANTT TTAGCTCAGG 420
 NTATAATNA GTCAAATNCN NNGGTNNNGG NTNNGNTGN 459

SEQ ID NO:498

LENGTH:481

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00555

SEQUENCE DESCRIPTION:

GATCCAGCAG AGAAGGATGA AAAGGGCATG CCTGTGACAG CTCGTGTGGT GTTGTTTTT 60
 GGTCTGATA AGAAGCTGAA GCTGTCTATC CTCTACCCAG CTACCACTGG CAGGAACCTT 120
 GATGAGATTC TCAGGGTAGT CATCTCTCTC CAGCTGACAG CAGAAAAAAG GGTGCCACC 180
 CCAGTTGATT GGAAGGATGG GGATAGTGTG ATGGTCCTC CAACCATCCC TGAAGAAGAA 240
 GCCAAAAAAC TTTTCCCGAA AGGAGTCTTC ACCAAAGAGC TCCCATCTGG CAAGAAATAC 300
 CTCCGCTACA CACCCAGCC TTAAGTCTCT TGGAGAAGCT GGTGCTGTNA GCCAGAGGAT 360
 GTCAGCTGCC AATTGTGTT TCCTGCAGCA ATTCCATAAA CACATCCTGG GTGTCATCAC 420
 AGCCAAGTTT TTTANGGTTN CTATACCAAT GGGTTTATTT AAATGAAAAT GGGCACTTAA 480
 A 481

SEQ ID NO:499

LENGTH:453

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00556

SEQUENCE DESCRIPTION:

GATCCAGATG CAGAGGCCAG GATGTGGGCC CAGCCCTGTG CCAGGAGGCT GGCTGGAATA 60
 AAGGTACAGA TAGAGGCCTC ACCCCCTCTG GGACCACTGG CACTCAGGCT GTTGCCAGCC 120
 TCAGAGCCCA CCTGCCCCCA GGGCCACAGC TGCATCTCCT GCCCTGCTGT CATTACAGGG 180
 ATGGGCAGGC TGGCATGGGG GCACCCGCTG CCCCTGCCTG GNTGTTGCTG TGTATTCCTG 240
 CCGGCCAGGG GCACTGCCAG GACCACGCCT CCNTTTTAT ATCCNGATTC TTAAGTTCTG 300
 CTATTGTGGT ATTCTGGTGG AGAAAAAGA CCGNGTGGCT GTTTTGAAC TGCCTGGAAC 360
 CTAAGACCTT GAATTCTTT CCCCCAAGG GAAAATCTAT ATGGAAACAT TTATTTAAAT 420
 ACAGGATGAA GTAATTAAAA GNTTTAATTC AAA 453

SEQ ID NO:500

LENGTH:446

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00557

SEQUENCE DESCRIPTION:

GATCAAAGTT GGCAAGGTGC GGAATCGAGA CATGGGCGGC TACAGACCAC AACCGACTTC 60

ATCAAGTCTG TCATCGGTCA CCTGCAGACT AAAGGGAGCT AGAGCCCTTT ATTTCTTCCA 120
 ACCTTGCAAG GACCACACTN CCCATACCNT TCAGTGCAGT GTACCAGGGA AGAGCCTTGT 180
 GCCTCTAAGC AGTGGACCAT GGTCACCTTG CTGGGTAGAG CCTAGGTTGT CCTTGGGCCG 240
 GCTTCCTTAG GGGACAGACT NTTGGGTGGT GATGGGGATT GTAGGATGGA GCCAGGCACA 300
 TGGATGATGA TGATTCTCCC NCACAGGTTT GAACCTCTGA CATGGGTGGC TATGCTACTN 360
 GCNATGCTTA NTGAGGNTGT CATTGCTGCT TTNCCNAACC ATAGGCCTGT CATACNNTGT 420
 AAGNGTCAA TAAGGACATG ACCAAA 446

SEQ ID NO:501

LENGTH:434

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00558

SEQUENCE DESCRIPTION:

GATCCAATTC AGGTTAGGCT TGTGTTGATTT TTTTTCAG AAAATGTATT CCATAAAGTT 60
 TGTACTTAGA CCAGACGGGT GTACTAAGAA TCATTCATGA GTAAATGTGT GTTGAATATC 120
 TACCCTTGAC CTTTTTTGA GAAATAGAGT AAACACAGTC CCTGTAGTCT GACAGCTAAT 180
 GGGGAGAGAG GGTAGACTTT TCATCGAATT AAATTTCTAC ATGCACCTTT CCCCAGAAA 240
 TCTTACTCAT GGCTGGTCTC AAGTAAGTCT TTATTGAAAA ATATNGACAT ATCTNCTTCC 300
 TCTTCTTCT CCTCACTGTC TTCCTTTTAG TAGTTAGGCA GAGTTAATAG GTAAGAAAAA 360
 TTATCTGCAT TTATGTGTAG TTTGTAATCT ACTAAAGGGG TTCTAGAATA AATGTNGNCA 420
 TNTNGTAACN GAAA 434

SEQ ID NO:502

LENGTH:430

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00560

SEQUENCE DESCRIPTION:

GATCAAAACAG GTTCAAAGTA AAACGTAAAA TTTACATTT NTTTTAAAGA ACTCTTAAAG 60
 TGTAACAGTT ACGCCATACT TCATAAGTGG TAAAGAAAGG TATAAAATTT GGAAACATTT 120
 TGTTGGGCAT AGTAGTGATT GGGTGAAAAG GATAAATTAT ATCAAAATGA GAATGTNCTG 180
 TAATTGGAAG TAGGGAGCTA AAGGATGTTT CTTTCAGTTT AGTAGAACTG GAACGTTTTA 240
 CTATTAAACA TGGCTTTTAT AAATNCATGG TCCAATAATT TTATTCAGTG TTAGTATTTA 300
 ATTCACTGTC AGCTTATTAA TGTTTTCTGT ACCCATTAAT GAATTTTAAA TTACAAAAAA 360
 TTGTCTAGCA GCTTCAGTT TAANAAATGG AACCTAGGCC ATTAATAATTA AATTTGGTAA 420
 ATTTTTTAAA 430

SEQ ID NO:503

LENGTH:428

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00561

SEQUENCE DESCRIPTION:

GATCCTAAAT GTGTTGCTGA AATCAGGCAG CCCGAGCCTC TGGTCTCTCC AGAGAGCCCG 60

TNTTCACATT TGTNTATTCC TCAGCACTCA CCCGAAACTG AACAGATGGG GAGTGGTCTT 120
 GATTGTCAAG ATAAACTGG TGAAGAAAGC TAAATGCTGA GAAACTGAGC ATCTATTGTG 180
 GTGTTTAAGC TTAGCTGGGT CCTTTCTAGT TTGTTTTTAC AGCTTACTAG GTGAAGTAGT 240
 TTGCACTATT TTNGCAATAA ATTCATGGAA AACCTAACAG TTACTIONT NGTTTCTNAC 300
 TGTGTGTATA TAANCTAATA CTAAANGTNT GGCATAGTGT TTNTGCACCT NCNTACATAA 360
 CCNCTAACAT GCACAGAATG CTGGTAAATN TGATAAANTA TGANGTGANT GATGATNNGA 420
 TANAGTGN 428

SEQ ID NO:504

LENGTH:422

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00562

SEQUENCE DESCRIPTION:

GATCCTCACC CTCCTGAGGC CCAGTGGGGA AGAATGAACA TGGCTTCATC CAGGTAACT 60
 NATGCTGCCA TTGCCCAGC CTCTCCATC CCAGCCCTGT CAGTNAGCCC AGGTCTGGTG 120
 CAACTNCTGC AGGATGCCTG TAGTAGGGA CTCTGGAAGT GTATTGGGCT GAGGTGGGAT 180
 TTTCCCTCCC CACAGTGCAC TGAGCAATGG AGGGTGGTGA GGGAGCCATG CTGCTGAATT 240
 CTGGTTGGCA TTTCCCATT ATGTAAATG GGGTGTGGG TAGGGCAGAC TCTGCTGGG 300
 TTTGGTTGTA AGATAAACCT GGAGGAGAAG CACAGTTGTC CCATTGAATT ATTTGAGCAA 360
 AAACTACTGT AAATAACTTT TTTGGGCTNT TGTCAAATAA AATTTTTTTT TGTNTTTA 420
 AA 422

SEQ ID NO:505

LENGTH:417

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00564

SEQUENCE DESCRIPTION:

GATCTGATTC AGAAGGGCGT CATCCAACAC AAAGAGAAAT GCAACCAATG AAGAATCAAG 60
 CCACTGAGGC AGGGCAGAGG GACCTTTGAT AGGCTACGAT ACTATTTTCC TGTGCATCAC 120
 ACTTAACTCA TCTAACTNNT TCCCCGGACA CCCTCCACCT CTAGTTGTTA CTAAGTAGCT 180
 GCAGTAGGCA TTGCTGGGGA AGAAACAAAC ACACACAAA CAGTACTGCT ACTTAGTTTC 240
 TAAGGCTGCA CAGGAAGGG AAAGACTGGG CTTTGGACAA TCTAGAGGTA ATTTATATCC 300
 GCCCCAGGT GGAGCAACAT GCGATTNTGG AGGCACGGGG GTAAGTAAA GTGAGTACAT 360
 ATAGTNTTC TGGTTTCTGG GGATAACCCA TCAATAAAAG CTGCTCCTC TNGTAAA 417

SEQ ID NO:506

LENGTH:421

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00565

SEQUENCE DESCRIPTION:

GATCTTCTTT ATAATTCTAC TTTGAGTGCT GTCTCCATGT TTGATGTATC TNAGCAGGTT 60
 GCTCCACAGG TAGCTCTAGG AGGGCTGGCA ACTTAGAGGT GGGGAGCAGA GAATTCTCTT 120

ATCCAACATC AACATCTTGG TCAGATTGGA ACTCTTCAAT CTCTTGCACT CAAAGCTTGT 180
 TAAGATAGTT AAGCGTGCAT AAGTTAACTT CCAATTTACA TACTCTGCTT AGAATTTGGG 240
 GGAAATTTA GAAATATAAT TGACAGGATT ATTGGAAATT TGTATAATG AATGAAACAT 300
 TTTGTCATAT AAGATTCNNT ATTTACTTCT TATACATTG ATAAAGTAAG GCATGGTTGT 360
 GGGTAAANCT GGGTTTATTT TTNGTTCAC AAGTTAAATA AAATCCATAA AACCTTGGAA 420
 A 421

SEQ ID NO:507

LENGTH:413

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00567

SEQUENCE DESCRIPTION:

GATCCCANAC TGGTCNTTGA ACAGACAGAA GGANGTAAAG GNTGGAACT ACAGCCAGGT 60
 GTGTACTGAA ATNAGGGCAG GATTAGAGGA AGGGTGGAGG GTCCTAACAG AATTGGGCAT 120
 AGGAGGTCAG GGGATAAAAC ATCCCTTGCC CCCTCCTCTG AATCCAGGNC CTAGCCAATG 180
 GNCTGGACAA CAAGCTCCGT GAAGACCTGG AGCGACTNAA GAAGATTCGG GCCCATAGAG 240
 GGCTGCGTCA CTTCTGGGGG TGAGTGGGGG GTCTCATCTC CCTGCCTACC TCGACTCAGC 300
 ATTCCTCCTA CTCGNTCTTC TTNTTTTCCC AACCTTTTGG TTTCTTGCTT GTNCATGACC 360
 TNGTGACTTN TTCNTNTTTT TACCNTGCAN GCCTTTNGTN GTCCTAGGGN CAN 413

SEQ ID NO:508

LENGTH:407

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00568

SEQUENCE DESCRIPTION:

GATCTNAGGG TGAACCACTT CATTCTGCAG GGTTCCTCCCT CCCACCTTAA AGAAGTTCCC 60
 CTTATGTGGG TTGCCTGGTG AATGGCCTTC CTTCCCGCCA NAGGGCTTGT AAACAGACCG 120
 GAGAGGACAG TGGATTGTTT ATACTCCAGT GTACATAGTG TAATGTAGCG TGTTTACATG 180
 TGTAGCCTAT GTTGTGGTCC ATCAGCCCCT CACATTCCTA GGGGTTTNG ATGCTGTAGG 240
 TGGTATGTGA CACCAAAGCC ACCTCTGTNA TTTGTNGTGA TGTCTTTNCT TGGCAAAAGC 300
 CTTGTGTATA TTTGTATATT ACACATTTGT ACAGAATTN GGAAGATTTT CNAGTCTAGT 360
 TGCCAAATCT GGCTCCTTTA CCAAAGGAN ATTACCCTTG NGGNAAA 407

SEQ ID NO:509

LENGTH:402

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00569

SEQUENCE DESCRIPTION:

GATCAAACAG TTTCTGGAGT GTGCCCAGAA CCAGGGTGAC ATCAAGCTCT GTGAGGGTTT 60
 CAATGAGGTG CTGCANCAGT GCCGACTTGC AAACGGATTG GCCTAATGAA GAAGTTCAAC 120
 CTGGAGAGAT GGAAATCAG CTCTCATAAC TANGTTAATT TAGTATAAAA NTAGAATTGA 180
 TAGTGAGGGT ATAAAGTGTA ACCATCAGTT AAACCTCTCC TGTCATTCTT GGCTTCCTTG 240

CTTCAGANTT GAAATGGAAG TGGGGGTGTC CCTACTCTGT AGAATCTGGG NCTGGGCAAA 300
 TGTTTGTGTTG GCCTCCTTAA ACTAGCTGTT ATGTTATGAT TTTTNTTCTT TGTGAGTTAA 360
 TTAGGAATAA AGTCATTTTC TTTCCAAGGG TATGGTTCCA AA 402

SEQ ID NO:510

LENGTH:396

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00571

SEQUENCE DESCRIPTION:

GATCATGAGA AGGAATGGAA ACTAGGCCGG TGCATTTTAC GGTTCCTGA GATTCTGCAA 60
 AAGATTTTAG ATGACTTATT TCTCCACACT CTCTGTGATT ATATATATGA GCTGGCAACT 120
 GCTTTCACAG AGTTCTATGA TAGCTGCTAC TGTGTGGAGA AAGATAGACA GACTGGAAAA 180
 ATATTGAAGG TGAACATGTG GCGTATNCTG CTATGTGAAG NAGTAGCTGC TGTCATGGCC 240
 AAGGGGTTTG ATATCTGGG AATAAACCT GTCCAAAGNA TGTAATCCTT CATAGGTTTG 300
 ACACTGTGTG TTTTACCCAA GTGGCCATTG GNACTGTTTG CTTTTTTACA ATCATGTGGG 360
 CACAAGCNTA AGAAAGGAAA TTNGCAACCA GGGAAA 396

SEQ ID NO:511

LENGTH:384

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00572

SEQUENCE DESCRIPTION:

GATCCAATCA GATCAGAGA ATGTGGATAC AGAATAATGT ACAAGAAAAG GACTAAAAGA 60
 TTGGNCGTTT TTNATGCTCG ATGAATGCTG GGAATTCAGA GGAATGTNTT CACTTATACT 120
 TGGATTTGCT CTCTCCCAT TTCTGATTGT NGTATAGCTT TCGATTTTNC TTACAGTAGT 180
 TCCCCCTTAT CTNCGGGAGA TACATTCCAA GGCCCCCAGT GAACTCCTGA AACCTCAAAC 240
 AGTACCAAAC CTTTATACAC TGTTTTTTCC ATATATATAT ACCTATGATA AAGTATAATG 300
 TATANNTTAA GCATAGCAAG AGATAATAAT AATGTNATAG NCCATTGNTA CNANCTATAN 360
 TAANNGGTTA TGTGANTGTG AAAA 384

SEQ ID NO:512

LENGTH:383

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00573

SEQUENCE DESCRIPTION:

GATCAGAGCA AAACATGCAG AGCCCTTAGC AGAAACCCAC TTTAATGCAT TTTCTTCATA 60
 TCCCTAAAGT TCCTTAAAAA TATGTGACAA TGCATCAGGA AGAGGAGAAC TGAAGAGTAG 120
 AAGTTCCCTT GCAGATTTTT TTATCAGTGA CATGTAATGA GCAATTCACA GATGAGCGCA 180
 GGCAGAGCTC TGTGTGCCGT GTACATATGG ACCGTGCTAT GATGTGTCTC ACATTGGATG 240
 ATATTCCACT TTGGGAATTT TAGTATTTGT ATATAGAAAA TGGGTTTAAT AACTCACCAT 300
 GGTTTTNATT NGTCTTATAT TCGTTATTTT TTAAGAACTCT NGTATGTGTT TTTATAATAA 360
 ANAATAAAAG TAAGCCATGG AAA 383

SEQ ID NO:513

LENGTH:381

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00574

SEQUENCE DESCRIPTION:

GATCCAAAAT CATACTGTCA AGACCATCAA ACAAACAAA GAAGCTTAAG TGAAC TAAGC 60
 ACAGGGAAAA GTTGT TTTT CACTCGTTCA TTTTGT CATC TGCTTCTAGA TGCTGCAATC 120
 AAGAAGTAGC AAATGCCCAA GTTGCCATAG TGTTTGCAGG AAAAAAGAG AAAAAATAAT 180
 AAAAATAAGG AAGGAGCAAT GCCAAAAATT GAAGGAAATA TTATATAATT AANGCAAGAA 240
 GNTATCTATC CATTGAGNGA AACAATTTT ATATTATTG CTTT TAGCNG CAAAGCATT A 300
 GGAATTCTGA GATTGTTATA GCACTAAGAA GGTTT NATT CTGTGTACAC ACTGGAAAAAT 360
 TAAAATTCTG GGTAAAGGAA A 381

SEQ ID NO:514

LENGTH:381

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00575

SEQUENCE DESCRIPTION:

GATCCCCCTG GAAGAGGGAC TCCAATGGGC ATGCCCCCTC CGGGAATGCG GCCTCCTCCC 60
 CCTGGNATGC NAGGCNTTCT TTNACCCTTG GCCACAGAGT ATGGAAGTAG CTCCGCAGAG 120
 GCGTGGGCTC GATTCTCAG GGCCACGTTA CCACAGACCT GTTGT TTTCT NATGCTGTTG 180
 TTCGTGGAGT CTCATGGGAT TGTNTGGTTT CCNTTACAGG GCCCNCTCCC CNGGGAATGC 240
 GCCACCAAG GCCNTAGACT CATCTGGCC NTCCTCAGCT CCCTGCCTGT TTCCGGTAAG 300
 GCTGTACATA GTNCTTTTAT CTNCTGTGG CCTATGAAAC TGGTTTATAA TAACTNTTA 360
 AGAGAACATT ATAATTGCAA A 381

SEQ ID NO:515

LENGTH:377

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00576

SEQUENCE DESCRIPTION:

GATCTGCGTG GGGCTGGTGG TGGTTGGTGT CCTGCTCATC ATCCTGATTG TNCTGCTGGT 60
 CGTCTTTCTC CCTCAGAGCA GTGACAGCAG TAGTGCCCCA CGGACCCAGG ATGCAGGCAT 120
 TGCCCTCAGG CCTGGGAACT GACCCAGCTG GTCCTGAAGG AGAAGCCAAA TGGCTGCACT 180
 GGCCGATTCT GGTCTCCAGA GGACCTTGGT GTTGTCTCTC CCTTGACCCA CCCCAGTNAG 240
 TGCCAAAGGG CAGCCCCAAC ATGTGCACCC CTGCATTTC TGTCATGCCA CAGACTGGCC 300
 CTTGAGGGCA GCCTGTGTA CTGGCCATGC TGGGCCAGCC NCACCTGGAG CTCAGTAAAA 360
 ACTGCTGTTT GATTAAA 377

SEQ ID NO:516

LENGTH:375

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00577

SEQUENCE DESCRIPTION:

GATCACACCA GTTCAGAGAG CTACACTTTA TGGGTAACAG TTTCACCTGT NATACAGTTC 60
 CCTAGAACAT TTTCCCAAAA GTAGTGAAGT GCAAAGTGCT TAGGTTTGAC ATTTATTGTA 120
 GCAGAACAGT AATATCACAG TATGGGACAA AGGTTTACAC TTTCAGGGT ATTCTTTGGG 180
 GGAATGTAA ATACTGTAAT AAAAACATGT TCAATCATGG TAAAATGTTC AACTNGTTAA 240
 ANTTACAAAT GGNCAAAAAA NATTTTTTTC CTNATATATN GCCTAANTAC CAAATGAAGN 300
 GCTTAANCTT AAGNTTCAAT GTGAAANCGA GTAAATNTGT TCCTAAATTT GCAGNAATAA 360
 NAGATANCCN GTANN 375

SEQ ID NO:517

LENGTH:374

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00578

SEQUENCE DESCRIPTION:

GATCCATGTA CTGTTCATGTT TTTTTCAGG AACAAGCACA TCATGATTGA TTTGGGGACT 60
 GGCAACAACA ACAAGATTAA CTGGGCCATG GAGGACAAGC AGGAGATGGT GGACATCATC 120
 GAGACGGTGT ACCGCGGGGC CCGCAAAGGC CGCGGCCTGG TGGTGTCCCC CAAGGACTAC 180
 TCCACCAAGT ACCGCTACTG AGGCGCCTCA GTCTGCGCGG ATAAATGTCG TGGAGCCCTT 240
 TTTGTATGGA AACGTTTTAA GCTATTTAAA GCCTTTGGAA AATACAGGAN GTNCAGGGCT 300
 GGAGCACCTC TGAGATGGAA TTGATAACAT GGTCTTAACT CACCGAAATA AACAAGCACG 360
 TNGTGAGNGG NAAA 374

SEQ ID NO:518

LENGTH:374

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00579

SEQUENCE DESCRIPTION:

GATCTCACCG TGGGTCCGAT TAGCCTTTNC TCTGCCTTGC TTGCTTGAGC TTCAGCGNAA 60
 TTCGAAATGG CTGGCGGTAA GGCTGGAAAG GACTCCGGAA AGGCCAAGAC AAAGGCGGTT 120
 TCCCGCTCGC AGAGAGCCGG CTTGCAGTTC CCAGTGGGCC GTATTCATCG ACACCTAAAA 180
 TCTAGGACGA CCAGTCATGG ACGTGTGGGC GCGACTNCCG CTGTGTACAG CGCANCATCC 240
 TGGAGTACCT NACCGCAGAG GTACTTNAAC TNGGCAGGNA AATTGCATCA AAANGACTTA 300
 AAGGTNAAAN GGTTTTACCC CTNGGTNANT TGCAACTTTG GTTATTNGN TGGGGGATGA 360
 AGGNTTTGGG TTNN 374

SEQ ID NO:519

LENGTH:372

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00580

SEQUENCE DESCRIPTION:

GATCAGAGAG ATTAGGATTG TATTTTGACA TAGGATTGG AACCCTCTA AATGTTGAAG 60
 TTCCCTGAGA CAGCTCTCCA GCTGCTNNGC CTGCGCCAGG GGCTANGCAG CCCCTAATGA 120
 GAGGCTCTGC TCCCTTTCCC ACCTCGCCAA TGTGTTGTT GCTGCCTTTT TGATTTGTAT 180
 CCTCTGTTAT AGACATTTT NAAAAACGAT TTCCTCTTC ATTGTGCACA AGTGCTGAGA 240
 GTCTNAGGCC CCATTTCTGC TGTGTATATA TATCCTGACT CGGGGCTTTT ATTCAGCAAA 300
 CTGTTCAATC TTCTGTCAGA CAATGTCATA TTCAACTCTG TTCATATTAA ACCACTTGTN 360
 AAGCANTNNA AA 372

SEQ ID NO:520

LENGTH:371

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00581

SEQUENCE DESCRIPTION:

GATCTGGTCG CTGCCCCAGG GGGACTGATG GGCAGNGTCG CCCCTGTGGC TGGACTGTNA 60
 CCATCCCTGA TGGGGCTGA CCGCGGGAGC TGAGGAAGCG CCGCTCCACC GTCTGCCCTC 120
 CAAGGACCCG CATGGAGGCA GTGGGCTGGC AGCTTCCTGC TGCTCCGTGT NAGAGTCAAA 180
 GCACAAATCC TCAGGACGGG CTCAAGGGCC AGGGCAGCCG AGGGAAGTNC AGGTGGGGAC 240
 CACGTCTTCC TGAGGTTGGT GCCACTGCTT GGNACCGTTT GCAGTGGGGT GGCTCCCCCT 300
 CTGTTTGCTT GGTGNAGNNA GCGTGCGCTG GGGACGTGAC TGAATAAAGC ACCATGGGTG 360
 ATGTGTTGAA A 371

SEQ ID NO:521

LENGTH:382

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00582

SEQUENCE DESCRIPTION:

GATCTNTGGG ACGTCAGCTG CTGAGAGGAG CAAGCGGTAG TACCACCCT TAGTTGAGGG 60
 AGTCAGCACA GTCCTTTCTG CAGCTTCTAA CCCAGGACCA TGAAGTCAAG TGCCTAGAGA 120
 AGCCAGGCAG CNNAAGGACA AGGAATGCTG GGGGCTGTGG GAACAGGAAT GCAGATACCC 180
 TTTGAAGGAG CATTCTGCT AAAAGAAGCT GAAAATGTAG ACCTATGTGA AGTGCTCTGA 240
 TTTCTAAATA TTGTGAAGGT TAAGAAAAAC ATANATTTN GGGTCTATGG GCTAGGATTN 300
 AGNCCCACAG TTGGCCANTT TNTAGNGGT NCCCAAATGG ANTGGTAAA CCNNNGGTTT 360
 NGNTTCCTAG CCTAGGGGTA AA 382

SEQ ID NO:522

LENGTH:382

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00583

SEQUENCE DESCRIPTION:

GATCAAGAAC AATGCCTCCA CTGACTATNA CCTATCTGAC AAGAGCATCA ACCCTCTGGN 60
 TGGCTTTNTC CACTATGGTG AAGTGACCAA TGACTTTNTC ATGCTGAAAG GCTGTGTGGT 120

GGGAACCAAG AAGCGGGTGC TCACCCTCCG CAAGTCCTTG CTGGTGCAGA CGAAGCGGCG 180
 GGCTCTGGAG AAGATTGACC TTAAGTTCAT TGACACCACC TCCAAGTTTG GCCATGGCCG 240
 NTTCCAGACC ATGGAGGAGA AGAAAGCATT CATGGGACCA CTGAAGAAAG ACCGAATTGC 300
 ANAGNGAAGA AGGAGCTTAA TGCCAGGNAC AGATTTTGCA GTTGGTGGNN GTCTCAATTA 360
 AGNGTTATTT NNCCACTGGA AA 382

SEQ ID NO:523

LENGTH:367

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00584

SEQUENCE DESCRIPTION:

GATCTCCAAG CNAACTCAGC CTCCANCCAA NCTCCCTGTG GGTCTAGCC ACAAGCTCTC 60
 CAACAATTAC TATTGCACTC GCAATGGCCG CCGGGAATCT NTGCCCCCTT CCATCATCAT 120
 CNCGTGCGAG AAGTCGCTGG TGTCAGGCAA GCCAGCAGAG AGCTCTGCTG TAGCTGCCAC 180
 TGAGAAGAAG NCGGTGACTC CAGCTCCTCC CATAAAGAGG TGGGAGCTGT CCTCGGACCA 240
 GCCTTACCNG TNACACTGCA CCCTNACGGC ACCNGACTAC TTTGCCTGCT TGGATTTCTT 300
 CCAGGGGAAT GTGACCTAAT TTATGNCAA TACGTAGAGT CAGGTATCAC TTCTAGTTTA 360
 CTNTAAA 367

SEQ ID NO:524

LENGTH:365

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00585

SEQUENCE DESCRIPTION:

GATCAAGAGG AAAGAGAAG TAACAACCAG AACCCTGGA CATTTGAGCG AATAGCCACT 60
 GCCAACATGC TGGGCATACG GAAAGTACTG AGCCCATATN ACTTGACCCA CAAGGGGAAA 120
 TACTGGGGCA AGTCTACAT GCCCAAACGT GTGTAGTGAG TGTAGGAGAT AACTGTATAT 180
 AGGCTACTGA AAGAAGGATT CTGCATTCT ATTCCCCTCA GCCTACCCAC TGAAGTCTTT 240
 GGGTAGCTCT TAAGCCATAA CTAAGGAGCA GCATTTGAGT AGATTTCTGA AAAACAATGT 300
 TATTTGTTGA TTAAAAAGA AAAGTGTATT NTTATTAAAT AAAATTTAAA CATCACTTCA 360
 GGAAA 365

SEQ ID NO:525

LENGTH:396

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00586

SEQUENCE DESCRIPTION:

GATCTATGGG TTGACTAATT AAACAATAAT TCAAGTAGAG TGTCCCAGAA AAAAACCCT 60
 TGGGCTCCCT GTTTGGAGTC TGGCTGGCTC TGAGCATTGC CAATGGCCCC TACTCACCTG 120
 ACTTTGTATC CTCTCCTTTT AGAGGCTTTG CATTCTGCAC CCAGCTTCAC TAACAGTGGG 180
 CTGAAAACAT CCTTGGGTTG AGTGTTCAT TTGGGAGTTA TTTGGCCAGG GCCTTTTGAA 240
 CAGTAGTGTC CCCATGAAGT GCTAGATAAT ATATGTGTAA GAGTCAGCTT TTTTTTTTTT 300

TAAACTNTAA CACCNTTNAG AANTTTCTAA CTA CTCTTNGNA ACTGNATGGT TTANCCCGGN 360
GNTAAAAGCN GTTTTAAAA GTNTANGTTT TCCAAA 396

SEQ ID NO:526

LENGTH:360

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00589

SEQUENCE DESCRIPTION:

GATCCGCGGG CTTCCACTNC ACCATCGGAT GTTTGCCACT CAGACTGAGG GGGAGCTCAG 60
AGTGACCCAA ATTCTCAAAG AAAAGTTTCC ACGAGCTACA GCTATAAAG TCACTGACAT 120
TTCAGGCACT AAAAGAAGAA ATCAAAGAGA TGCATGGATT GCGGATATTT ACCTCTGTCC 180
CCAAACGCTG ACCACGGCCT GGCTGCATAG ATGCTGCTGC TTAAGACCTT GGATGAACTT 240
CACTGACATC ATTCTTCCCT AAGCAGTCAC CAAAAAATTT ATATATNTNG CTCATATACA 300
NTNCCATATN ATANTTATAG AAGATGTATA ATCTATTTTA GATGTNANTN AAAGGGTAAA 360

SEQ ID NO:527

LENGTH:267

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00590

SEQUENCE DESCRIPTION:

GATCGGGTTT GGCCCCCAGC CCCGCTCAGC CCAGTCCCTC TTCCTCTGCC GGGAGGGTGT 60
TTTCAACTCC AAACCCAGAG GAGGGGTGT AGATTGGGTC CAGCTTTGCT TCAGTGTGTG 120
GAAATNTCTC GTGGGGTGGC ATCGGGGCTG CGGGGTGGGG ACCCCAAGGC TTTCTGGGGC 180
AGACCCTTGT CCTCTGGGAT GATGGGCACT GCTATCCACA GTCTCTGCCA GTTGGTTTTA 240
TTTNGAGGTT TNTGGGCTTT TTTTAAA 267

SEQ ID NO:528

LENGTH:352

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00591

SEQUENCE DESCRIPTION:

GATCAATCAC CTCTGCTGC TTGGATGGGT GGATTGGTG CTCAGCCTCC CCAAGGACAA 60
GCTCCTCCCC CTGTAATACC TCCTCCTAAC CAAGCCGGAT ATGGTATGGC AAGTTACCAA 120
ACACAGTGAG CCGGGACTCT AAAAAAAT TGTAATTCAT GATAGGCTTC GATTCCTGT 180
GACACTCTGA AGACATGAAA GTAGACATCG GAAAATGNAA ATATTTATTT TAAAAATTGA 240
AATGTTTGGA ACCTTTAGCA CAGATTGCT TTGGTGAAGG ACACGTGTCT TCTAGTTCTG 300
CCTTTTNAAG GTTNTTGT CATGNTGGAT NTTGAACATN GNTTTTNTT TN 352

SEQ ID NO:529

LENGTH:351

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00592

SEQUENCE DESCRIPTION:

GATCAAGCCT TTCTTTCATT CCCTCTCTGA AAAGTATTCC AACGTGATAT TCCTTGAAGT 60
 AGATGTGGAT GACTGTCAGG ATGTTGCTTC AGAGTGTGAA GTCAAATGCA TGCCAACATT 120
 CCAGTTTTTT AAGAAGGGAC AAAAGGTGGG TGAATTTTCT GGAGCCAATA AGGAAAAGCT 180
 TGAAGCCACC ATTAATGAAT TAGTCTAATC ATGTTTTCTG AAAACATAAC CAGCCATTGG 240
 CTATTAAAAA CTTGTAATTT TTTTAATTTA CAAAAATATA AAATATGAAG NCATAAACCC 300
 AGTTGCCATC TGCCTGACCA ATAAAACATT AATGCTAACC ACTTTTTTAA A 351

SEQ ID NO:530

LENGTH:348

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00593

SEQUENCE DESCRIPTION:

GATCCAGAAT ACCCTGACCT CGCCCCAGTT CCAGCAGGCC CTGGGCATGT NCAGCGCAGC 60
 TTTGGCCTCG GGGCAGCTGG GCCCCTCAT GTGCCAGTNC GGTCTGCCTG CAGAGGCTGT 120
 GGAGGCCGCC AACANGGGCG ATGTGGAAGC GTTTGCCAAA GCCATGCAGA ACAACGCCAA 180
 GCCCAGCAG AAAGAGGGCG ACACGAAGGA CAAGAAGGAC GAAGAGGAGG ACATGAGCCT 240
 GGACTGAGCC ACGCGCCGTC CTCCGAGGAA CTGGGCGNTT GCAGTGCGTT GCACACCTTN 300
 ACCTTCNACN TACTGATTAT TAATAAAGTT TTTTCTTTA CCTGCAAA 348

SEQ ID NO:531

LENGTH:347

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00594

SEQUENCE DESCRIPTION:

GATCCTGAAG AGATTGAAAA AGAAGAGCAG GCTGCTGCTG AGAAGGCAGT GACCAAGGAG 60
 GAATTCAGG GTGAATGGAC TGCTCCCGCT CTTGAGTTCA CTGCTACTCA GCCTGAGGTT 120
 GCAGACTGGT CTGAAGGTGT ACAGGTGCCC TCTGTGCCTA TTCAGCAATT CCCTACTGAA 180
 GACTGGAGCG CTCAGCCTGC CACGGAAGAC TGGTCTGCAG CTCCCACTNG CTCAGGCCAC 240
 TGAATGGGTA GGAGCAACCA CTGACTGGTC TTAAGCTGTT CTGTCATAGG CTCTTAAGCA 300
 GCATGGAAAA ATGGTTGATG GAAAAATAAC ATCAGTTTCT ATTTAAA 347

SEQ ID NO:532

LENGTH:346

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00595

SEQUENCE DESCRIPTION:

GATCCGGTNT TGGTGCCAAT GTCTCCAAC TCACTTTTGC TCCTAGCAGC ATTATATTTT 60
 ACCTGGGACA TGCTGTATG CTGGGACTCA TGTATGTCTA CTGGACTCAG CTCAACATGT 120
 TCCAGACCTT GAAGTACCTG GCCATCTTGG GCAGTGTGAC GTTTCTGGCT GGCAATCGGA 180
 TGCTGGCCCA GCAGGCAGTC AAGAGAACAG CACATTAGTT CCAGAAGAAA GATGGAAATT 240

CTGAAACTG AATGTCAAGA AAAGGAGTCA AGAACAATTC ACAGTATGAG AAGAAAAATG 300
GAAAAAATA CCTTATTTA AAAANGAAAA AAGTCCAGNT TGTAATA 346

SEQ ID NO:533

LENGTH:346

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00596

SEQUENCE DESCRIPTION:

GATCTTGTAG CCTAGATAGG ATAGTNTGAC CTTCTAGCAT AGTCTTTTGG GCAATNATT 60
TGTGTTTCA GTGTGTGGGG AAGCTGTCCT GGGGGCTGGG GCGACAGATA GCACATAGGC 120
TGTTCCTGGG GCTGCAGGGG CTTCCNTGAG CTGGATGTTG TGGGTNTTGC CGTGCTTCAG 180
GAAGTNTGGC GACCAGAAAG CGTAGACCCG GGGCCCAGGG TCTGCCCCGC CCTGCAGCNT 240
GGCCTCCCCG CACAGGCTGT GGCTTGCACT CCAGCCGNTC TAGTNTCTNA GGAATTTNCT 300
TGTNACTGT ACTGTGTAATA TAAAGCTTC TGGTTCAATA CCNAATA 346

SEQ ID NO:534

LENGTH:345

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00597

SEQUENCE DESCRIPTION:

GATCCTATGG CCATGACCCA GAAGTATGAG GNGCATGTNC GGGAGAGCAG GCTCAAGTAG 60
AGAAGGAGGA CTTCAAGTAC ATGGTGGCTG AGCAGCTGC CAAACAGAAG CAAAAAATC 120
GGAAAGCTCA GCCCCAGGAC AGCCGTGGGG GCAGCAAGAA ATATAAGNG TTCAAGTTT 180
AGGTCCCCTC AACTAGCCC TTTTGTGGC CCTACGTCTG GATGCCTGGG CTTACACAA 240
GAACCACCTC TCCGCGAGT CCAAGGNTC TGTCATTTCA TGTCTTATT TTAGACCTGT 300
TTTGTAATA AGCTGTTTC CCAAGGAAAG AGATGAATAT TTAATA 345

SEQ ID NO:535

LENGTH:354

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00598

SEQUENCE DESCRIPTION:

GATCGTGTAT ATGGTGAATC CAAGTTGGGA GGAATGAAA TAGTATCTTT NTTGAAAGGA 60
ATATTGACTC TTTTGTCTAC TACATAAAG AAAGATACTC ATTTATAGTT ACGTTCATTT 120
CAGGTAAAC ATGAAAGAAG CCTGGTACT GATTTGTATA AAATGTACTC TTAAAGTATA 180
AAATATAAGG TAAGGTAAT TTCATGCATC TTTTATGAA GACCACCTAT TTTATATTC 240
AAATTAATA ATTTAAAGT TGCTGGCCTA ATGAGCAATG TTCTCAATTT TCGTTTTCAT 300
TTTGCTGTAT TGAGACCTAT AAATAAATGT ATATTNTTTT TTGCATAAAG TAAATA 354

SEQ ID NO:536

LENGTH:343

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00599

SEQUENCE DESCRIPTION:

GATCCGTGAC AAGCGCACAG GCAAGACCAA GGGCTACGGC TTCGTCAGCT TCAAGGACCC 60
 CAGCGACTAC GTGCGCGCCA TGCCTGAGAT GAATGGGAAG TATGTGGGCT CGCNCCCCAT 120
 CAAGCTTCGC AAGANCATGT GGAAGGACCG GAATCTGGAC GTGGTCCGCA AGAAGCAGAA 180
 GGAAAAGAAG AAGCTGGGCC TGAGATAGGG TCTGTGGCCA GGCACCCGCT CCCACCTGGC 240
 CGGGCGCTGG CTCCTCCCTC AGTTCTCTTT GGGAAAACCC CCAGCTNGTC CACCCATCCN 300
 NTGCCCCAAA ACCAGTTTCA GTAAATTTAC GTTCATTTC AAA 343

SEQ ID NO:537

LENGTH:341

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00600

SEQUENCE DESCRIPTION:

GATCGAACGG ACTGTGAAAT CCGCTCTTTG TCGGAAGCTG AGCAAGCTGT GGCTTTTTTC 60
 CAACTCCGTG TGACGTTTCT AAGTGTAGTG TGGTAGGACC CCGGCGGGTG TGGCAGCAAC 120
 TGCCCTGGAG CCCAGCCCC TGCNTCCATC TGTGCTGTGC GCCCCACAGT AGACGTGCAG 180
 ACGTCCCTGA NAGGTTCTTG AAGATGTTTA TTTATATTGT CCTTTTTTAC TGGAAGACGT 240
 ACGCATACTC CATCGATGTT GTATTTGCAG TGGCTGAGGA ATTCTTGAC GCAGTTTTCT 300
 TTGGCTTTAC GAAGCCGATT AAAAGACCGT GTGAAATGAA A 341

SEQ ID NO:538

LENGTH:339

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00601

SEQUENCE DESCRIPTION:

GATCCTCGGG TGTTCTTCCC ATCAGATAAA ATAGTTCAT ACAGACAGAT GTTTTTATCT 60
 ACTGAACTAC AAAGAGTAGA AGAGCTTTAT GATTCATTAT TACAAGCTGT TGCTTCTAT 120
 GANTTAGCAG TGTTGACTC TCAGCCTTAG AATTCTGAGG TTAACGTGCT AAAGTATAAT 180
 TNTTAGCTCT AACGTAACAC CAACTGTTGT GAACATCCAT GTTATTGGAA AAGAACACAT 240
 TTTAGTGTA TTTTAGATGT TTAANTTCTG ACTTTTGGCT ATTAAATGGT TTACACAATA 300
 AGCCAAGACC AAATCAATAA ACATTTTNTG AGAACGAAA 339

SEQ ID NO:539

LENGTH:339

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00602

SEQUENCE DESCRIPTION:

GATCATCATC CGAGTGCAGA CCACGCCGGA CTACAGCCCC CAGGAAGCCT TTACCAACGC 60
 CATCACCAC CTCATCAGTG AGCTGTCCCT GCTGGAGGAG CGCTTTCGGG TGGCCATAAA 120
 AGACAAGCAG GAAGGAATTG AGTAGGGGCC AGAGGGGGCT CTGCTCGGCC TGTGAGCCCC 180

GTTCTACCT GTGCCTGACC CTCGCTCCA GGTACCACAC CGAGGAGAGC GGCCGGTCCC 240
AGCCATGGCC CGCNTTGTGG CCACCNTCA CCCTGACACC GACGTGTCCT GTACATAGAT 300
TAGGTTTTAT ATTCCTAATA AAGTATAGCG GAAGAGAAA 339

SEQ ID NO:540

LENGTH:339

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00603

SEQUENCE DESCRIPTION:

GATCGTTATG AATATCAAAT GTCCATTTCT ATNGTAATGA ATTCAGTGGG ACCATCACAC 60
AAAAGCACAC AAAGACCTCC TCCTCCACAG GGGAGACAGA GGTGGGGAGG CTCTCTTGGC 120
TCACATAATC GTGTCTGTGT CACAAATAAT CATTAAATTA GCTATTTTCA GCTAACACAT 180
TTGTNGTTGC ACTGAAAAA GAGTTAGTGA GCCTGTCTTG GAGTTTAAAGT AGTTTCAAAT 240
AAAAAAGGC TACAGTGCCT CACAAAGGAT GTTCCCAGCA AGTNGTTTAA ATTCCCAGCA 300
AGTTGTAAA GTGTAATAN AANTATATGA ANTTGTAAA 339

SEQ ID NO:541

LENGTH:355

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00604

SEQUENCE DESCRIPTION:

GATCCTGAAA TCTACTAGAG ACACCCCTAA GCCATGAATG AACTACATCC AAATACCTGA 60
NTTTTGGAA TCTGTTTCAT GGATTTNCA TCTTCTACCG TATGTNAAAT TGCAAGTNTT 120
TGAAGATTA TAAGTACAAA TTTGGGAACA TACAAATCTT TTAGGTAGTA GAGTTTAACG 180
TGTAAGCT AAAAGTGAAG GTAAGTGAAG GTTCTCTTGT TTCTTTGCAT TAATGTAAGT 240
GTGTGGTTTG CCTTTGTCCC CCTGGATAGA ACGTGCATTT AAAGAATATA TTGTACTTAC 300
TGTGACAGCA GATAATAAAC CAGTCTCTTG GAGGGCACAA CCCTTATTTG ACAA 355

SEQ ID NO:542

LENGTH:331

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00606

SEQUENCE DESCRIPTION:

GATCTTTTT ANATAAANT TATGTATTGT GGCATAATCC TTTTTTTGAG CTCTACAGAG 60
AACAGTCTTT TGGTAATAGT GGCAGGTATT TATCCTTCT GAATATATAC CCCATTATAG 120
GAATAACTGT TACTTATTTA GGATTCCATC ATTGAAAATT TTNACCCAAG GCACAGCAGT 180
GAANTTTATA GTNCTCANTT TAGTTGNCAT TATTGACAGG CATTGGNATT ATTAGTCATT 240
GCTAAGCAAC TAAAACTTCA TCAGTTCAAN TAAGTTTAN TTGTCANATG GCNGTATAAN 300
CACATGANCT TTCTAGGAAA TATTCCTCN N 331

SEQ ID NO:543

LENGTH:330

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00607

SEQUENCE DESCRIPTION:

GATCGGTGTG CCCCGCTGCG AGGGGCCCC CATGGGGCTG NTGGCCCNCT CGCAGTCAGG 60
ACATCCCAAC CCCTGGNTGG GACTGAACCA CCCAGAGCGG AGGGCNCTCC TTTNAGCCT 120
TGTNAGTCAC CTGGCAGGCC CCAGCTGGGC TGGCTGTCCG TGTCCCTCAG CCTGGNTGGT 180
GATTCCTTGC AGGCCAGAAA TNAAGAGTCC CTGTAGGTTT TGGTTTTGTT TGTTTTATTT 240
TGTTCTTTCA CCTTTTTTCC TCATTAAAA AAAAANGNCC CTGNGGAGTG TACTNATTNA 300
TTTTTTGATN AAAGGGANGT AAAATGNAAA 330

SEQ ID NO:544

LENGTH:329

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00608

SEQUENCE DESCRIPTION:

GATCCAGACT GTAAGATGTT GTTTTAGGGG CTAAAGGGGA GAAACTGAAA GTNTTTTACT 60
CTTTTTCTAA AGTGTGGTC TTTCTAATGT AGCTATTTN NTTGTTGCAT CTTTCTACT 120
TCAGTACACT TGGTGTACTG GGTAAATGGC TAGTACTGTA TTGNCNCTGT GAAAACATAT 180
TTNTGAAAAG AGTATGTAGT GGCTTCTTTT GAACTGTAG ATGCTGAATA TCTGTCCACT 240
TTTCAATCCC AATTCTGTCC CAATCTTACC AGATGCTACT GGACTTGAAT GGTAATAAA 300
ACTGCACAGT GCTGTTGGTG GCAGTNAAA 329

SEQ ID NO:545

LENGTH:329

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00609

SEQUENCE DESCRIPTION:

GATCACTAGA TTTATGGAGG AATTNGTCAC AAATNACTN TAGAAAAATG CTGTCATATA 60
GTTCAATTCA TCATTTTCTG TTGCAGGAAG CCACTCCACC ACAGAATGCT AATATGCCAG 120
TGGTACCCAG TACCTCTTGT ATATAGGTTA TTGCAAATAT TGTNCTGAAA TGCTTAACTT 180
CAGAATTACA TTTTAAAG TAAATAATTG TTTTAAATCT ATTTTGTAAG GNTATAAAGT 240
ACAATAGAAT TTCTGGAGTA CAGATTAAAC TATTTGCACT AACACACGTG CCGTGCATGA 300
TTTAATAAAA TANCTNNACT CTCNTAAA 329

SEQ ID NO:546

LENGTH:328

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00610

SEQUENCE DESCRIPTION:

GATCACCGTG TGCTCAGGCC AGGTGTGAAT CCTGAGGTCC ATGGAGGTGC AGAGATGAGA 60
TTACTCTAT TCACGTTGAA GTGATTTGCT TTGTTAACAA AAAATTGCAG CTATTGTCTA 120

GCTTTCATTT TTTTACTGAG AACTTTAAAT TAGTCCCCTA TTAGAATAGG GTTGCTACTC 180
ANCTNTTTTN AAAAACCGAA TTTTCATCATT TATCTAAAGA GNAAATATGC AGANTAAGTG 240
GTCTTGTTAA GAGTGCAATA TTATATNNNN ANGTAAGT AAAANTNAAT TTGGGGGGAT 300
TATTTATNCA GCATGANACC TANTNTGN 328

SEQ ID NO:547

LENGTH:328

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00611

SEQUENCE DESCRIPTION:

GATCCCNNGG ACGTGAGACT TANNCTTCCA GCCAGTGTGA ATCATTGTAT TTTGTCTCAT 60
AATCACAGCA CNCCTGCATG ACACAACAAC GTGCAGCATT TTTTACATAA AAATATGGTA 120
GANTTAATTT ATGACATGGA AATGCCTTAC GTGGTATCAC ACTTAGTCTT GAAAAAACA 180
CCNAGGTGAC GTTTAAATTT TTAGTACAT ATCCTCAAAT TGGAGCTAAG TTATACTTCT 240
TTTATAACCT TTTGGGCATC TGGTCGAGAG AAGACAAGAT TTTNTCTATT TACAGTGATG 300
CAATAAATAT GTTGGCCACC TTTGAAA 328

SEQ ID NO:548

LENGTH:322

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00612

SEQUENCE DESCRIPTION:

GATCTTGAAG AGACCGCTGG CAGCACCAGT ATTCCCAAGA GGAAGAAGTC TACACCCAAG 60
GAGGAAACAG TTAATNACCC TNAGGAGGCA GCCACAGAAG TGGCTCCAAG AAAAANAGGA 120
ATTNTCCAAA GAGGAGCCGG TCAGCAGTGG NCCTGAAAGA GCGGCTGGC AAGANCAGCT 180
CCAAGAAGAA GAAATGTTC CATAAAGCAT CCCAGGANGA TTAGAATCAA ATGGACANTC 240
TCTNGGAGGT GGNATACCA TAGNCCAAGG TNCATTTCCC ACCNTGTGCC GTGTCCCAA 300
TAAANACAAA TTCACAAGGA AA 322

SEQ ID NO:549

LENGTH:318

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00614

SEQUENCE DESCRIPTION:

GATCCACCTA GCCTCAGCCT CCCAAAGTGC CGCCGGGATT ACAGGCGTNA ACACCATGAC 60
TGGCCTTCAT TATCTCTNTT TTAATAATGA AAAAGTTTAT AATTACATT CAGTAAATC 120
ACCTTTTTTA GTGTCTAGTC TGTGAATTTT GACAAATGCA TGGTTTTGTA ACCAATCGAT 180
AGGNCAGTTC TGCCACCCAG GACATTCCCN TCTGTTCTC TGTCTCTC TTCTCTGCC 240
CCCTAGCAAC CACTGGTGT TCTGTCCNT CTGTTTCATT TGACATTTAT TTTAAATAA 300
AATATTTTAA AATCTAAA 318

SEQ ID NO:550

LENGTH:318

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00615

SEQUENCE DESCRIPTION:

GATCCTCACC GTGGAGGACC ATNATAATNA AGGTGGCATT GGTGAGGCTG TGTCCAGTGC 60
 AGTAGTGGGC GAGCCTGGCA TCACTGTCAC CCACCTGGCA GTTAANCGGG TACCAAGAAG 120
 TGGGAAGCCG GCTGAGCTGC TGAAGATGTT TGGTATCGAC AGGGATGCCA TTGCACAAGC 180
 TGTGAGGGGC CTCATNACCA AGGCCTAGGG CGGGTATGAA GTGTGGGGCG GGGGTCTATA 240
 CATTCTGAG NTTCTGGGAA AGGTGCTCAA AGATGTACTG AGAGGAGGGG TAAATATATG 300
 TTTTGNNGNAN AATGCAAA 318

SEQ ID NO:551

LENGTH:314

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00616

SEQUENCE DESCRIPTION:

GATCCCCTCT CTGAAGAGAA AGGAGGAAAG AAAAGAAAAA AACAGAAACA GAAGCTCCTG 60
 TTCAGCACCT CAGTCGTCCA CACCAAGTGA CACTACTGGN CCAGGCTACC TTCTCCATCT 120
 GGTTTTNTT TTTNTTTTT TTTCCCCCAT GCTTTTGTTT GGNTGCTGTA ATTTTAAAGT 180
 ATTTGAGTTT GANCAGATTA GETCTGGGGG GAGGGGGTTT CCACAATGTG AGGGGGAACC 240
 AAGAAAATTT TAAATACAGT GTATTTTCCA GCTTCCTGTC TTTACACCAA AATAAAGTAT 300
 TGACACAAGA GAAA 314

SEQ ID NO:552

LENGTH:313

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00617

SEQUENCE DESCRIPTION:

GATCCCTACT TGGNAGTTAA CCCTAACTAC TTGCTCGAAG ATTGAGATAG TGAAAGTAAC 60
 TGACCAGAGC TGAGGAAGTG TGGCACAGCA CCTCGTGGCC TGGAGCCNGG CTGGAGCTCT 120
 GCTAGGGACA GAAGNTTNC TGGAAGNNAT NCTTCCAGGA TTTNTTTTTC AGAAACAAGA 180
 ATTGAGTTGA TGGTCCTATG TNTCACATTC ATCACAGGT TCATACCAAC ACAGGCTTCA 240
 GCACTTCCTT NGGTGTGTTT CTNTCCCAGT GAAGNTGGAA CCAATAATG TGTAGTCTCT 300
 ATANCCANTA CCN 313

SEQ ID NO:553

LENGTH:310

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00618

SEQUENCE DESCRIPTION:

GATCTTAGCT AGTTCATCAC TTCCTCAGGG AACATTCCC TAATTTCTGT CACAGAGTAA 60

GACCCGTTGT TATACGTCTC ACCTGACCAT GTACCTCTAC TTAGCATTTA ACACGTGTAA 120
TNTTGTATGT ATTGGTTTGA TTAATGTCAG ANCCACTAGA TTGTAACTC CATGAGGACC 180
GGAATTTNGT TTCTGTCATT GTCATTGTTT AACCTTGTAT TTTTATGCGC TCATACAGTG 240
CCTGGCACAT AGTAGGTGCT CAATTAACCT NATTGAAAG AATAAAATGA ATGGATGAGG 300
TATCAAGAAA 310

SEQ ID NO:554

LENGTH:310

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00619

SEQUENCE DESCRIPTION:

GATCTGGGGG CCACCACCCT GTGCCGGTGG CCTCTGGGCT GCCTCCCGTG GTGTNAGGGC 60
GGGGCTGGTG CTCATGGCAC TTCCTCCTTG CTCCCACCCC TGGCAGCAGG GAAGGGCTTT 120
GCCTGACAAAC ACCCAGCTTT ATGTAAATAT TCTGCAGTTG TNACTTAGGA AGCCTGGGGA 180
GGGCAGGGGT GCCCATGGC TCCCAGACTC TNTCTGTGCC GAGTGTATTA TAAATCGTG 240
GGGNAGATGC CCGGCCTGGN ATGCTGTTTG GAGACGGAAT AAATGNTTTC TCATTCAGTC 300
TNCAGTCAAA 310

SEQ ID NO:555

LENGTH:308

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00620

SEQUENCE DESCRIPTION:

GATCCNGTGC TGAAAGAGAA ACCAAGAAAA AAGATGACAT TCCAGAAGAA GACAAAGGAA 60
ATGTAAACA ATGTGAAATC AATTATGTAA AGAAATTTCA GAGCTTCCAA GACCACAAAC 120
TTAAATAAG TAAAGANGAC AGTAAATTN TAAAAAGGC TCGGAAAGAT GGATTTTTC 180
ATGAGACGCT TCTGGACAGG NGAGCCAAAT TGAAAGCCGA CAGATACTGC AAGTNACTGG 240
GATTTTNTT TCTGCCTTAT CTTNCTGTNG TTTTCTGA NTAAATATT CAGAGGAATG 300
CTTTTAAA 308

SEQ ID NO:556

LENGTH:300

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00621

SEQUENCE DESCRIPTION:

GATCTTCCTG AAGTNTCTCC CCGTTTNGTG CAGCTGGCCA TACCCAGGT GGACATNATG 60
AGTCAGGCTG ACTTAATTNC TCATGAGCAG ACCATCCCAG TGAATGCAA GGGCATGGGC 120
TCCACAGCCT GGACCCTGGC ATGGAGTCCA GCNNCCTGCT CACCGGCCAG GAGGCCTGGG 180
GGGGGTAC TTACCTTNT NAGCCTCANT TTCTNTTCT GGAAGCGGAG ATGGTAATAG 240
CTTNACATT NGAGGTGAAT GTNAGAATTA AACTTGGCA CATGGAGGAA TACACCTAAA 300

SEQ ID NO:557

LENGTH:299

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00622

SEQUENCE DESCRIPTION:

GATCACTTGT CCTATTACCC TATACCTAGC ACTTGTGACA CCACCCCTAA ATCACTTTGA 60
GCCTGGGAAA TAAGCCCCCT CAACTACCAT TCCTTCTTTA AACACTCTTC AGAGAAATCT 120
NCATTCTATT TCTNATGTAT AAAACTAGGA ATCCTCCAAC CAGGCTCCTG TGATAGAGTT 180
CTTTAAGCC CAAGATTTTT TATTGAGGG TTTTTGTTT TTTAAAAAA AATTGAACAA 240
AGACTACTAA TGACTTTGTT TGAATTATCC ACATGAAAAT AAAGAGCCAT AGTTTCAA 299

SEQ ID NO:558

LENGTH:301

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00623

SEQUENCE DESCRIPTION:

GATCTGCTTC TCCAGTTTTT GAGGAGCCAG CCAGGGGTCC AGCACAGCCC TACCCCGCCC 60
CAGTATCATG CGATGGTCCC CCACACCGGT TCCCTGAACC CCTCTTGGAT TAAGGAAGAC 120
TGAAGACTAG CCCCTTTTTC TGGGGAATAA CTTTCCTCCT CCCTGTGTA ACTGGGGCTG 180
TTGGGGACAG TGCCTGATTT CTCAGTGATT TCCTACAGTG TTGTCCCTC CCTNAAGGCT 240
GGGAGGGTGN TAAACACCAA CCCAGGANTT CTCAATAANT TTTNATTAC TAAACCTGAA 300
A 301

SEQ ID NO:559

LENGTH:297

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00624

SEQUENCE DESCRIPTION:

GATCAGATTT TGCTAAATGG AAATAATATA ACAATGCTGG TTCCTGGAGG AGAAGGACCT 60
GAAGTGTGAA TGAGTTTCCT TGACTTACAC TAGATTTTGT TTTGGCTTAT AATGACAAGA 120
AAATGGAATT TTTTTTCCC ACTTTCTAAT GTTTAAATCC CATAAAGCTA AGTTTCCCGT 180
TAAAGGGAAG TGCTTTGAAG ATGTGTACCC ATTTTGTAA GTTAATCATG ATTATCCTGG 240
AAAAAGAAGA AAAGAGCTTC TTCTTTGCAG ATGAAAATAA AGGTGTTTTT GGTAAA 297

SEQ ID NO:560

LENGTH:304

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00625

SEQUENCE DESCRIPTION:

GATCTATTTG TAGATTAGGA TTAATGGA TTTAATCCAT TTTAAGGCT GTGTGAATTT 60
TTCTAAACAA GAACCATTTG CAATATGGAT TTCTTAGAGA TTAAACCAAT TATAACTTAT 120
TAGCAGTCGC GAGCACATGT TCATATAGTC AATGTAAAA TACACTAATG AGTATTTGGT 180

AAATCCCACT AGGCTTTTAC CATTAGCATA ATTTTGTGTT GTACAATTAA GTTACAATTA 240
CATCTCTAAT TTTGGATAAT ATTCATTGGT TAACANTANA GTGACAAAAG CTCATGCCTT 300
CAAA 304

SEQ ID NO:561

LENGTH:301

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00626

SEQUENCE DESCRIPTION:

GATCTGGAAC TTTGCACATG TCACTACTGG GGAGGTGTTT CTGCTCTAGC TTCCACGATG 60
AGGCGCCCTC TTTACCTATC CTCTCAATCA CTACTCTTCT TGAAGCACTA TTATTTATTC 120
TTCCGCTGTC TGCCTGCAGC AGTACTACTG TCAACATAGT GTAAATGGTT CTCAAAAGCT 180
TACCAGTGTG GACTTGGTGT TAGCCACGCT GTTTACTCAT ACAGTACGTG TCCTGTTTTT 240
AAAATATACA ATTATTCTTA AAAATAAAATT AAAATCTGTA TACTTACATT TCAAAAAGAA 300
A 301

SEQ ID NO:562

LENGTH:294

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00627

SEQUENCE DESCRIPTION:

GATCTNAGGA GCTTTAGGGA GAAGACTTGG TGGGGCTGGA GCACACCTTG GGNCTCANTG 60
GTTTCTGTGT CCCNGTGGTG CCANTCCTTC TGGGCAGTGC AGGCGGCTGC CAGGCCCAGC 120
CCTGACTTCC ACTCTGGCTC AGCAACCTGG TTATTTATGT GGGGCCGTGC AGGCATGGGC 180
CCACTGCCTG TCCATCCTGT TTCTNTTATA AATTGAACT CACCATTGCC CTATCCTTGT 240
GTCTCCACCC GCTTCCATGT GTTGAATAAT AAAAGGTGGG AAAGTGCTGT CAAA 294

SEQ ID NO:563

LENGTH:296

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00628

SEQUENCE DESCRIPTION:

GATCTGCCAT AAGAAAATCT AGTTCAACTC TAATTTTATG TAGTAAATAA ATTGGCAGGT 60
AATTGTTTTT ACAAAGAATC CACCTGACTT CCCCTAATGC ATTAAAAATA TTTTATTTA 120
AATAACTTTA TTTATAACTT TTAGAAACAT GTAGTATTGT TTAAACATCA TTTGTTCTTC 180
AGTATTTTTC ATTTGGAAGT CCAATAGGGC AAATTGAATG AAGTATTATT ATCTGTCTCT 240
TGTAATACAA TGTATCCAAC AGACACTCAA TAAACTTTTT GGTGTGTTAA CTGAAA 296

SEQ ID NO:564

LENGTH:307

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00629

SEQUENCE DESCRIPTION:

GATCGACTAC AGAGTACTTN TTTCTTATGA TGATTGGTGT AGAAATGTGT GATTTGGGTG 60
 GGCTTTTACA TCTTGCCTAC CATTGCATGA AACATTGGGG TTTCTTCAAA ATGTGTGTGT 120
 CATACTTCTT TTGGGAGGGG GGTGTTTTT TTTCTGTTAT TTTCTGAGAC TCCTACAGGA 180
 GCCAAATTG TAATTTAGAG ACACTNAANT TTGTTAATCC TGTCTGGGAC ACTTAAGTAA 240
 CATCTAAAGC ATTATTGCTT TAGAATNNNC AAATAAAATT TTCCTGACCA AATTGTTTTG 300
 TGGGAAA 307

SEQ ID NO:565

LENGTH:296

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00630

SEQUENCE DESCRIPTION:

GATCTTGCTC CTTCAGACTC TGACCTGAGT GGAGACCTTT CCACCAGACA CAGCTCGGGC 60
 CTGTGTAATT GTAGGAGAAG ACACTCAGCA GTGATTGCCA TGGCAGAGAG CCGTGGTCAT 120
 TGTGCTGTT ACAAGAAGA AAACCATCTG AGTTCTAACT CCTTGGTTGC TTAAGTAG 180
 TTCCAAGAG TCTGAGAAGC TATTTCTATT TTTAAGAGTC ATTTTTGTA ATNTTGTAA 240
 NACAAAAGTA CCAATCTGTT TTGTAAATAA AANTCATCCT AAAATTCGAN GTTAAA 296

SEQ ID NO:566

LENGTH:288

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00631

SEQUENCE DESCRIPTION:

GATCTTTNGC TAGGTGGATG ACTAGTNATA TTCAAAGCCT TTTCTCAAAG CCCTTTCAGT 60
 TACAACCACC CCACTATGGA ATCAGTATTT AGTTATACAT TTGTATAAGA NCCTGTATTT 120
 TGAAAAACAC ATTCATGTAT ATTTATTCCT GGAATTATTT GCCTGTAAAA CAGTGTCTTT 180
 CATGTTCTCT CCCAGATTG TAAACTCTGT AAGAAGCTGC TNGTATCTGT ATCCCTTGT 240
 GAAACTCTGA AAACACTGAA TAACTAAANT CTTCTTCTCA TCCNTAAA 288

SEQ ID NO:567

LENGTH:292

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00632

SEQUENCE DESCRIPTION:

GATCTTGATA TTCTGTACAA GTTGATGTAA TACCCTGATG CGTTTTAGAG GACTTGGCAT 60
 AAAATNAAAG NTTGGCAAAG GCCCTTGAGG GGCTTGGGGA TGAGAGTATG GAACTGTCTG 120
 CATTGGACCC TAACTGGAC TAGANGAGGC ATCTTCAAGG TTCATACGTT GTCCAGCTGT 180
 AAGTTCATTT GAGTAGCAGA GCTAACAAAT ATTTGAGGTC AAAACCCTAC CATGTTAAAA 240
 CAAACAAAAA CTTATCATGT TAATAAAGT ATTCATTGTC TTGANANANA AA 292

SEQ ID NO:568

LENGTH:291

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00633

SEQUENCE DESCRIPTION:

GATCCTGACA AGAAGAAAAT NAAGCTCAAA GTCAAAAAAT CTCGTGAAAA ACGGAGTTTG 60
GCCTCTCATC TCAGTGGATA TATCCCTNCC AAAAGGAAAC AAGGGCAAGG CTTATCTTTG 120
TGTCAAAACG GAGAGTCACC CAACTGTGTG GAAGACAAGA TGCTCTCGAC AGTTGCAGTA 180
CTTACCCTTG GCTAAGAACT GCACTGCTTT GTTTAAAGGN CTGCAGACCA AGGAGCGAGC 240
TTTCTCTCAG AGCATGCTTT TCTTTATTAA AATTACTGAT GCAGANAAAA A 291

SEQ ID NO:569

LENGTH:285

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00634

SEQUENCE DESCRIPTION:

GATCANGCTG GCTGCAAAGA AGGGACTGGA CCCATACAAT GTACTGGCCC CAAAGGGAGC 60
TTCAGGCACC AGGGAAGACC CTAATTTAGT CCCCTCCATC TCCAACAAGA GAATAGTAGG 120
CTGCATCTNT NAAGAGGACA ATACCAGCGT CGTCTGGTTT TGGCTGCACA AAGGCGANGC 180
CCAGCNNTGC CCCCCTNGT GGAGCCCATT ACAAGCTNGT NCCCCAGCAN CCTGGCACAN 240
TGAGGNACCT GCATAAATT ACTNAAAATG TGCTGTAAAG NTTTN 285

SEQ ID NO:570

LENGTH:285

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00635

SEQUENCE DESCRIPTION:

GATCACCTT GTAATGTGT ACGGGTCCAT TTTCTGGA ATCGTTTAAT CTAAAGCAGT 60
TTCCCCTGTT TTGGAGATT TTAGTTAAT TTTAATTTG GCTATTGTTT GGAAAAGATG 120
AGCTGTCTGT GTAGATATGA AGTATAGTT TTNCCATAAA ACAGATGTTT ATTTGTATT 180
AAAAAATACC ACTGTACTT TTTACACCA TTTGTATACA TGTGGTGATA TTAATGCTAA 240
ACTGTAAAT TCAGGAATTA AAATGTGACC CTGTAATTCC ATAAA 285

SEQ ID NO:571

LENGTH:287

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00636

SEQUENCE DESCRIPTION:

GATCTAACCA TTTTCATACT CTTAACTGAT TGAAACAGAT TCAAAGAAGT ATCGAGTGCT 60
ATGCATTGAA ACTTGTTTTT AAATGTTAGA TGGCACTATG TATATTAATG TAAANCAATG 120
TTAATTTACT CAAGTTTCA GTTTGTACCG CCTGGTATGT CTGTGTAAGA NGCCAATTTT 180

NGTGTATTGT NACAGTTTCA GGTNATTNAT ATTCGATGTT TTGTAAANCT CAAATANCGA 240
CTATACTNAT GGGNCCAAAT AAATGGGCAT CTGCATTCTN GGTAAAA 287

SEQ ID NO:572

LENGTH:282

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00637

SEQUENCE DESCRIPTION:

GATCTNTGGT GGCAATGNCT GACCAGTAGA CTGGTGGCTC ACTTCTNCCC ACCTGCCGGC 60
AACACCAGTG CCAGGAAAAG GCCAAAAGAA TGTNTGTTTC TAACAAATCC ACAAATAGCC 120
CCGAGATTCA CCGTCCTAGA GCTTAGGNCT GTTTTCCACC CCTCCTGACC CGTATAGTGT 180
GCCACAGGAC CTGGGTCGGT CTAGAACTCT CTCAGGATGC CTTTCTACC CNATCCCTCA 240
CAGCCTCTTN CTGCTAAAAT AGATGTTTCA TTTTNTGGA AA 282

SEQ ID NO:573

LENGTH:279

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00638

SEQUENCE DESCRIPTION:

GATCTACTGG CGAGCGATGA AAATGTTGCA GGGAGAGTCA GCAGAGGCAT TTGTAGCTAA 60
ACATGCTATG CATCAGACTG GCCATTTATG AAGATGAAGA ATACAGTCAG CTTTGTGAAA 120
TAGTATTGCA AGCAAGCCCC GTGGGCAAAT TTGTATTGAG TCCATCTGTA ATTTGCTCAG 180
TGATGGCAGA CAAGATGGCT GTCTGGTTTT GAGACACACT TTAATTTTAT GTTAACTTGT 240
TAAATCTTTT TAAAAATTAA AAAATTTTAA TGATTGAAA 279

SEQ ID NO:574

LENGTH:279

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00639

SEQUENCE DESCRIPTION:

GATCATTGCA TTTTCTGTGA TTTTCTAAAA TGGCTCCAAT TTTGTNTTTT AAGCTTCAGC 60
TTAAGAGGAA GTTTATGTTC TAATTCCTGA CTGAGAATAC AGTATTGAGA TTCNTGTGTT 120
TACAGATAAC AACTGGTTTT TATTACTCAT TAAGTTCATT TGCATCCCGT AGCCCTCTGT 180
AAATGTTTCC CCTAGTTGTA TGTACGTAAA TGCACGCTTA TCCAGTNTAT ATTAGACATT 240
TTTGTGCTAA AATATATTAA GTGGGATTTT TGTAGCAAA 279

SEQ ID NO:575

LENGTH:280

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00640

SEQUENCE DESCRIPTION:

GATCTTTGCA AGGGCAAAAC TACAAGTAAC GAGTTTTATA TAATTAATTT AAATTTNTNA 60
 CAGGTTTTCA TGTTCAGGAT AAACCATACT TCCACCTTGG GTGAGAACAC TTGCAACAGT 120
 TTATTAATGA GGTGACTTTC ACCTTAGGAC AACTGTTGCA TGCCAAGTTT TTTGTGTGTG 180
 TGAAACACTN TCAAACTGA TTAAAAAGAT GTAAATTTAA AATTGGTTGT ATCTAATATG 240
 CCCCAGGTTC GGTAAATAAA CAATTCTTTT TAAAAACAAA 280

SEQ ID NO:576

LENGTH:300

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00641

SEQUENCE DESCRIPTION:

GATCTGCCTG TCCCTTTTTC CCCTGGGGTT TGACACACAG GCTCCTCTCA GCATGAGGTG 60
 GAGCAGTGAC CAGGTGGAGC AGTGACCAGG ACGCCTCTGG CCCAGTGCTG CCCAGCCTCC 120
 CCGNCCGCTC CCAGGCGCCC CATGTCCTCA CAGGCCAGGA CGCCATGNCA GGATGGAGAG 180
 GACTTGGTGG ATTTTGTGTT CTTGCCTGAC CTCAGTTTCA TGAAAGAAAG TGGAAGCTAC 240
 AGAATTATTT TCTAAATAAA AGGCTGAATT GTCTGAAAAA TAAATATAT TGTATTAAA 300

SEQ ID NO:577

LENGTH:278

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00642

SEQUENCE DESCRIPTION:

GATCTGGGAC GTGGTTCGGC GGANAGTCCC CAGCCCGGCC CCCTGCCTGG GACCACCAGG 60
 CCCCAGGAG AAGCCGCCTG AGCCACAACC TTGCGGCATG CAAATNAGAT GGCCGCTCCA 120
 GGCCTGGAAT GTTCCGTGGC TGGGCCCCAC GGGAAGCCTG ATGTTCAGGG TTGGGGTGGG 180
 ACGGGCAGCG GTGGGGCACA CCCATTCCAC ATGCAAAGGG CAGAAGCAAA CCCAGTAAAA 240
 TGTTAACTGA CTTCCAGCCT CACCCGTGGG CGGTCAAA 278

SEQ ID NO:578

LENGTH:277

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00643

SEQUENCE DESCRIPTION:

GATCAGGGCC CACTGATGAT GGTGAAGAAG AGATGGAAGA AGACACAGTC ACAAACGGGT 60
 CCTGAGCAGT GAGGCAGATG TATAATAATA GGCCCTCTTG GAACAAGTNT TGCTTTTNGA 120
 ACATGGTATA ATAGCCTTGT TTGTNTTAGC AAAGTGAAT CTATCAGCAT TGTTGAAATG 180
 CTTAAGGCTG CTGCTGATAA TTTNNTAATA TAAGTTTGA AATCNAAATG TCAATTTNCT 240
 ACAAATNATA AAAATAAACT CCACTCACNA TGCTAAA 277

SEQ ID NO:579

LENGTH:277

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00644

SEQUENCE DESCRIPTION:

```
GATCCGAGTC GTCCGGAAAT CCATTGCCC GTNTTCTCAC AGTTATTAAC CAGACTCAGA 60
AAGAAAACCT CAGGAAATTC TACAAGGGCA AGAAGTACAA GCCCCTGGAC CTGCGGCCTA 120
AGAAGACACG TGCCATGCGC CGCCGGCTCA ACAAGCACGA GGAGAACCTG AAGACCAAGA 180
AGCAGCAGCG GAAGGAGCGG CTGTACCCGC TCGGGAAGTA CGCGGTCAAG GCCTGAGGGG 240
CGCATTGTCA ATAAAGCACA GCTGGCTGAG ACTGAAA 277
```

SEQ ID NO:580

LENGTH:276

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00645

SEQUENCE DESCRIPTION:

```
GATCAGGACC CACCTNCAGT NCTTCTGAAA GTGTGACAGT GTCCAGCCGG TTCTGCAGCA 60
CTAGGGGAGG GGGCAGATGG TGGTTGCATG GGCTTCCTGG GTCTCCACTC TCCGTCTGGC 120
CTAAAGGTGA TGTATTTGGT GTTTGGCCCT GCAGTCCCCA CTCTTGAGGC TTAAGGCGCA 180
TGTGGCAGAN CACTNCTTCC AGCAGTAGTC GCTTTACTGT TACCNGTTTA GGCCTAGAAG 240
TTTTCCNCA TCTGTAAATG TGATTAAAA TATAAA 276
```

SEQ ID NO:581

LENGTH:275

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00646

SEQUENCE DESCRIPTION:

```
GATCTACTTA CTCAAGTCTN ATGAATNCTG NGCCTTTCAT CACATTCCTA GCCCACTCTC 60
ATCATTACTG CAGAAGGGTG TTGTGATGAC CAGTNTTATA CTGTGTTTTG ATATGTCTAG 120
CAATAACTTA AAGAAAAAAA AACCTGGGAA ATCTTCAACA TGNNNTNGGA ACATATATGT 180
ATGTATTAAT GNATATACAT GGCTTAACTT ATACGGTTAT GGCAGCNCCT GTATACAGTT 240
TGAACATG NACCTGAAAA ANAATTCTTA ANTTN 275
```

SEQ ID NO:582

LENGTH:307

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00647

SEQUENCE DESCRIPTION:

```
GATCGCCATC ATGAACGACA CCGTAACTAT CCGCACTAGA AAGTTCATGA CCAACCGACT 60
ACTTCAGAGG AAACAAATGG TCATTGATGT CCTTCACCCC GGAAGGCGA CAGTGCCTAA 120
GACAGAAATT CGGGAAAAAC TAGCCAAAAT GTACAAGACC ACACCGGATG TCATCTTTGT 180
ATTTGGNTTC AGAACTCATT TTGGTGGTGG CAAGACAACT GGCTTTGGCA TGATTTATGA 240
TTCCCTGGNT TATGCAAAGA AAANTGGAAC CCNAACATAG NCTTGCAAGT CATGGCCTGT 300
ATGNNGN 307
```

SEQ ID NO:583

LENGTH:272

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00648

SEQUENCE DESCRIPTION:

GATCTGAATT TTTTCCTCCT TTTGGTTTTA TTTTGTGGT TTATTTTGTG TTTTCTTTTC 60
TCCTTTTGG GGGGTATTCA GAGTGGGCTG GGCCCTGGG CGAGACACAG CTACCTCTGT 120
TGGCATCTTT TTAATACCAG GAACCCAGCG GCTCTAGCCA CTGAGCGGCT AAATGAAATA 180
AAGTGGAAAA AAAAAAANGG GAAAAACCCA AAGGNTTAAA AACCCACNGG AATTTTNTTG 240
TNGAAANTNG AAAATAAAGG TTTCCNNGTA AA 272

SEQ ID NO:584

LENGTH:279

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00649

SEQUENCE DESCRIPTION:

GATCTATACC AATTAAACAT TTTCATAGTT CTGCCTATTG TCCTTCCCTG AGGCTCCATT 60
GCTGCTTGGT GGCCATTCTC TGCCTTTTCA CAGTCACCTG AACAATGACC CATCATCTCT 120
TGCTTGCTTG AAATCTTGCT GAAATGTTCT CATTTCTGTG TTGCTGTATG GGCTCGGGTG 180
GGATGTTTGT TGGCTCTGTT GTGTTTATTC ACCAATTTGT ACATTATTG TTGTCCTTTA 240
CTACTGTAAA CAGTAAATAT AGTTTGGTAT TCTGTCAA 279

SEQ ID NO:585

LENGTH:273

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00650

SEQUENCE DESCRIPTION:

GATCCCAGAC TGGTTCTTGA ACAGACAGAA GGATGTAAAG NATGGAAAAT ACAGCCAGGT 60
CCTAGCCAAT GGTCTGGACA ACAAGCTCCG TGAAGACCTG GAGCGACTGA AGAAGATTCG 120
GGCCCATAGA GGGCTGCGTC ACTTCTGGGG CCTTCGTGTC CGAGGCCAGC ACACCAAGAC 180
CACTGGCCGC CGTGGCCGNA CCGTGGGTGT GTCCAGNAAG AAATAAGTCT GTAGGCCTTT 240
GTCTGTAAAT AAATAGTTTT ATATACCTNN AAA 273

SEQ ID NO:586

LENGTH:275

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00651

SEQUENCE DESCRIPTION:

GATCTNCCAC GTCTCCATCT CAGTACACAA TCATTTAATA TTNCCCTGTC TTACCCCTAT 60
TCAAGCAACT AGAGGCCAGA AAATGGGCAA ATTATCACTA ACAGGTCTTT GACTCAGGTT 120

CCAGTAGTTC ATTCTAATGC CTAGATTCTT TTGTGGTTGT NGCTGGCCCA ATGAGTCCCT 180
AGTCACATCC CCTGCCAGAG GGAGTTCCTC TTTGTGAGA GACACTGTAA ACGACACANG 240
AGAACAAGNN TAAAACAATA ACTGTGTGTG TTAAA 275

SEQ ID NO:587

LENGTH:269

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00652

SEQUENCE DESCRIPTION:

GATCTTATGG ATAAACTCA GAAAGTGAAG GTGAAGAAAG AAACGGTGAA CTCCCAGCT 60
ATTTATAAAT TTCAGAGTCG TCGAAAACGT TGACGTGTTA TAGATAAGCC TTGTCATTNT 120
GTATCAAAAA TCTGTTGTCG TTTTCTAGTA ACTTCAAATT CCATTACTCC AAATGGCATG 180
GTTTCCGGT TTGTAACCAT AACTAAATTG TCAGTCTGAC ATTTAATGTC TTTCTATGGA 240
CAACATTAAA TCNCCCTCCC TTCTGTAAA 269

SEQ ID NO:588

LENGTH:272

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00653

SEQUENCE DESCRIPTION:

GATCAAGTGG CTTTCCCTGG GACCTGCCCC GCTTTGAGAA TCTCTNCTCA TCCACCCTCT 60
GGCACCAGC CTCTNAGGGA AGGAGGGATG GGGCATAGTG GGAGACCCAG CCAAGAGCTG 120
AGGGTAAGGG CAGGTAGGCG TGAGGCTGTG GACATTTTCG GAATGTTTTG GTTTNTTTT 180
TTTTAAACCG GGCAATATTG TGTTCAATTC AAGCTGTGAA GNAAAATATA TATCANTGTT 240
NNCCAATANA ATACAGTGAC TANCTGAACA AA 272

SEQ ID NO:589

LENGTH:268

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00654

SEQUENCE DESCRIPTION:

GATCGTCAAA TCTTTNCAA ATTTAATNTA TATGTGTATA TAAGGNAGTA TTCAGTGAAT 60
ACTTGAGANA TGTACAAATC CTTTATCCAT ACCTGTGCAT GAGCTGTATT CTTACAGCA 120
ACAGAGCTCA GTTAAATGCA ACTGCAAGTA GGTTACTGTA AGATGTTTAA GATAAAAGTT 180
CTTCCAGTCA GTTTTCTCT TAAGTGCCTG TTTGAGTTTA CTGAAACAGT TTACTTTTGT 240
NCAATAAAGT TTGTATGTTG CATTAAAA 268

SEQ ID NO:590

LENGTH:267

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00656

SEQUENCE DESCRIPTION:

GATCAAAAAT AAAATGTTAT TTTTAAAGTT TCTNTTTGAG ATTTTNCCTA AGTTTTGGTA 60
 GATATTCTTA AGTTTTAGTG ACCTCAGTTT GGGAAATTAAG TAAGCTAAAC ATTGTGTCCT 120
 TATTATNAGT TATATAAAAC TATGCTTTAG ACTTTGTNAG AAACTTCTGC CCCACCTGA 180
 CTGACTGCTT TNCCATTNTT GGTGTACAA AATGAATCA CACTTTAATG CTATGGCCAC 240
 CTTTAAATAA AGTACAGCGT GACTAAA 267

SEQ ID NO:591

LENGTH:265

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00657

SEQUENCE DESCRIPTION:

GATCTAGATT CTACATGTTA CCATTGGTTT ATTCTTGTGC TTTCTGTATT TAAACTTTG 60
 GCTGTACTAA GCAAAATGCAA GGTATAATT TAGCTAATAG TAGTTACAG ACAATTCTGA 120
 TGATTATGAT TTCATTGGT TTAATAAGC TGTACTAGTT CATTTCATAA GGAAATGATA 180
 CTGTAGACAA ATGTAAATAA AGCCTGTGAG TCAAGCATCA AGTGGTGTGTT GTTAGAAATA 240
 ANCTAGAGAT TTTAANCTC TGAAA 265

SEQ ID NO:592

LENGTH:264

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00658

SEQUENCE DESCRIPTION:

GATCTGGGGC CAGCTCACCG CTCACGTCCC CGTCATCGAC AACTCCACCC TNTACATCAG 60
 TAGAGCATGC ACCATTTTGA ACGTGACATT TNCGGTAAAG TAACTATGC TGATTTCTCA 120
 GACTTTAAAG ATGCTCTNNT TCTGTGTGN AAATAGGACC CAAAGTGTCT CGATTGCTGA 180
 AGTGATGAAC AAGTGGGAAA GCAGATTGA GACTATTTCC TTATCTGAAT ATTTAAATGA 240
 AATACAGCAT CTTTAAAANG CAAA 264

SEQ ID NO:593

LENGTH:262

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00659

SEQUENCE DESCRIPTION:

GATCTTTTAA AAAGATGATG CAGTTCTGTA TTTATTGTGC TGTGTCTGGT CCTAAGTGGA 60
 GCCAATTAAN CAGGTTTCAT ATGTATTTN CCAGTGTTGA ATCTCACACA CTGACTTTG 120
 AAAATTCCT TCCATCCTGA ATACGAATA GAAGAGGCCA TATATATTGC CTCCTTATCC 180
 TTGAGATTC ACTACCTTTA TGTAAAAAGT TGTGTATAAT TGTAAAAATC TGTGAAAGAA 240
 TAAAAAGTGG ATTTAAATTA AA 262

SEQ ID NO:594

LENGTH:260

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00661

SEQUENCE DESCRIPTION:

GATCCATCCA AAAACAAGGA CTGCAGCCTA AATTCCAAAT ACCAGAGACT GAAATTTTCA 60
GCCTTGCTAA GGAACATCT CGATGTTGA ACCTTTGTTG TGTTTTGTAC AGGGCATTCT 120
CTGTACTAGT TTGTCGTGGT TATAAAACAA TTAGCAGAAT AGCCTACATT TGTATTTATT 180
TTCTATTCCA TACTTCTGCC CACGTTGTTT TCTCTCAAAA TCCATTCTT TAAAAATAA 240
ATCTGATGCA GATGTGTAAA 260

SEQ ID NO:595

LENGTH:259

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00662

SEQUENCE DESCRIPTION:

GATCCCTTTA TGAAACCTTG TGAATAGATG AATGTNTGGA GATGGCGACT AGTGGACAAC 60
AGAACAATAT TGGAATGGTG GTAATACGAG GAAATAGTAT CATCATGTTA GAAGCCTTGG 120
AACGAGTATA AATAATGGCT GTTCAGCAGA GAAACCCATG TCCTCTCTCC ATAGGGCCTG 180
NTTACTATG ATGTAAAAAT TAGGTCATGT ACATTTTCAT ATTAGANTTT TTGTAAATA 240
NNCTTTTGTA ATAGTCAAA 259

SEQ ID NO:596

LENGTH:257

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00663

SEQUENCE DESCRIPTION:

GATCNNGGCT AAGCCAGCCA GCCCNCCCGC GCCAGGNAAA ACAGGGCTGC AGGTGTCCTG 60
TCTCCAGCC TCATCTGGCC GGCCTCCCCA AACATTTGCC TGTCCATCAG CTCTCCTCC 120
TTTCGAGTCA TGTGAAAAGG GACAGGNCCA AGTGGCCTTG GTGTTAAAT CTTGCCCTAA 180
ATTGTAATC ACATGATTAT TTAAAGTCAC TAGANATAAG TAAGCACAGC AATAAAGNTT 240
TAATGGAATA AAAGAAA 257

SEQ ID NO:597

LENGTH:252

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00664

SEQUENCE DESCRIPTION:

GATCCCAGAA TTCAACCTGT ATTTATAAAT GTATAATGTA TTTAGCTACT TTTTGGTTTA 60
AATGAACTTG TTGGTTAGC TTGGTAAATG TTATAATTTT NACTATTTTC TACAAAGAAA 120
ATATTTTCTA ATTTAAGTTG GAGCTATCTG TGCAGCAGTT TCTCTACAGT TGTGCATAAA 180
TGTTTTNCT ATAAATGAG CTAATGTATA ANATACTGCT GTATACCATA ATAANGATAG 240
TAATACTTGA AA 252

SEQ ID NO:598

LENGTH:250

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00665

SEQUENCE DESCRIPTION:

GATCATTAGT TGAATCGGTA TCATCTTCAC CAAATAAAGA AAGTAATGAA GAAGAGCAAG 60
TGTGGCACTT CCTTGGCAAG TGATTGAAAC ATCTGAAATT CTGCTGTCAA GATTCCCATC 120
TCTAAGGACT CCAAGTGCTA GAGACAAGGG GGTCTATGAG CATTACTGA CTCCTGTGA 180
AAACTTCATT TTTTCAAAC TTTTGAGCTA TGCAATATAT AANTAACAG TAAGAATTTT 240
AAATTACAAA 250

SEQ ID NO:599

LENGTH:250

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00666

SEQUENCE DESCRIPTION:

GATCCTTCTT CCTTTCAC TGTCGTGCCTC CCANNAGGTG CAGAGATTCT TAGAAGAGGA 60
GGTGTATCCC CTGTTAAAC CATATGAAAG CGTGATGAAG GTGAAAGCAG AATTATGTCT 120
GTAGAGTTGG AAGAGAATTA AACGAAAATC ATTGTTAATT GCTGAGGCAT GAAAATTGTG 180
TTACTATAAT GCCTTATTTT ACCTCGAGAA TTGTTACCTT AAATTAGTAC AGCACTTTCT 240
TCTTCCAAA 250

SEQ ID NO:600

LENGTH:247

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00667

SEQUENCE DESCRIPTION:

GATCCTTCAG TTACATACAA TTTGTTAAT GAAATGTCAT GGCTCTGTTT ATATTTTNT 60
NTTGTNCTTC CAATTGGTAT ATACAACTTT CAGAGCCTCT TGTATTTGGA AGGCTGGAAG 120
GGCCCAGACT TTGGAATAGT GTCTTGGTTT CACTGTTTTN GTTTTGATT TTTTTTGT 180
TNGATTTTTT TAAACTAAA GCTATATAAA GCTTGNGGAT TAANCAGANT AAATTCCTAA 240
ATTAAA 247

SEQ ID NO:601

LENGTH:246

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00668

SEQUENCE DESCRIPTION:

GATCCAGGGT GTGTGTGAGT TGAGGGTGGG TGGAGGGGTT TGCAGTGTGG GAATGTGGCC 60
CTGCAGTTGA CCTGAGCTGC TTCACATGGT TGTCCATTCT GGGGCTTAAA GAACTGGGAC 120

CAGACCAAGT AGAGGCCTTG GTGCTGNTTG GGGTGGGGCC TGCAGANTCT TAGTTACTGA 180
 TTTCATTTTC AATAAATGTA GGTTCGTTAC ATGAGTTTCC CAATTAAAAA AAAAATGACT 240
 TCTAAA 246

SEQ ID NO:602

LENGTH:284

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00669

SEQUENCE DESCRIPTION:

GATCAGAATT TCACCAGGGA GTAAAATTAC CTGAAAACGT AAGANGTTTT AAACAGCTTT 60
 TCACACAAAT TAGATGCAAC TGTTCCTATG TCTGAGTACT TATTTAAAAG AAAGGTAAAG 120
 ATTGGCCTGT TAGAAAAAGC ATAATGTGAG CTTTGGATTA CTGGATTTTT TTTTTTTNA 180
 AACACACCTG GNGNGGNCAT TTGAAAACAC TTTTCTTACC CTCGANCCCT GATGTGGTNC 240
 CATTATGTAA ATATTTCAAA TTTTAAAAAT GTATATATTT GAAA 284

SEQ ID NO:603

LENGTH:249

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00670

SEQUENCE DESCRIPTION:

GATCGAGGTG GAGAAGCCCT TTGCCATCGC CAAGNAGTAG GGCACAGGGA CATCTTTCTT 60
 TNAGTGACCG TCTGTGCAGG CCCTGTAGTC CGCCACAGGG CTCTGAGCTG CACTNGCCCC 120
 GGTGCTGGCA TCTGGTGGAG CGGACCCACT CCCCTCACAT TCCACAGGCC CATGGACTCA 180
 CTTTTGTAAC AAATCCTAC CAACACTGAC CAATAAAAAA AAATGTGGGT TTTTTTTTTT 240
 TTAAATAAAA 249

SEQ ID NO:604

LENGTH:244

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00671

SEQUENCE DESCRIPTION:

GATCGGAATG GTGGAGAACT TCAACCAGGC ACTCAAGGAA ATTGGGGATG TGGAGAACTG 60
 GGCTCGGAGC ATCGAGCTGG ACATGCGCAC CATTGCCACT GCACTGGAAT ATGTCTACAA 120
 AGGGCAGCTG CAGTCTGCCC CTTCTAGCC CCTGTTCCCT CCCCCAACCC TATCCCTCCT 180
 ACCTCACCCG CAGGGGAAAG GAGGNAGGCT GACAAGCTTG AATAAAACAC AAGCCTCCGT 240
 TAAA 244

SEQ ID NO:605

LENGTH:244

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00672

SEQUENCE DESCRIPTION:

GATCCCCTTT CCGTAAAAGC GTGTAACAAG GGTGTAAATA TTTATAATTT TTAATACCTG 60
 TTGTGAGACC CGAGGGGCGG CGGCGCGGTT TTTNATGGTG ACACAAATGT ATATTTTNC 120
 AACAGCAATT CCAGGCTCAG TATTGTGACC GCGGANCACA GGGGACCCCA CGCACATTCC 180
 GTTGCCTTAC CCGATGGCTT GTGACGCGGA GAGAACCGAT TAAAACCGTT TGAGAAGCTC 240
 CAAA 244

SEQ ID NO:606

LENGTH:242

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00673

SEQUENCE DESCRIPTION:

GATCTTTCCC ATNTCTACCT AAGTCAGCTT TCATCTTTGT GGATGGTGTG TCCTTTACTA 60
 AATAAGAAAA TAACAAAGCC CTTATTCTCT TTTTTNTTG TCCTCATTCT TGCCTTGAGT 120
 TCCAGTTTCT CTTTGGTGTA CAGACTTCTT GGTACCCAGT CACCTCTGTN TTCAGCACCC 180
 TCATAAGTCG TCACTAATAC ACAGTTTGT ACATGTAACA TTAAAGGCAT AAATGACTCA 240
 AA 242

SEQ ID NO:607

LENGTH:245

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00674

SEQUENCE DESCRIPTION:

GATCCGGGTG GATGCACAGC CCGTCAAGGT CTATGCTGAC GNCTCCCTGG TCTTCCCCCT 60
 GCTTGTGCTT GAAACCTTTG CCCAGAAGAT GGATGCCTTC ATGCATGAGA AGAACGAGGA 120
 CTGAGCGGCT GCGGTCCAG GAAGGTCTTA CCCCCTCTNC TATTTATNAA TTTGCAGACC 180
 CAGCCCNCC CTTACTTTTT GGTCAGCTAC GNCTCTAGAA TAACNCCGG TATCTGAAGT 240
 CCAAA 245

SEQ ID NO:608

LENGTH:245

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00675

SEQUENCE DESCRIPTION:

GATCTCTACC ATTTAATTAA GAAAGCAGTT GCTGTTGAA AGCATCTTGA GAGGAACAGA 60
 AAGGATAAGG ATGCTAAATT CCGTCTGATT CTAATAGAGA GCCGGATTCA CCGTTTGGCT 120
 CGATATTATA AGACCAAGCG AGTCCTCCCT CCCAATTGGA AATATGAATC ATCTACAGCC 180
 TCTGCCCTGG TCGCATAAAT TTGTCTGTGT ACTCAAGCAA TAAATGATT GTTTAACTAA 240
 ACAA 245

SEQ ID NO:609

LENGTH:241

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00676

SEQUENCE DESCRIPTION:

GATCTAAAT GTCACATTCA GATTTTNAGG AAGAAAATCT TCATTACAGT GGAGCACAAA 60
TNTCCATAC AAGACATCAT TGAGGNAGCA TGCTGTCCCC TTCTAACCTG AAACACATTC 120
TTTCCCATCC NGGTTGGGCT TCTNTACCNC CTTATTAATT TATGAACCNG AAGTTGCTTG 180
AAGTGTTTG GCGTTAATAA ATGGGGTGAA AGTATAGGTA GCAGTAACAC CTACATGNAA 240
A 241

SEQ ID NO:610

LENGTH:240

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00677

SEQUENCE DESCRIPTION:

GATCTTCTGA GGTCAGGAGT TTGAGACCAG CCTGACCAAC ATGGAGAAAC CCAGTCTCTA 60
CTGAAAATAC AAAATTAGCC GGGCATGGT GTGCACGCNT GTAGTCCCAG CTAATTGGGA 120
GGCTGAGGCA GGAGAATCGC TTGAACCCAG GAGGCGGAGG TTGCGGTGAC CCTCCAGCTT 180
GGGCAACATG TTATGANTGA AACTCCATCT CAAAAAATAA AAAAAAAAAA GGGNNGCAA 240

SEQ ID NO:611

LENGTH:240

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00678

SEQUENCE DESCRIPTION:

GATCTGTGAA GGCTCCCTG ACCNNTGCCC AGGAAGAGTT CACTGGTCCG TCTGTTGTGC 60
CCCACAGCAC TTTGTTATAC CTCTGCCACA CACTTCACGC AGCGCGTTGT AACTCATGTG 120
TTTACATGTC TGTCCCNCCA GACTGTNAGC TCCTTGAGGG CAGGGACTGT ACATTCTCCA 180
GCTCTGTGTC CCCAGGGCCT GGCACATTGT AGACGCTTAA TAAATTTCTG TTAAATGAAA 240

SEQ ID NO:612

LENGTH:242

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00679

SEQUENCE DESCRIPTION:

GATCAGCTCC TTGACCTCTG AGGGGCAGGN GTGCTTCCTG GTGTGTGTAT TAGAATCCCT 60
TCCTGCCTTG TTTCATGGCA GTGAAATGCC TCTTGGTCTT GTCCAAGTGT ATCTTTCACT 120
GATTTCTGNA TCATGNTCTA GTTGCTTGAC CCTGCCANAT GGGTCCAGTG TTCATCTGAG 180
CATAACTGTA CTAAATCCTT TTTCCATATC AGTATAATAA AGGAGTGATG TGCAATAGCA 240
AA 242

SEQ ID NO:613

LENGTH:239

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00680

SEQUENCE DESCRIPTION:

GATCGCAACA ATNAGCCATC CACATNCGTT TTTCAGGGTC ACACCCAAGT AATTGAAAAG 60
ACACTCCTCC ACTTATCCCC TCCNTAATAT GGCTCTNCGC ATGCTGAGTA CTGGACCTCG 120
GACCAGAGCC ATGTAAGAAA AGGCCTGTCN CCTGGAAGCC AAAGGACTCT GCATTGAGGG 180
TGGGGGTAAT TTTTCTTGG NGGGCCAGT TAGTGGGCTT NCGNANTGTN TGTATGNGN 239

SEQ ID NO:614

LENGTH:238

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00681

SEQUENCE DESCRIPTION:

GATCCAAATA AACAGACCCC GTCTGGCAAG AAATGCATTG CAGCCAAAAA AATTAAACAG 60
TCGGTGGGAA ACAAAGCAT GTCCTTTCCA ACTGGAAAGT CAGACAGAGG CTTCAGGTAC 120
AACTGGCCAC AGAGATAGTC CTGGAAGACA CGTGGCGCCT GTGGACCGGA AGCACCAAAT 180
GCTGGTGCTG CTTTGTACA TACATATTTT TAAACCATTA AAATTCTTCC TGAAGAAA 238

SEQ ID NO:615

LENGTH:254

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00682

SEQUENCE DESCRIPTION:

GATCCATAGT CAGAAAAGTT ACTGCAGCTT AAACAGGAAA CCCTTCTTGT TCAGGACTGT 60
CATAGCCACA GTTTGCAAAA AGTGCAGCTA TTGATTAATG CAATGTAGTG TCAATTAGAT 120
GTACATTCTT GAGGTCTTTT ATCTGTTGTA GCTTTGTCTT TTTCTTTTTC TTTTCATTAC 180
ATCAGGTATA TTGCCCTGTA AATTGTGGTA GTGTACCAG GAATAAAAAA TTAAGGAATT 240
TTTAACTTTT CAAA 254

SEQ ID NO:616

LENGTH:247

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00683

SEQUENCE DESCRIPTION:

GATCAAAGAA AGAAGGCATA CGCNGATTTT TACAGAACT ATGATGTCAT GAAAGATTTT 60
NAGGAGATGA GGAAGGCTGG TATCTTTCAG AGTGTAAGT AATCTTGGA TATAAAGAAT 120
TNCTTCAGGT TGAATTACCT AGAAGTTTGT CACTGACTTG TGTTCCTGAA CTATGACACA 180
TGAATATGTG GGCTAAGAAN TAGTTCCTCT TGATAAATAA CCANTTAACA AATNCTTTNG 240
ACAGAAA 247

SEQ ID NO:617

LENGTH:235

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00684

SEQUENCE DESCRIPTION:

GATCTGCACC TGAGCCAAAG AAACCTGAGG AAAATCCAGC TTCTAAGTTC AGTTCTGCAA 60
GCAAGTATGC TGCTCTCTCT GTTGATGGTG AAGATGAAAA TGAGGGAGAA GATTATGCCG 120
AATAGACCTC TACATCCTGT GCTTTTNTCC TAGTTTCTCT CCACCCTGGA ACATTGAGA 180
GCAAATCAAA ACCTCTATCC AGACAAGACA AAATAAACT CAACATCTCC TGAAA 235

SEQ ID NO:618

LENGTH:238

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00685

SEQUENCE DESCRIPTION:

GATCTGTTCC TTGGCAGTGG ACTCAGAAAG CCAACATGTG GCTCCTCCCA GCCCATAACC 60
AGTATTTTTC CTGCTTCTAA ATACAAATNG GTTGGTTTTA ACTTCANATT GANCTTACTG 120
TAGCCTCAAA TGATTTCCTC CCTCCGCCTC CAGGAAGAAA GAATGTNACT GCCTTAATAA 180
AAAATGAAAA GAGAATGATG CTCAAAATCT TTCAAATAA AATGTTCCCT ATATTAAA 238

SEQ ID NO:619

LENGTH:234

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00686

SEQUENCE DESCRIPTION:

GATCCGCCCT CGAATGGACA CATTACCAGT GAAGGGGCAT TTNTNGTCAA TGTAGGTGCC 60
CTCAATAGCC TCCTTGGGTG TTTTGAAGCC CAGACCGATG TTCTTGTAGT ACCGCGGGAG 120
CTTCTCCTTG CCAGTTTCTC CCAGCAGGAC CCTCTTCTNG TTTTGAAAGA TGGTCGGCTG 180
CTTTTGGTAG GCACGCTCAG TCTGAATGTC CGCCATCTTC CCGGCCGGCT GAAA 234

SEQ ID NO:620

LENGTH:251

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00687

SEQUENCE DESCRIPTION:

GATCCCAAG CCTGGCAAGG GAATTTNTTC AACTCCCTGC CCCCCAGCCC TCCTTATCAA 60
AGGACACCAT TTTGGCAAGC TCTATCACCAGGAGCCAAA CATCTACAA GACACAGTGA 120
CCATACTAAT TATACCCCTC GCAAAGCCCA GCTTGAAACC TTCACTTAGG AACGTAATCG 180
TGTCCTCTAT CCTACTTCCC CTTCTAATT CCACAGCTGC TCAATAAAGT ACAAGAGCTT 240
AACAGTNAA A 251

SEQ ID NO:621

LENGTH:241

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00689

SEQUENCE DESCRIPTION:

GATCCATCAT CCGNCAATGT TAAAAGGCCCG GTGCGCGAG GGCACGTGC TCACCCTTTT 60
GGAGTCAGAG CGAGAAGCCC GGAGGTTGCG CTGAGCTTGG CTGCTCGCTG GGTCTTGGAT 120
GTCGGGTTTC ACCACTTGGC CGAGGGGAAT GGCTGTGAC AGTCTGCTCC TTTTTTTTGT 180
CCGCCACACG TAACTGAGAT GCTCCTTTAA ATAAAGCGTT TGTGTTTCAA GTTAACTCAA 240
A 241

SEQ ID NO:622

LENGTH:231

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00690

SEQUENCE DESCRIPTION:

GATCTCCTG CCTNGGCCCTC CAAAAGTGCT GGGATTACAT GCATACCTGA NCTACTGAGC 60
ACTTTNATCT TGAATGAGTG TTGGATTTTG TCAAATGCTT TTCCTGTACC TATTAATACA 120
ATCATGATTT TNNCTCTTT AGTATGTTGA TATGATGGGT TACATTAATT GATNNTCAAA 180
TGTTGAATCA GTCTNGCATA CCTGGAATAA ATCCCACTG GTCATAATAA A 231

SEQ ID NO:623

LENGTH:231

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00691

SEQUENCE DESCRIPTION:

GATCTATGAA ATCTGTGTAG GTTTTAAATA TTTTAAAAAT TATAATACAA ATCATCAGTG 60
CTTTTAGTAC TTCAGTGTTT AAAGAAATAC CATGAAATTT ATAGGTAGAT AACCAGNTTG 120
TCNCTTTTTC TTTAAACCAA GCAGTTGANA TGGCTATAAA GACTGACTCT AAACCAAGAT 180
TCTGCAAATN NTGATTGGNA TTGCACAATA AACATTGCTT GNTGTTTTAA A 231

SEQ ID NO:624

LENGTH:231

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00692

SEQUENCE DESCRIPTION:

GATCCCATTT AGGAANCGGC ATTCACTTCA GAAGGTACTT TTTAACTGCT CAGTTTTTGA 60
CTATTTTAAA TAGTTTGCTG AAAACTCCTG ATAACACTTG CTACATATCA TGTTTTAATT 120
GCTTGACAG TTAACCTTTA ATTTTATTTA GTAAAGTGTA TCAAAGTAGG ACTTTTTTGA 180
ATTGTAAATA GGTGGTTTAA TTAAATAAAA GTCAATGTAA AAATTGTAA A 231

SEQ ID NO:625

LENGTH:230

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00693

SEQUENCE DESCRIPTION:

GATCCGGAGG GAAATGTGTT AGAGGGTCTG GAAAATTCAG TGCTTTTGAG TTA CTGTGTTT 60
TTATTAAAAA TTCTCACA AAAGAGAGTC CTCAAGTTGT GGCTGTTCTT GGGAAAGGG 120
TCACCGTGTC TGACAAAGTG TAACTTTAAA AAGCACGTTG ATTTT TACA AATGTAAGTG 180
TGCTGGGAA TTCCTAAAT TTTGTGCAAT AA ACTATTTT TTGGAAGAAA 230

SEQ ID NO:626

LENGTH:202

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00694

SEQUENCE DESCRIPTION:

GATCCAATCA TATTNCTGT AGGGTGGAGG AGGTTTCAGA CCATCCCGCT CTGTTATATC 60
GAAGACCACA ATGGAAGACA AAGGCTTCTA AAGTATACCC CACAGCACGT GCATCGCGGA 120
NAGCCTNCTT GGGATAAAAT ATGTTTACAA TAACTTGCCT ATTGCTGAGA TTAAACCTTA 180
CAGGCTGCGT TATTTAGCA AA 202

SEQ ID NO:627

LENGTH:226

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00695

SEQUENCE DESCRIPTION:

GATCCATTGT ATCAGTACCT CACAATCAGA GTTGGCAAAT GATGGATGAG TGATTCAAGC 60
AGTGACCCG GTGGAAGCTG AAATCCATCT GTGAATGGAA CTGAAGTGAA CGTGAATATG 120
CTGACTATAT CCTGGAAGCA TTTTATACC ATCTTGAAAT TTCAACANAC TGGCTTTTGC 180
CAGTTAATCC AGCTGTCTTT CAAGAATAAA AGTTGGGGTT TTCAA 226

SEQ ID NO:628

LENGTH:226

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00696

SEQUENCE DESCRIPTION:

GATCACCTGA GGTCAGGAGT TCGANACCAG CCTGGCCAAC AGGGTGAACC CCGTCTCTAC 60
TAAAAGTACA AAAATTAGCT GGGCGTGGTG GCGGACGCTG TAATCTCAGC TACTTGGNAG 120
GCTGAAGCAG GAGAGGTGCT GGAACCTGGN AGGCGGAGGT TGAAGTNAGC CGAGATTGCC 180
CTATTGCACT CCAGCTCGGG CGNCAACTGC AAGACTCCAT CTCAA 226

SEQ ID NO:629

LENGTH:226

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00697

SEQUENCE DESCRIPTION:

GATCTGTAA TTTCTATCT AATAAATGCC TTNAATTGTN CTCATAATNA AGAATAAGTA 60
GGTATCCCTC CATGCCCTTC TGTAATAAAT ATCTGGAAAA AACATTAAAC AATAGGCANA 120
TATATGTNAT GTGCATTTCT AGAAATACAT AACACATATA TATGTCTGTA TCTTATATTC 180
AATTGCAAGT ATATAATAAA TAAACCTGCT TCCAAACAAC AATAAA 226

SEQ ID NO:630

LENGTH:226

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00698

SEQUENCE DESCRIPTION:

GATCAGAGTA ATTCTTTTGT ACATTGAAAT NAGGGGCTTG GTTTAAAAAA AGACCTTTCC 60
CTCTCCCTGC CCCTAGAACA ACCAGTATTA GAAGGTGCCA CCATTGGTGC TGCCTTCTNT 120
TCCCACAGCC TGTAAGTCAG TGTTTGTAC TTCACTGAAT TGTGATGGNT AGAAACTTCG 180
TGGGTAGNNN NTGGGAATCA TCCNGTTAAA CAANACGGGN TTTAAA 226

SEQ ID NO:631

LENGTH:222

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00699

SEQUENCE DESCRIPTION:

GATCCTTGGT GTACTGAGCA GTTCTTTTGG GGCTTTTCT TTCTGGGAAG CGGGAGGGAA 60
AGGAGCAAGG TGTCATCCTG CTCTTCATTT GTATTTTGGT CCCAAAATGT AAATACAATT 120
TNTTATGTTA CTTTTTGTG GTAAGTACCG AGATGAATAT TTTAATTAGA TAAGTTATAT 180
GAAAAGGAAA ATTCCATGTC TAAATAAAAA ACAAACTCCA AA 222

SEQ ID NO:632

LENGTH:222

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00700

SEQUENCE DESCRIPTION:

GATCTTCTGG ACAAACTTCT GCGATACGAC CATCAACAGA GACTGACTGC CAAANAGGCC 60
ATGGAGCACC CATACTTCTA CCCTGTGGTG AAGGAGCAGT CCCAGCCTTG TGCAGACAAT 120
GCTGTGCTTT CCAGTGGTCT CACGGCAGCA CGATGAAGAC TGGAAAGCGA CGGGTAATGC 180
GGCATTGATG CTTNCCAATA AAACCAACCA ACCAAACACA AA 222

SEQ ID NO:633

LENGTH:221

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00701

SEQUENCE DESCRIPTION:

GATCCACCCA GTTCTTTAGG CAACCACTGA TAGCATTTTC TTAAGTATTC TTCCAGATAT 60
CGTCTATGCA TATGTAAAAG TATCTGNCTT TCTCCNTTTA AAAACACAAT TGGNAATATA 120
TCATACTNGC TGGTTTGCAC CTNGCTTTTT TTGCTTAATA TATCTAGTTT ATAATGNCCN 180
AATGNGCAAA TTTTNGCATC NGCCCTAAAT ATCTACTGGN N 221

SEQ ID NO:634

LENGTH:220

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00702

SEQUENCE DESCRIPTION:

GATCACTCGT TTAAGTCCTT AGTTGTATGT NATCTCTTCT CTAGCAGGAA TTGGCAAAC 60
TTTTTGTAAG GGGGTAGAAA GTGAAGATTT TAAGGCTTTG CAGGCCATAT ATCCTCTNCT 120
GCAAATNCTC AGCCCTGCTG TTGTAATGTA AAANCTNCCA CAGACACTAC ATGAACACGA 180
ATGAGTGTGG CTGGTGTTCC AATAAACTT TATTACAAA 220

SEQ ID NO:635

LENGTH:220

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00703

SEQUENCE DESCRIPTION:

GATCATCAAA CCAGTCCACA AGCACAGGGA GATGCGTGGG CTGACATCTG CAGGCCGAAA 60
GAGCCGTGGC CTTGAAAAGG GCCACAAGTT CCACCACACT ATTGGTGGCT CTCGCCGGGC 120
AGCTTGGAGA AGGCGCAATA CTCTCCAGCT CCACCGTTAC CGCTAATATA NGTAAAGTTT 180
NGTAAATTC ATACTTAATA AACAATTTAG GACAGTCAAA 220

SEQ ID NO:636

LENGTH:219

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00704

SEQUENCE DESCRIPTION:

GATCCACATC TCAAAGAAGT GGGGCTTCAC CAAGTTCAAT GCTGATGAAT TTGAAGACAT 60
GGTGGCTGAA AAGCGGCTCA TCCAGATGG CTGTGGGGTC AAGTACATCC CCAGTCGTGG 120
CCCTCTGGAC AAGTGGCGGG CCCTGCACTC ATGAGGGCTT CCAATGTGCT GCCCCCCTCT 180
TAATACTCAC CAATAAATTC TACTTCCTGT CCACCTAAA 219

SEQ ID NO:637

LENGTH:215

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00705

SEQUENCE DESCRIPTION:

GATCCTCTCT CGACTNGCCA TACATTTCTT TCACAGCATT TACATAGTCC ATGATAGTTT 60
 ACTTGTGGGA TTATTTGGTT AATCTTTGCC TTAAACACCA GGGTTCCTTG GGTGAAGGAG 120
 CTTCTTTATC TNGGTAACAG CATTATTCA AGCATAACTN GTAATATAGT NATATTACAT 180
 ATATANCATA TATATATATN NCANANCANA TATAN 215

SEQ ID NO:638

LENGTH:214

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00706

SEQUENCE DESCRIPTION:

GATCTGGTTT CTTAGCAAAT TTCCAGTAG GATGTCATGT AAGTNCCTTC CCCCTCTTAG 60
 AGATTGAAGG CTGTAAGAGT CCAGATGGTG GAGCCAGGCT GTCTGGGTTC AAATGCCATC 120
 TTTGACACTT GCAAGCTAAA TNACATTACT CAAATTAATC GTTCTGCACT TCAGCTTCN 180
 TGTCTATCAA ATAAAAAGAA TAGTACCNGC CAAA 214

SEQ ID NO:639

LENGTH:215

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00707

SEQUENCE DESCRIPTION:

GATCATTGTA GATGANCTGA AGCAAGANGT TATCAGTACC AGCAGCAAGG CAGAACCACC 60
 CCAGTGCAAC TCCCTGGCCT GGNCTGCTGA TGGCCAGACT CTGTTTGCTG GCTACACGGA 120
 CAACCTGGTG CGAGTGTGGC AGGTGACCAT TGGCACACGC TAGACGTTTA TGGCAGNGCT 180
 TTACATGTGG GGGGAATAACN TGGCTTTTCT GTAAA 215

SEQ ID NO:640

LENGTH:220

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00708

SEQUENCE DESCRIPTION:

GATCAAACCA AGGCCCAGGC TGCAGCCCCA GCTTCAGTTC CAGCTCAGGC TCCCAAACGT 60
 ACCCAGGCCC CTACAAAGGC TTCAGAGTAG ATATCTCTGC CAACATGAGG ACAGAAGGAC 120
 TGGTGGGACC CCCCACCCCG GCCCCTGGGC TACCATCTGC ATGGGGCTGG GGTCTCCTG 180
 TGCTATTGTG ACAAATAAAC CTGAGGCAGG ATTTGTAAA 220

SEQ ID NO:641

LENGTH:210

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00710

SEQUENCE DESCRIPTION:

GATCGAGAAC CACATCCTCA AGCTCTTCGA GAGCAACCTG GTGCCCGCTA AACCTGAGT 60
GAAGGCCGCC TGCCGGGGAC TCAGACACTC AGGGAACAAA ATGGTCAGCC AGAGCTGGGG 120
AAACCCAGAA CTGACTTCAA AGGCAGCTTC TGGACAGGTG GTGGGAGGGG ACCCTTCCA 180
AGAGGAACCA ATAAACCTTC TGTGCAGAAA 210

SEQ ID NO:642

LENGTH:208

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00711

SEQUENCE DESCRIPTION:

GATCTGGTTT TATTCCTGTA ATTCAAGCCAC CTGATTTTGT GAGGGGGGGG AATAATATGT 60
GGTTTTTGTA CAAACATGTT TCTCAGTGTG TTGTNATTTT GGAAAAAATG AGGGGAGGGA 120
GTTTGGCAAG AATGGAGAAA ATGAATGAAG AAGGCCTAAT CTCTCTCTTT TTCAGTNAAT 180
AAATGGAACA CCATTCTGG ATTCTAAA 208

SEQ ID NO:643

LENGTH:206

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00712

SEQUENCE DESCRIPTION:

GATCTGTACA TTGTAAACA CCATTCAAGT GTCAGAATCA TTATTTTCCA CCACTTATCA 60
TGGTGCTTGA CAAGCTTCC CAATAAATAC TGAATGAACA AATGAATGGC AGAAACATTA 120
AAATGAACAC TATGGGGAAA GGGGAAGAGA GGCAGAATCA GAAATTATCC NGAATAAATA 180
TTTATNCCAT TTGTCATCCN NCNAAA 206

SEQ ID NO:644

LENGTH:244

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00713

SEQUENCE DESCRIPTION:

GATCTATGTG GTGAAAATGC ACAGGAGCTT GGTAGACTGC GGGGGAAAGA GAGAGCTCCT 60
TTGCGCATGT TTTACCAGTN TGCTGTTATA ACCTCTTAGG TTGTATCCTT TAATTTCCAG 120
CCTTTTAGGT TAGTTTCTGT AACAGAACAA GTGAGTCTGG GATGAAGTCC TCAAAGTACT 180
TCAAATGGTA ATTTTTTTGT TTTTGTAAATA GCTNAACAAA TAAACCNAGG GTTCTATAT 240
TAAA 244

SEQ ID NO:645

LENGTH:231

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00714

SEQUENCE DESCRIPTION:

GATCTATGAA TGANAGGAGG GCAGACCACA TTGCTTTTNA CATCCATTTC CCCTCCTTCC 60
CATGGGCAGA GGACCAGGCT GTAGGAAATC TAGTTATTTA CAGGAACTTC ATCATAATTT 120
GGAGGGAAGC TCTTGGAGCT GTGAGTTCTC CCTGTACAGT GTTACCATCC CCGACCATCT 180
GATTAATAATG CTTCTCCCA GCATAGGATT CATTGAGTTG GTTACTTCAA A 231

SEQ ID NO:646

LENGTH:200

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00715

SEQUENCE DESCRIPTION:

GATCTACATC TTTTCTAAA GAAAAGTGGG GCTTGCCTCC AGTTCAATTC ACAAGAGCAT 60
TTTCCCTCCC ATGCCACCT TTTCTGTGG CTGTCGCTAG GAAGGATGCA GAGGCTGTGT 120
GGTTACCAA ATGCCTTAAC TTAGCAGTGA ATGACAACTG TCAAACACAT GTTGAGGGGA 180
AATTTTACT GATTACAAA 200

SEQ ID NO:647

LENGTH:200

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00716

SEQUENCE DESCRIPTION:

GATCTGCCGC AAGTGCTATG CTCGCCTTCA CCCTCGTGCT GTCAACTGCC GCAAGAAGNA 60
GTGTGGTCAC ACCAACCAACC TGCGTCCCAA GAAGNNGGTC AAATAAGGTT GTTCTTTCCT 120
TGAAGGGCAG CTTCTGCCC AGGCCCGTG GCCCTGGAGC NTCAATAAAG TGTCCTTTN 180
ATTGACTGGG GNNGNANAAA 200

SEQ ID NO:648

LENGTH:199

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00717

SEQUENCE DESCRIPTION:

GATCCAGAAG GGGTTTGGTC TGGGACTTCC TTGCTCTCCC TCTTCTCAAG TGCCTTAATA 60
GTAGGGTAAG TTGTTAAGAG TGGGNAGAG CAGGCTGGCA GCTCTCCAGT CAGGAGGCAT 120
AGTTTTTACT GAACAATCAA AGCACTTGA CTCTTGCTCT TTCTACTCTG AACTAATAAA 180
TCTGTTGCCA AGCTGGAAA 199

SEQ ID NO:649

LENGTH:206

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00718

SEQUENCE DESCRIPTION:

GATCTTTTGT CCTACTGCT TTCTAATGGG GAGGGCTGAG GGTTCCTGT CCCCACAGCA 60
 GGTATGTTGG GNTCTGCCCC AGCCCCACAC TTGCTCTGAA AACCAAGTGN NAGAGCCCCT 120
 TCCCCTTGT TTTATTTTAC TGTATAATA ATTATTAAT TCCTTGTAAT AGAAATAAAG 180
 TTTGTAATTG GAGTTCAGCT CAGAAA 206

SEQ ID NO:650

LENGTH:201

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00719

SEQUENCE DESCRIPTION:

GATCCTCGTT TTCTNGGTTT TGGTGATGTT GGAGGAGTAC CCCCAGCCC ACCGCCCCGA 60
 TTCCTTTTGT CTCTGGTTT GGAGCTCCGG ACCAGGACCT TCGTCCTGGT CAGTTTTTAA 120
 ATAATNATT AGCAGTGTA CTTTTAAACC TGC GTGACAT CTACANNNG CCCAATAAAG 180
 AAAGAGGAAG CCACGGTCAA A 201

SEQ ID NO:651

LENGTH:198

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00720

SEQUENCE DESCRIPTION:

GATCTGTTAT CTAGCTGAGT TCATTCATC TCTCCCTTTT TTATATCAAG TTTGAATTTG 60
 GGATAATTTT NCTATATTAG GTACAATTTA TCTAACTGA ATTGAGAAAA AATTACAGTA 120
 TTATTCCTCA AAATAACATC AATCTATTTT NGTAAACCTG TTCATACTAT TAAATTTTGC 180
 CCTAAAAGAC CTCTTAAA 198

SEQ ID NO:652

LENGTH:197

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00721

SEQUENCE DESCRIPTION:

GATCTTAAAC ATCGGTCAGA TGAGTCATAC ATTGGGTTAT TTTTATATA CATGTATACA 60
 CAAAATATTT CAAATTGAAA GCAACATCTT AATGGATTCA AACTATTAC AAGCTGTTGT 120
 CTAAAACAGG TGAGAAAAAA ATTTATAACT GTAAAANCAA ATGCACATAT TGATATTTAA 180
 AATGCGTAAT TAAGAAA 197

SEQ ID NO:653

LENGTH:197

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00722

SEQUENCE DESCRIPTION:

2153480

GATCTGGACT GTCCTGGCAT CGAACTCTCC CTCTGTGTGT AATTGGAGGA GACCACAAGC 60
TGTTGTTTTG GGTGACTGAA GTATAAAGTG TTTNCTGTAC CTTAGATTCA CAAACTTTGT 120
ATTTTNAGTA CATATTTNNA AGAATTTCTA TAGTACATAT NTNNAAGAAT TTTNATATCA 180
AATATACCGT ATACTNN 197

SEQ ID NO:654

LENGTH:201

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00723

SEQUENCE DESCRIPTION:

GATCACCGCC GCGAGTAAAA AAGGCTCCAG CCCAGAAGGT TCCTGCCCAG AAAGCCACAG 60
GCCAGAAAGC AGCGCCTGCT CCAAAAGCTC AGAAGGGTCA AAAAGCTCCA GCCCAGGNNN 120
GCACCTGCTC CAAAGGCATC TGGCAAGAAA GCATAAGTGG CAATCATAAA AAGTAATAAA 180
GGTTCTTTTT GACCTGTAA A 201

SEQ ID NO:655

LENGTH:199

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00725

SEQUENCE DESCRIPTION:

GATCTGCAGT TTAAGTTGCC ATGCTGCTAG GAAATTGTCC TTTNCTTTC TAGCTGTAA 60
CCTACTTCCT GGAAAAAGTA GTAGCTCTCT GTAGCATTAT GGAGTTTCAG TGGAACCAAA 120
TNTTTGCCAT TAAAACTGG CATTATACTG AACTATACAT TGAGAAATCA ATCAAAATAA 180
AANTTTTAC TTTCACAAA 199

SEQ ID NO:656

LENGTH:196

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00726

SEQUENCE DESCRIPTION:

GATCTGGTTT CTAGCAAATT CCCAGTAGGA TGTCATGTAA GTCCTTCCCC CTCTTAGAGA 60
TTGAAGNTGT AAGAGCCAGA TGGTGGAGCA GGCTGTCTGG GTTCAAATGC ATCTTTGCAC 120
TTNAAGCTAA ATGACATACT CAAATTAATC GTCTGACTCA GTTCCTTGCT ATCAAATAAA 180
AAGATAGACC TGCAAA 196

SEQ ID NO:657

LENGTH:201

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00727

SEQUENCE DESCRIPTION:

GATCTGCCTG CCTCAGCCTC TCAAAGTGTT GAGATTACAG GCGTGAGCAN CCGCTCCCTG 60

00462

2153480

CCCAACACAT ATACCATCTG AAAATGTTAG AATTCTGAGT TGTGATTTTA TTGACTTGTT 120
GCTTGCTTTT CCTNAGGCTT TGTAAGTGT AATATGTAA AGTGTACTAT CCTAATAAAC 180
TGAATACTTT GGTATCTTAA A 201

SEQ ID NO:658

LENGTH:197

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00728

SEQUENCE DESCRIPTION:

GATCCTCCAT TGGAGTGGCC CAAATCTTTC CATCTAGGGC AAGTCCTGAA AGGCCCAAGG 60
CCCCCTCCCC AGTCTGGCCT TGGCCNCCAG CCTGGAGAAG GGCTAACATC AGCTCATTGT 120
CAAGGCCACC CCCACCCAG AACAGAACCG TGTCTCTGAT AAAGGCTNTT GAAGTGAATA 180
AAGTTTAAAA ANCTAAA 197

SEQ ID NO:659

LENGTH:195

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00729

SEQUENCE DESCRIPTION:

GATCGTNTTT GTTTGTITT TAAAGAAAGG TGAGATTGGC TTGGTTCTTC ATGAGCACAT 60
TTNATATAGC TCTTTCCTG TTTNCCTTG CTCATTTCTG TTTGGGGAAG AAATCTGTAC 120
TGTATTGGGA TTGTAAAGAA CATCTCTGCA CTCAGACAGT TTACAGAAAT AAATGTTTTT 180
TTTGTNNC AGAAA 195

SEQ ID NO:660

LENGTH:196

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00730

SEQUENCE DESCRIPTION:

GATCTCAAAC TCCAGGCTCA GAACTGTGAA GACTGTTTCC AGCCTGGCTG TGAGCCAAGA 60
CCTGGTTCCT GGTGGACCCT GAGGACAAAG TGTGATAAAA CCTCTGGCTC AGACTTGCTC 120
TACTGAAGGC TTCTGGTTA TAAGATGCAT AAAGTCACTG GGGCTAGCTA AACAATAAAG 180
AGTTTATTGT GAGAAA 196

SEQ ID NO:661

LENGTH:194

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00731

SEQUENCE DESCRIPTION:

GATCTAATGT ACTGTAAGT TATCAGTGAA AGGTAAAATC TCAAATAACA AGTACAAACA 60
TTGAACAATT ACCTATAAAG ATTTNTAAAA GTAAAATTTT TCCAATAGAT TTCATTCTTG 120

00463

TCATTTTGTA AGACGACCCT GCAGTCCACC NGTTTGTAAC TTTTSTAATA AAATAGACAT 180
CTGTATTACT GAAA 194

SEQ ID NO:662

LENGTH:246

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00732

SEQUENCE DESCRIPTION:

GATCAAGAAA ATAAGGACAA CGTGAAGTTT AAAGTTCGAT GCAGCAGATA CCTTTACACC 60
CTGGTCATCA CTGACAAAGA GAAGGCAGAG AAAGTGAAGC AGTCCCTGCC CCCCAGTTTG 120
GCAGTGAAGG AACTNAATAA ACCAGACACA CACAGAACAG GCGATTATTT ATTTGTTTTT 180
AATTTATTTT GTCATATTTT TGTAAAACGG CAGAAATGCA ATAAAACCTA TATTTCAACA 240
GTGAAA 246

SEQ ID NO:663

LENGTH:192

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00733

SEQUENCE DESCRIPTION:

GATCATATTT TATACATGTG TAATAGATAA AAATAAACCA GATTGCAAAT CCTTTTTTAA 60
AATCCTAAAC CATGTACCAA GTTTTTGGTC CAAATTATGT AGGATAAGTT AAAGTAAAT 120
TGCATTCTAT TAACCAATAT GAGTGTATTT CTGTAAGCAT AGTTATGTTG AAATAAGTT 180
TTAAAAACCA AA 192

SEQ ID NO:664

LENGTH:191

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00734

SEQUENCE DESCRIPTION:

GATCTTCACA CTAATGATGA GTGTGTGGCT ACATACAAAG GAGTTCCCTT TGAGGTGAAA 60
GGGAAGGGAG TATGTAAGGG CTCAAACCAT GAGCAACAAG TGGAATCAAA TAAATGCTT 120
CCACNACCAA AAGACATTAG AGAAAACCTT AAAAGTAATA AAGNGAAATA TATTTNTCAC 180
TTATACCTAA A 191

SEQ ID NO:665

LENGTH:188

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00735

SEQUENCE DESCRIPTION:

GATCTGAATC TNCCGGGGCC CCAGCCCACT CCACCCTGCC AGCAGCTTCC AGCCAGTCCC 60
CACAGCCTCA TCAGTCTCT TCACCGTTTT TTGATACTAT CTTCCCCAC CCCCAGCTAC 120

CCATAGGGGC TGCAGAGTTA TAAGCCCCAA ACAGGTCATG CTCCAATAAA AATGATTCTA 180
CCTACAAA 188

SEQ ID NO:666

LENGTH:186

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00736

SEQUENCE DESCRIPTION:

GATCTNAAAC CCAAGGGTCT GAGGCCAGGG CCGACTGCCG TAAGATGGGT GCTGAGAAGT 60
GAGTCAGGGC AGGGCAGCTG GTATCGAGGT GCCCATGGN AGTAAGGGGA CGNCTTCCGG 120
GCGGATGCAG GGCTGGGGTC ATCTGTATCT AAAGCCCCTC GGAATAAAGC GCGTTGACCG 180
NCGAAA 186

SEQ ID NO:667

LENGTH:184

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00737

SEQUENCE DESCRIPTION:

GATCTGTAAA TAATCATTGC CAGTNTGACT TTTGTTCAAC AAAAGGATTG TACTGTATTA 60
AGAACCGATG AAAAAAATTN TCCTGTAACA TTTTTTAAG AAAACTTTGT TTGTTTAAAG 120
AAAAAGTATT GTATAANTNA TAATTTAAT TTAAATAAAC CTAAAATGCT TTGTGCTAAG 180
GAAA 184

SEQ ID NO:668

LENGTH:180

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00738

SEQUENCE DESCRIPTION:

GATCCCAGAA AAGTTCTAAT TTTCATTAGC AATTAATAAA GCTATACATG CAGAAATGAA 60
TACAACAGAA CACTGCTCTT TTTGATTTTA TTTGTACTTT TTGGCCTGGG ATATGGGTTT 120
TAAATGGACA TTGTCTGTAC CAGCTTCATT AAAATAAACA ATATTTGTAA AAATCATAAA 180

SEQ ID NO:669

LENGTH:179

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00739

SEQUENCE DESCRIPTION:

GATCTATCCA AGGTTTTGAC ATGTATCGAG AGTTTATTCC TTTTATTGTC TGAATAGTAT 60
TAATATTCTA TAGTATGGAT GTAACATAGT GTGTTTAAAC ATTGCCTGT TGAAGGACAC 120
TTGGGTTGTT TCCAGTTTCA GGTTCTTACA AATAAAGCTA CTCTGTGTGT TCATGTAAA 179

SEQ ID NO:670

LENGTH:179

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00740

SEQUENCE DESCRIPTION:

GATCAAATGC CAGTGTTCATT TTGTACTTAA GTTCCAAAGT AGGAACATTN TATACTTTTT 60
NCTGTATTGT AATAGGTAGT TTTGTATGAA ATCTTTTCTC CTCTCCCGTT GTACCGCATT 120
CTTCCAGCA TTGTGCTTTT TCCCTGGNCT TATTTGAAAA TTTTACTGTT TTATACAAA 179

SEQ ID NO:671

LENGTH:177

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00741

SEQUENCE DESCRIPTION:

GATCCAAGAA ACCAGGGCCA TGACCAGGTC CACTGTGGAG CAGCCATCTA TCTACCTGAC 60
TCCTGAGCCA GGCTGCCGTG GTGTCATTTT TGTCATCCGT GCTCTGTTTC CTATTGGAGT 120
TTCTTCTCCA CATTATNTTT GTTCCTGGGG AATAAAAACT ACCATTGGAC CTAGAAA 177

SEQ ID NO:672

LENGTH:175

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00742

SEQUENCE DESCRIPTION:

GATCTGCAAG TCCCGGAGAG CAACAGCACA GCTCTGCCTG ACGCTCTCAT TAAAATCTAT 60
GCAGCCAAGC TCGGCACTTT GTAGCAGCCG GCCTTGCGAA GCCTCCTCAG CTCGGGGGGC 120
CGGGGACCCA GTGAGCCGAG AGCCCTCTGG NCTCCACTTA TGCATATGCA CCAAA 175

SEQ ID NO:673

LENGTH:180

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00743

SEQUENCE DESCRIPTION:

GATCCGGAGA ATAGGGCINN AATATGTGCC GCCAGTGTTT CCGTCAGTAC GCGAAGGATA 60
TCGGTTTCAT TAAGTTGGAC TAAATGCTCT TCCTTCAGAG GATTATCCGG GGCATCTACT 120
CAATGAAAAA CCATGATAAT TCTTTGTATA TAAAATAAAC ATTTGAAAAA ACCCTTCAAA 180

SEQ ID NO:674

LENGTH:176

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00745

2153480

SEQUENCE DESCRIPTION:

GATCTATTCA GATGGTTCTG ATGAAGTGAA ACGNGCCATG AACAAATCCT TTATC>NNGT 60
CGGGTGGTAC AGTTTGGAGT ACCAACTGGT CTGATGTAGG TAAAAGGAAA GTTGAAATCA 120
ATCCTCCTGA TGATATGGNN NGGAAAAAGT ACTAAATAAA TTAATTGCT CTCAAA 176

SEQ ID NO:675

LENGTH:173

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00746

SEQUENCE DESCRIPTION:

GATCAAAACC AGTTTGATTT GGGAATCTTC CCCTTTCCAA ATGAAATAGA GATGCAGTAC 60
TTAACTTTCC TTGGTGTGTTG TAGATATTGC CTTGTGTATT CCACTTAAAA CCGTAATCTA 120
GTTTGTAATA GAGATGGTGA CGCATGTAAA TAAAGCATCA GTGACACTCT AAA 173

SEQ ID NO:676

LENGTH:173

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00747

SEQUENCE DESCRIPTION:

GATCCTAGCA TCCCTTTTCA CATGGTTTCT CCATGTATAT AACAGAATCA AGAAACAAAT 60
TTNAATTAATA CAATCTGTAA CAGAAATCAAG AAACAAATAC ATTTTAATTA AACAATCTAT 120
ATGGAACAAA CATTCCTAAA TNCTAAGAAT AANTNTTCNT NTAAGTTTTC AAA 173

SEQ ID NO:677

LENGTH:182

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00748

SEQUENCE DESCRIPTION:

GATCCAAATA ATTTATTAATA TGAAGTGTCT CAGAAACTGA ACTCATTAAAT GTCTCTGGTT 60
AACAAACTA CGCATCTCAT AGCCAAAGAG GAGATGATAC ATAATCTACA ATAAGGGTCT 120
TAGTGCTTTA GAAAAAGTT AAAATTGGAA GTCATTAATA AAAGACTGTT ATAATGGTGA 180
AA 182

SEQ ID NO:678

LENGTH:173

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00749

SEQUENCE DESCRIPTION:

GATCTTATGA GAAGAGGAAG GAGAGANGTC TCTNCCTATG CTCACACACA AAGGAAAGTC 60
CACATGAGGA CACAAGGAGA AGCCAAGAGN GCCCTTACCA GGANTTAAAC CTGCTAATCC 120
CTATTTTAAT TAGAACAGTG AGAAANTAAA TATCTGTATT TAAGCCTCAC AAA 173

SEQ ID NO:679

LENGTH:173

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00750

SEQUENCE DESCRIPTION:

GATCCAGAGA AAGCCAAAGC TCTTAGTAAA CACTTGCCAT CGTCAGTNTN ATGTCTCTAA 60
AAGTAGATGT TGAGGCTCTT NAAAATNCTC CTGGTGCTAC ATACATTCGG AAGAAGGGTG 120
GAAAAGTTAC TGGAGATAGT CAACCAAAGG AACAAGGACA GGNAGATTG AAA 173

SEQ ID NO:680

LENGTH:172

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00751

SEQUENCE DESCRIPTION:

GATCCAATCC ATTACAGAGT CCATTGAAAG GCTCTTAGTC TAAACCTGTG GCCTCTGCCA 60
CGTNGCTCCC TGCCAGCTTC CCCCTGAGG TTGTGTATCA TATTATCTGT GTTAGCATGT 120
AGTATTTTCA GCTACTCTCT ATTGTTATAA AATGTAGTAC TAAATCTGGA AA 172

SEQ ID NO:681

LENGTH:170

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00752

SEQUENCE DESCRIPTION:

GATCAAATTT AAACCTCATT TTGGGGGGTA TTTTGGTACT GTAATGGGGT CATCAAATNA 60
TTAATCTGAA AANAGCAACC CAGAATGTAA AAAAGAAAAA ATTGGGGGGA AAAAGACCAG 120
GTCTACAGTG ATAGAGCAAA GCATCAAAGA ATCTTTAAGG GAGGTTTAAA 170

SEQ ID NO:682

LENGTH:239

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00753

SEQUENCE DESCRIPTION:

GATCGGAACA GCTCCTTACT CTGAGGAAGT TGATTCTTAT TTGATGGTGG TATTGTGACC 60
ACTGAATTCA CTCAGTCAA CAGATTGAGA ATGAGAATGG ACGTTTGTT TTTTTTGTT 120
TTTGTTTTG TTTTTCCTT TATAAGGTG TCTGTTTTT TTTTNAAAA AATNGCANCA 180
GTNCATGGCC CCCATCATT ANANGNGAGG ANTNCANCAG AAAATAAAAT ATNCACTCN 239

SEQ ID NO:683

LENGTH:170

TYPE:nucleic acid

2153480

TOPOLOGY:linear

CLONE:HUMGS00754

SEQUENCE DESCRIPTION:

GATCCAGACA GCCATCAGGG AAAGCTTGTN TTAAACCGAA CTGTCACACT GAAGGAAGAC 60
CCAGGAAAGG TGTGAGCTGG AAGCACTGAA CCTACCTCAT CCTCCTGGAG GGTGTGGCTA 120
CGCTCGCCAC CCCAAATTCC ATGTCAATAA AGAACAGCTA AATTCTCAA 170

SEQ ID NO:684

LENGTH:168

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00755

SEQUENCE DESCRIPTION:

GATCTTTCCA TTGGAATATA CTGGAAGTGA AGAGGTTTTG TTGCTTGAC AGTGTGAGAT 60
GAGGAACACC ACTATCTTAA TTTGTGATA CACTGCATT GCTGGTGCTA TTTNATACA 120
GTGAAGCAAC AGCTTGCAG CAAAATAATA AAATACTTCT ANGTTAA 168

SEQ ID NO:685

LENGTH:169

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00757

SEQUENCE DESCRIPTION:

GATCCATCGT NATGTCTTAT TTAAGGGGAA CGTGTGGNCT ATTTAGGCTT TATGGCCCTG 60
AAGTAGGAAC CAGATGTCGG ATACAGTCA CTTAGCTAC CCCCAAGTNT TATGGGCCCG 120
GAGCGAGGAG AGTAGCACTC TTGTNCGGGA TATTGATTTC ACGGAGAAA 169

SEQ ID NO:686

LENGTH:171

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00758

SEQUENCE DESCRIPTION:

GATCTGCTAC TAAACAGAGT TCAAAACTT TCCAGAGTAA TTAATATGTA AAGCCANGTA 60
ACTAACAAAN GATTTGCTTT AGAGATAATT ATTTGGAATT TTTATAGCTN ACTTCACAAT 120
GTGCCCAGGT CAGCTGTATA AAATAAATAC TGCATTNTNG TTTCTTTCAA A 171

SEQ ID NO:687

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00759

SEQUENCE DESCRIPTION:

GATCCTGACA CTAAGGAAAT GCTGAAGCTT TTGGACTTCG GCAGTCTGTC CAACCTTCAG 60
GTCACTCAGC CTACAGTTGG GATGAATTC AAAACGCCTC GGGGACCTGT TTGAATTTT 120

00469

NCTGTAGTGC TGTATTATTT TCAATAAATC TGGGACAACA GCAGAAA

167

SEQ ID NO:688

LENGTH:166

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00760

SEQUENCE DESCRIPTION:

GATCAGCGAT GAAGAGGAAG AAGATGATGA TTGAAGTATG AAATATGAAA ACATTTTATA 60

TATTTNATTG TACAGTTATA AATATGTAAA CATGAGTTAT TTTGATTGAA ATGAATCGAT 120

TTGCTTTTGT GTAATTTTAA TTGTAATAAA ACANTTTAAA AGCAAA 166

SEQ ID NO:689

LENGTH:175

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00761

SEQUENCE DESCRIPTION:

GATCTATTTG GTCTTTCTCA TGTCCCCAC TGGTCTGTAC CCCAGGGAGC GGGTGCTTGT 60

ACTGTGTGAA TCCAGTGTC ACATTCACAC TTAATGACTT CCTTGGCACC AATCATGTAT 120

TTCACCGTTT GCACTTNTTG TATTTCAATA AAAATGTTGA TGCAAACTG CTAAA 175

SEQ ID NO:690

LENGTH:165

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00762

SEQUENCE DESCRIPTION:

GATCGACTCT ATCATCCAAC GCTCCGAGGA CAGCCCATGT CCCCACCCN GNGACCCGGA 60

CCCGGCCAGC AGGACCCACT GAGANGGGCT GCCCGGNGCT NCTCAGCTGC CCACACCCAC 120

ACTGTCCAGC ATCTGGCACA ATAAACATNC TCTGTTTTGT AGAAA 165

SEQ ID NO:691

LENGTH:164

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00763

SEQUENCE DESCRIPTION:

GATCAAGAAA TAAACATAAA CATCTCAGAA TGCTCCTTCA TTACCAGAGT CACTACCTGA 60

TTATGTCTTA ATGGGTTACA TAATGACAGA GGGTATCTCA TATATGTNCT TTTCCAAACA 120

TAAATAACT TTTGTTTTG TTTGATTGAA AAAAAATTA GAAA 164

SEQ ID NO:692

LENGTH:171

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00764

SEQUENCE DESCRIPTION:

GATCCAGATT CTCACTTAAT GGGGTTTATA TGGACTTTCT TCTCATAAAT GGCCTGCCGT 60
CTCCCTTCCT TTGAAGAGGA TATGGGGATT CTGCTCTCTT TTCTTATTTA CATGTAAATA 120
ATACATTGTT CTAAGTCTTT TNCATTAAAA ATTTAAAACT TTTCCCATAA A 171

SEQ ID NO:693

LENGTH:164

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00765

SEQUENCE DESCRIPTION:

GATCGACTCT ATCATCCAAC GCTCCGAGGA CAACCCNTGT CCCCACCCCC GGGACCCGGA 60
CCCGGCCAGC AGGACCCACT GAGAAGGGCT GCCCGGNTCA CCTCAGGGGG NCACANTTTA 120
CACTCTCCAG CATCTGGCAC AATAAACATN CTCTGTTTTG TAAA 164

SEQ ID NO:694

LENGTH:168

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00766

SEQUENCE DESCRIPTION:

GATCTAATGG TCTAAAACT GGAGTTTCCG GACACAAGCT CTCCCTTNC CTGCAACCAT 60
CCATGCAAGA TGTNACTTGC TCCTCTNTGC TTTCTGCCAT GATTGTAAGG CCTCCCCAGC 120
TACATGGAAC TNTAACTCCA TTAAACCTCT TTNTTTTGTA AATTGAAA 168

SEQ ID NO:695

LENGTH:160

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00768

SEQUENCE DESCRIPTION:

GATCCGCCCA CCTCAGCCTC CTAAAGTGCT GGGATTACAG CTGTGAGCCA CCCTGCCCGG 60
CCACTTTTGT ATGATTTCTA ATGTATTGT AATTTACCTA ACAAATTGCC TAATCTGCTA 120
TGTTAATGTA TTTATGAATT AAAATAAATA CGACTGCAAA 160

SEQ ID NO:696

LENGTH:161

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00769

SEQUENCE DESCRIPTION:

GATCCGTAGC GGCATGTTCT GGCTGCCGCTT CTAGGCGGGA AGCCTATGTA AGCAAGAGGG 60
CAGGGCCGGG GTTTGTGGTC CCCCCCCCAC CACAAACACA GCACTTCGGC TCCTCTAACC 120

TGTGCCACAG GTGACCACCA ATAAATCCT CTGCTGAGAA A 161

SEQ ID NO:697

LENGTH:159

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00770

SEQUENCE DESCRIPTION:

GATCTCCCTG CCCCCACCCC AGTTCCCCAA CCCACTCCCT TCCAACAACA ACCAGCTCCA 60
ACTGACTCTG GTCTTGGGAG GTGAGGCTTC CCAACCACGG AAGACTACTT TAAATGAAAA 120
AANGAAATTG AATAATAAAA TCAGGAGTCA AAATTCAAA 159

SEQ ID NO:698

LENGTH:159

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00771

SEQUENCE DESCRIPTION:

GATCTTTTNN TTTTTTTTAA GTCTCACAAG ACATGGGGCA TCTCCACAAA TTTAAGTTCC 60
TGTCCATTG GAAATTTGTT TCTATGTGTA CAGTTTGTCA GAGAAAAACA AAGTTTTTGT 120
ATGANTACAG AATGTGATT ACGCAAGATT TGACAGAAA 159

SEQ ID NO:699

LENGTH:161

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00772

SEQUENCE DESCRIPTION:

GATCTACCTA TCTTCAGGAT GGAACCTTGG GGAAAAATAA AATTGAGGGG AAGTAAAAAG 60
TATGTAACAC TTCCAGTTGT GAGCCAAGAT TGTACCAGA GAGCAGCCAG GAGCTTCCTG 120
TCAGTAACCA TTTTTTCAAT AAATACTCTT TCATGTACAA A 161

SEQ ID NO:700

LENGTH:157

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00773

SEQUENCE DESCRIPTION:

GATCCTCTCA CCTCAGATT CCAAAGTGTT GGATTATAGG TGTAAGCCAC TGAGCCCAGT 60
TTGAATGCTT TTTTATATAT TTTTGGCCA TTTGTATGTC ATCTTTGGAG AAATGTCTAT 120
NCAAAATCNT TGCTCATTAA AATNATTNC TGATAAA 157

SEQ ID NO:701

LENGTH:160

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00774

SEQUENCE DESCRIPTION:

GATCTGGCCG TNAGCCGCGA NCCGCTGNGA ACTCCACTCG GGGAACTCCT TTCCAAGCTG 60
ACCTCAGTTT TCTCACAAGA ACCCAGTTAG CTGATGTTTT ATTGTAATTG TCTTAATTTG 120
CTAAGAACAA GTAATAAGTA AATTTTAAA AAGCCTTAAA 160

SEQ ID NO:702

LENGTH:161

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00775

SEQUENCE DESCRIPTION:

GATCAAATTG TGCAGTACTT TGTGCATTCT GGATTTTAAA AGTTTTTNAT TATGCATTAT 60
ATCAAATCTA CCACTGTATG AGTGGAAATT AAGACTTTAT GTAGTTTNA TATGTTGTAA 120
TATTNCTCCA AATAANTCTC TCCTATAANC CACCAGGGAA A 161

SEQ ID NO:703

LENGTH:154

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00777

SEQUENCE DESCRIPTION:

GATCAGAGCT TATACTTAAT TAAGGTTTTA TACACACCAG TTCCCCAGTA AATNCAAATT 60
TAACAAGAAA ATCAGACATG TCATATGTNC AAAATGCTCA TGGCAAACAA TCATTTTGCA 120
TTCCTGCAAA TAAAATTGTT TTACTGTGA GAAA 154

SEQ ID NO:704

LENGTH:153

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00778

SEQUENCE DESCRIPTION:

GATCTGTTTG TTCCCTGAGC TTTTAAATA CCCTGTGAAA ATTTNTTTC CTCCCTTGGT 60
CATCATGCAT CTAATTGTGG GGAAATGTTT GTCAAACCAA CCTGCAAAGC AGCATGGTGT 120
AGTTGAGAAG AATAACAGA GAAGACTGGG AAA 153

SEQ ID NO:705

LENGTH:152

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00779

SEQUENCE DESCRIPTION:

GATCTTTGGA CAGAAGCAGC TCTTTCCCGA ACACTTGTGG CGTCTGGNAC GGCCCCACCC 60
NTCCCCCAC ACTCCCTCCC ACGGGGCTCC GGGAGACAGG CCGGCCCTGC ACCTNACCCC 120

ACCGTGACCT CAATAAACGT TGAAACTNCA AA

152

SEQ ID NO:706

LENGTH:152

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00780

SEQUENCE DESCRIPTION:

GATCTATCCT TTA CTGAAA GCTTTGAAA AGTGGAAGG TCATTTTGT GCATTTCCTC 60

ATTTCTGT TTTAAAGAC CAACAAATCT CAAGCCCTAT AAATGGCTTG TATTGAACTT 120

TTACATTGA ATTAAAGATG TTAAACATGA AA

152

SEQ ID NO:707

LENGTH:151

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00781

SEQUENCE DESCRIPTION:

GATCTAGTAT GCTCCTGGTC TAATGCATTT ACATTGTGTA GGTAAGTGGT TCCTAATAAA 60

AAGAATTATA AAATACCTC AAATTAACAA TTCAATNGCA TATAATAGCC TAACTCAGTA 120

AGANTATTAA AACTTACTAT TATNCTTCAA A

151

SEQ ID NO:708

LENGTH:152

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00782

SEQUENCE DESCRIPTION:

GATCTANTCT GTGCTACCTG ATTAAGTAC AGCAGGCTTA CTGANTGGCT TCATTTCAGA 60

TTTAGTTGAT TTCTCCACCA AATNCATGTC ATGTATTCTC AATAGGCTGT ATTCCCAGCA 120

GNCAATAAAT GGAACACCCG TANAANCNCA AA

152

SEQ ID NO:709

LENGTH:147

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00783

SEQUENCE DESCRIPTION:

GATCCCCAGG GTTCTTTGT CTTATTTATG GAGAAAAACC GGTCACTTTG TCCAGCGCAC 60

TGTGAGGCCC CCACTCAGGC CAGCCCTGGC CCCCCCTGG TACTTGAAC CGAAGTTACA 120

GATTATATTA AAATAATAAT GTACAAA

147

SEQ ID NO:710

LENGTH:146

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00784

SEQUENCE DESCRIPTION:

GATCTTATAA AAGGAAATTC TAGCAGTTTT AGAAATAGGT GGGAAAACT CAAATATTCC 60
TCCTATCTGC ACCAAAAAGT TTATTTGTGG TATATAAAT GAATATTGTT TTATAATAAC 120
TTGTTAATAA AGTACTTTCT AATAAA 146

SEQ ID NO:711

LENGTH:145

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00785

SEQUENCE DESCRIPTION:

GATCAATGAA GTGAGAAATT GTTGAGAAGG ATACAGTTTG TTTTAGATG TCCTTTGTCC 60
AATGTGAACA TTTATTCATA TTGTTTGAT TACCCTCGTG TTACTACAAG ATGGCAATAA 120
ATACTATGGG ATTGTTTGA TTAAG 145

SEQ ID NO:712

LENGTH:145

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00786

SEQUENCE DESCRIPTION:

GATCTCCCTT CAGCAACTTA TTTTGCTTTA ATTGCTTTAA ATCTTAAGCA ATATTTTAA 60
TTCAGTAAAC AAATCTTTC ACAAGGTACA AAATCTTGCA TAAGCTGAAC TAAATAAAA 120
NTGAAAAGGA GAGATTAANG GTAAA 145

SEQ ID NO:713

LENGTH:145

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00787

SEQUENCE DESCRIPTION:

GATCTAGAAG CAGAGGAATC CCAGCGCCTT TAAAAGTTG TTATGTGGTT TTCTTTTAA 60
AAGCTCCTGT TTTTGAAAG TAGAATTTAT GGTACAACG TATGTTTATT ATTGTACAT 120
AAAATAAAC CATTTAATAA GTAAA 145

SEQ ID NO:714

LENGTH:154

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00788

SEQUENCE DESCRIPTION:

GATCTATGCC TAACAGAGCC CCAGTACAAC TATTTTNCAG AATGGCTGTT ACCCTAGAAT 60
TACTATAGCA CATATTGAGA TATAGTTGTA CTCCTAGTA GATAGGAACT GACCCAACA 120

ATAAACTTTG ATAATAAAGA AAAAAAANCG NAAA

154

SEQ ID NO:715

LENGTH:144

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00789

SEQUENCE DESCRIPTION:

GATCAACCTT AAAGGAACT GCTATCCGAA CTTGGCTATC TCACAGCAGA GCCAGTTTGA 60
CGAATGGGTA AAACCTAAGG ACATGCTGGG TCCAAAGTGA TTTACATAAA TNTATAATGA 120
AAATAAACAT GTATAANATT TAAA 144

SEQ ID NO:716

LENGTH:149

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00790

SEQUENCE DESCRIPTION:

GATCCGTGAT GCCACTTACC TGTGTGTTTG GTAACAACAA ACCAACATCA TGGAGGTCCC 60
TGGATTGAAA AAGGAGCCTC TCCCACTCCT CCTACCACCA AAGTGGTTAG GACNCTATAT 120
AANTAAAAAC AAGGCTTTTG GAAAAATAA 149

SEQ ID NO:717

LENGTH:147

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00791

SEQUENCE DESCRIPTION:

GATCTGGCTG AACCAAGTCC ACAAGGTTAC TGTATACATA GCCTGAGTTT AAAAGGCTGT 60
GCCCACTTCA AGAATGTCAT TGTTAGACTT TGAAATTTCT AACTGCCTAC CTGCATAAAG 120
AAAATAAAAT CGTTTAAAT CAAGAAA 147

SEQ ID NO:718

LENGTH:115

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00792

SEQUENCE DESCRIPTION:

GATCTGGGGC AGCCACCTTG CTACCATGAA GGAAAGGCCA AGACAATCAT CCACAGCTAT 60
TCCCTCCAGC ATCTGGTTCT GTACAAAAAT TAAATGCTTA TTTNTTTAAG TCAAA 115

SEQ ID NO:719

LENGTH:142

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00793

SEQUENCE DESCRIPTION:

GATCGCCACT GTAAAGGTCC TAGAGTTGCC TGTTTGTCTC TGGAGATGGA ATTAAACCAA 60
 ATAAAGAGCT TCCACTGGAG GCTTGTATTG ACCTTGTAAC TATATGTAA TCTCNTGTTA 120
 AAATAAAATA TAGCTTGTGA AA 142

SEQ ID NO:720

LENGTH:142

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00794

SEQUENCE DESCRIPTION:

GATCTGTGCC TACNTTTTAC CACCCTCTTG ATTGGAGCTT TTGTNATGCA GCTACCATNN 60
 TTCAAAAAA TTAAAAATTA AAAAAAAAAA ATCTGCCACT TATCCAAGTC CACTAGAGGC 120
 CACTGTCTTC AAAGNTTNTN TN 142

SEQ ID NO:721

LENGTH:147

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00795

SEQUENCE DESCRIPTION:

GATCCAGGTG ACTCTGAACA TCATTAGAAG CATGCCAGAA CAGACTGGTG AAAAGTAAAC 60
 CTTTTCACCT ACAAATTTT ACCTGCAAAC CTAAACCTG CAAAATTTTC CTTAATAAAA 120
 ATTTGCTTGT TTTAANAACA NNNGAAA 147

SEQ ID NO:722

LENGTH:140

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00796

SEQUENCE DESCRIPTION:

GATCCAGAGC CTCCCGGCC TTCTCCGGTG TCCTGTACCA ACTCTTCTAT TTAAGAGAAC 60
 CTCAGATGAT GTACCTGAGC CTCAGGGTTT TGTTTCAGAG GGATATAAAT NATTTAAAAA 120
 TTAAATGAAA ACCTTGCAAA 140

SEQ ID NO:723

LENGTH:150

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00797

SEQUENCE DESCRIPTION:

GATCGGCCAC TACCTGGGCG AGTTCTCCAT CACCTACAAG CCCGTAAAGC ATGGCCGGCC 60
 CGGCATCGGG GCCACCCACT CCTCCGCTT CATCCCTCTC AAGTAATGGC TCAGCTAATA 120
 AAGGCGCACA TGA CTCCAAA AAAAAATAAA 150

SEQ ID NO:724

LENGTH:140

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00798

SEQUENCE DESCRIPTION:

GATCAGGGTA AGGCAGTCAG GCGGGTGTTC ACCACTGCCT TTCCTTCCTC TGAGCGTGAG 60
AACACTGAAC CCAGCCACTG CCCCTGGGTC CCTGTCTGG AAATNGTCTA ATAAATCCTT 120
TNCCCTTCTT GAGCTACAAA 140

SEQ ID NO:725

LENGTH:141

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00799

SEQUENCE DESCRIPTION:

GATCCGAATC GAGGCCAACG AGGCCCGGGA TGAAGGCCN GGAGTAGGCG AGCCAGACGA 60
CAAGGTTGAC CTCAGCTTCG GAGCCACCTC TGGATGAACT GCCCCAGCC CACGNCCNAT 120
TAAAGACCCG GAAGCCTGAA A 141

SEQ ID NO:726

LENGTH:136

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00800

SEQUENCE DESCRIPTION:

GATCAGCTTT ACCTATGGTG CTTTGCCTTT AACTAGAGTG TGTGATGGTA GATTATTTCA 60
NATATGTATG TAAACTNTT TCCTGAACAA TAAGATGTAT GACCCGAGC AGAAATAAAT 120
NCTTTTCCTA ATTAAA 136

SEQ ID NO:727

LENGTH:135

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00801

SEQUENCE DESCRIPTION:

GATCATGTCA TTCAATTCCA GTCACCTCTT CTGCAATCAT GACCTCTTGA TGTCTCCATG 60
GTGACCTCCT TGGGGGTCAC TGACCCTGCT TGGTGGGGTC CCCCTGTAA CAATAAAATC 120
TATTAAACT TTAAA 135

SEQ ID NO:728

LENGTH:135

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00802

SEQUENCE DESCRIPTION:

GATCTTAAAC ATTGTTTTGT AGTGTATATT ACTTGTCCAT TCCTTTAAGG GGAGCAGCCT 60
GCACTCTTTT GTAGATTACT TTTGGGGGAT ATATTNNAG AATNATGAAA CGGAATAAAA 120
TTGTAAAAAA CTAAA 135

SEQ ID NO:729

LENGTH:134

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00803

SEQUENCE DESCRIPTION:

GATCATGTTA CCATATCAAG CTGAAAATGT CACCACTATC TGGAGATTTC GACGTGTTTT 60
CCTCTCTGAA TCTGTTATGA ACACGTTGGT TGGCTGGNTT CAGTAGGGGG NTATTNAGG 120
CCTTTCTTTT TAAA 134

SEQ ID NO:730

LENGTH:134

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00804

SEQUENCE DESCRIPTION:

GATCTANGTT GCCTACCTTG AATTTTTTTT TAAATATATT TGATGACATA ATTTTGTGT 60
AGTTTATTTA TCTTGACAT ATGTATTTTG AAATCTTTTA AACCTGAAAA ATAAATAGTC 120
ATTTAATGTT GAAA 134

SEQ ID NO:731

LENGTH:134

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00805

SEQUENCE DESCRIPTION:

GATCTCACTA AAGGATTTCT ATTTGCTGTC AGTTAAAAAT AAAGCCCTAA ATACATTTTT 60
ATTCTTTCTA CTGAGGGCAT TGTCTGTTTT CTTGTAAAT GCCGTACAAT AAACAAATTA 120
TTTAATAACC TAAA 134

SEQ ID NO:732

LENGTH:137

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00806

SEQUENCE DESCRIPTION:

GATCTTGGCA CTCTCCATGT TCTCTACAAG AAGCTGTGGT GATTGGCCCT GTGGTCTATC 60
AGGCGAAAAC CACAGATTCT CCTTCTAGTT AGTATAGCGG ACTTAATAAA AGAGGAAAAA 120
ACTCTTGCTT CAGTAAA 137

SEQ ID NO:733

LENGTH:134

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00807

SEQUENCE DESCRIPTION:

GATCCTCGAA CGGAAAGCCA AATCTCGCCA AGTAAGGAAA GGAAAAGGGC AAATACAAGG 60
AAGAAACCAT TGAGAAGATG CAGGAATAAA GTAATCTTAT ATACAAGCTT TGATTAAAAC 120
TTGAAACAAA GAAA 134

SEQ ID NO:734

LENGTH:132

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00808

SEQUENCE DESCRIPTION:

GATCAGTGGC TTTGAATGAA ATACAGATGC ATTATCCAGA ACTGAAGTTG CCCTACTTTT 60
AACTTTGAAC TTGGCTAGTT CAAAGATAGA CTCTTCTTTT GTAAAGTAAA TAAATTCTTC 120
AAAATGCTTA AA 132

SEQ ID NO:735

LENGTH:132

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00809

SEQUENCE DESCRIPTION:

GATCNNAACC TTTTCAATAA AAGGCAAAAC AAACCAATNT CCNAACATAG CATTACAGCC 60
TTTAAACCA TTCACTNCTC ATAGTGATTC ACAGAGGACA AGAGATTAAA GTGCTGGATT 120
TTAAATGTCA AA 132

SEQ ID NO:736

LENGTH:131

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00810

SEQUENCE DESCRIPTION:

GATCANATGC AACCNCAAA CCTCGGCTGA GTCTTGAGAC TGAAAGATTA AGCCATAATG 60
TAAACTGCCT CAAATTGGAC TTTGGGCATA AAAGAACTTT TTTATGCTTA CCATCTNTTT 120
TTTTTCTTAA N 131

SEQ ID NO:737

LENGTH:383

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00811

SEQUENCE DESCRIPTION:

GATCATACAC CTGCTCACAG GCGAGAACCC TCTGCAGGTC CTGGTGAACG CCATCATCAA 60
 CAGTGGTCCC CGGGAGGACT CCACACGCAT TGGGCGCGCC GGGACTGTGA GACGACAGGC 120
 TGTGGATGTG TCCCCCTGC GCCGTGTGAA CCAGGNCANN TGGCTGCTGT GCACAGGCGC 180
 TCGTNAGGCT GCCTTCCGGA ACATTAAGAC CATTGCTGAG TGCCTGGCAG ATGAGCTCAT 240
 CAATGTGTCC AAGGGCTCCT CGAACTCCTA TGCCATTAAG AAGAAGGACG AGCTGGAGCG 300
 TGTGGCCAAG TCCAACCGCT GATTTTCCCA GCTGNTGCCC AATAAACCTN GTCTGCCCT 360
 TTTGGGGGAA GCCCCGAAGC AAA 383

SEQ ID NO:738

LENGTH:128

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00813

SEQUENCE DESCRIPTION:

GATCCAGCTG CCAGAGGATG AGTGACCAGT TGCTAAGTGG GGCTCAAGAA GCACCGCCTT 60
 CCCCACCCCC TGCTGCCAT TCTAACCTCT TCTCAGAGCA CCTAATTAAA GGGGCTGAAA 120
 GTCTGAAA 128

SEQ ID NO:739

LENGTH:128

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00814

SEQUENCE DESCRIPTION:

GATCTGGATT ACNATGTAAA TTCACAGCAG TAAGATAATA TAAATTTTGT TGAATGTATT 60
 AACATCATAT GGTCTGAAAA TGTGGGTTTT NATTTGGCAC ATTTAAATAA AATGTTTCTA 120
 ACTAGAAA 128

SEQ ID NO:740

LENGTH:128

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00815

SEQUENCE DESCRIPTION:

GATCAAGAAT GAAAAAGACA TCATATGAAN NGGGAGAAAC TATTGCACA CCATCTATCT 60
 CATGGTTTGG TTAATATTCA AACTATATNA GCAGAATGTG TAAGGATATC CTACAACTCA 120
 ATAGCAAA 128

SEQ ID NO:741

LENGTH:138

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00816

2153480

SEQUENCE DESCRIPTION:

GATCCAAGGG GAAACTGCAG GTCAAGGGCT GATAACGGCC ATGCAGGATG CTTGATGCTG 60
CGTCCCCCGC TGCTTGCCGC CCCCCACCCC GCCATTTTGT ATAATAAAGC TCCCTGTGTA 120
TTCTCAAAAA AAANCAAA 138

SEQ ID NO:742

LENGTH:127

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00817

SEQUENCE DESCRIPTION:

GATCCCTGAG ACTGAGGGGT TTACGGGCTG TGAATGGACC TTCAGCCCTN CCCACCCTCC 60
CTCCCCACTG CTGCTGAGTC TGTCTGATGT TTTGGTTGTG TGAATAAATA TAATCCCTCCT 120
CTGGAAA 127

SEQ ID NO:743

LENGTH:124

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00818

SEQUENCE DESCRIPTION:

GATCGGGTAG CTCAAAAGAA GGCAAGCTTC CTCAGAGCTC AGGAGCGGGC TGCTGAGAGC 60
TAAACCCAGC AATTTTCTAT GATTTTTTCA GATATAGATA ATAACTTAT GAACAGCAAC 120
TAAA 124

SEQ ID NO:744

LENGTH:124

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00819

SEQUENCE DESCRIPTION:

GATCAGAAAT TCTCTTGCTT GAGAGATTTT TTTTGTCTCT CTGTTGACTA CATAGTTTCA 60
AATCTCTCTN TATTTTATGA TGATATATAA ATNGCTTTTA ATTATATNAA ATNTTAATTN 120
NCCN 124

SEQ ID NO:745

LENGTH:125

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00820

SEQUENCE DESCRIPTION:

GATCTCATTG CCTGTTTCC GAATTCTGCC GTGTGTATCC CCAACCCTTG ACCCAATGAC 60
ACCAAACACA GTGTTTTTNA GCTCGGTATT ATATATNTTT TTCTCATTAA AGGTTTAAAA 120
CCAAA 125

00482

SEQ ID NO:746

LENGTH:123

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00821

SEQUENCE DESCRIPTION:

GATCCGTGGC TTAAGACAGG AGATTATCTC TNTACTCCAG TGGCATCTCC TTAGCCAAGA 60
TGTGAAATTA AAATCATAGT TCGCCTCATT TAAAAATNCT AATAAAGCAC TCAAAC TTG 120
AAA 123

SEQ ID NO:747

LENGTH:122

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00822

SEQUENCE DESCRIPTION:

GATCCAAATC TGGTTCAAAC ATTCAAACT TCAAAGATAA TTCATCTTTC AGCTAATGCT 60
TGTGGTCTG TTGTTCCCTT GAAAAAAAT AAAACAGTT GCCTTCNGGG AAAANTTNA 120
AA 122

SEQ ID NO:748

LENGTH:122

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00823

SEQUENCE DESCRIPTION:

GATCTTGTGT TTTAGGNTGG GCATTTTCAC TCTTCTGCCT TAAATCCCTA ACCCCATGGA 60
GCTGACATTC TAGTGCGGCT GAGGGGAGGG GAAACATTGT AAAATAATC ATAAAAATTA 120
AA 122

SEQ ID NO:749

LENGTH:122

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00824

SEQUENCE DESCRIPTION:

GATCTCTGGG CTGGGGACTG AATTCCTGAT GTCTGAGTCC TCAAGGTGAC TGGGGACTTG 60
GAACCCCTAG GACCTGAACA ANCAAGACTT TAAATAAATT TAAAAATGCA AAAACTCGGA 120
AA 122

SEQ ID NO:750

LENGTH:122

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00825

SEQUENCE DESCRIPTION:

GATCNTAGAA GGGCTTCCCA ACCNNATTG CAACATCCAA ATTGTCTTCA ATTNAAGGAA 60
 GGCCTTATCA GTTCATAGAT GANCTTCATT GTAAAAATAA ATGTACTTGG CACCACTTCA 120
 AA 122

SEQ ID NO:751

LENGTH:273

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00826

SEQUENCE DESCRIPTION:

GATCCACTTC TGTNATTANG TAAATGGATG TNTCGTGATG CGTCTACAGT TATTTATTGT 60
 TACATCCTTT TCCAGACACT GTAGATGCTA TAATAAAAAT AGCTGTTTGG TAACCATAGT 120
 TTCACTTGTN CAAAGCTGTG TAATCGTGGG GGTACTATCT CAACTGCTTT CGTATTCATT 180
 GTATTAAAG AATCTGTTA AACAACCTTT ATCTTCTCTN CGGGTTTAAG AAACGTTTAT 240
 TGTAACAGTA ATTAAATGCT GCCTTAATTG AAA 273

SEQ ID NO:752

LENGTH:144

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00827

SEQUENCE DESCRIPTION:

GATCAAAAAG AAACCTTGTGTT TTTCCGCAAT TGAAGGTTGT ATGTAAATCT GCTTTGTGGT 60
 GACCTGATGT AAACAGTGTC TTCTTAAAT CAAATGTAAA TCAATTACAG ATTAAAAAAA 120
 AAAGCCTGTA TTAAAGAAC GAAA 144

SEQ ID NO:753

LENGTH:132

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00828

SEQUENCE DESCRIPTION:

GATCAGAGGA AAAATCCAGT GTGACAGAGT GCAAGTNAGA AGACCTGGCT TTTNATCCCA 60
 GCTTTGAAAC TTGGAACCTT TTGATTGACA AATTAATAAA CCTCTCTATG CCTCAGGCTC 120
 CTCATCTGTA AA 132

SEQ ID NO:754

LENGTH:117

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00829

SEQUENCE DESCRIPTION:

GATCTAGGCT TGAGCTTGGT TGGGATTGCT NTTTTCTTCT TCTTCTTTAT AAACGATTCT 60
 NTGTAACNT TTGTATTGAC AGTTTCAAAC TTACAGTAAA ATTGCAACAC GAGTAAA 117

SEQ ID NO:755

LENGTH:117

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00830

SEQUENCE DESCRIPTION:

GATCAGTACA TAGCATTTGG CTCNTGAACN NAATTNTAAA CTTTCAGGTA TTTTGTACA 60
AATAAGGGAC TGATGTTCTG TTTCTTGTA TTAGAAATAA ACATTAATAC AGTGAAA 117

SEQ ID NO:756

LENGTH:119

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00831

SEQUENCE DESCRIPTION:

GATCTATCAT TACTGCAAAA ACCTGCTCTG TTGTGCTGGC TGGNAGGCC TGTGGCTGCT 60
GGCTGAGGGT TCTGCTGTCC TGTGGCACCC CATTAAAGTG CAGTTCCTC CGGGCCAAA 119

SEQ ID NO:757

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00832

SEQUENCE DESCRIPTION:

GATCTGAAAT TAAATACTCA ACAGACTCCT CCTTTTTAG CTGTATTTTT CAGGTACTGT 60
GTGGTGACCG CCCCACTGGT GTCTATTACA GGCCACTTG GTAGTTGTGT ATCTGNTCAT 120
GTATGTGATT TGACAAACCA GTTTTTTAAA ATAAATGGCT TTTTAAA 167

SEQ ID NO:758

LENGTH:379

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00833

SEQUENCE DESCRIPTION:

GATCCAATA GAAATGAATG GAAGATGATG GGAAATATGA CTTCACCAAG GAGCAATGCT 60
GGGATTGCAA CTGTAGGGAA CACCATTAT GCAGTGGGAG GATTCGATGG CAATGAATTT 120
CTGAATACGG TGGAAGTCTA TAACCTTGAG TCAAATGAAT GGAGCCCCTA TACAAAGATT 180
TTCCAGTTTT ANCAAAATTA AGACCCTCTC AACTANCAG GCTTAGTGAT GTAATTATGG 240
TTAGCAGAGG TACACTGTG AATAAAGNGG GTGGGTGGGT ATAGATGTTG CTANCAGCAC 300
CACAANGCTT TTCCATATTN GCNTCCTNTT AACCATGCNT GTCCATAAAC CCNGGGANGN 360
NNANTTGNGG GGTNAANN 379

SEQ ID NO:759

LENGTH:121

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00834

SEQUENCE DESCRIPTION:

GATCTACTAC TNGGCCTTCA GTGCGAAGAG CCACATCCAG GCCTGAGGGC GGCACCCCAG 60
CCCTGCCCTT GCTTCCTTCA ATAAACATCA CAGGACCTGG GACTGCACAG GNCCTGGGAA 120
A 121

SEQ ID NO:760

LENGTH:303

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00835

SEQUENCE DESCRIPTION:

GATCGAAGCA ATTGANGTAT CATGGATTGG ATTGTTACTG ATTCAGTAA AGTATGTTTT 60
GCCAATTAGA TACATATATA CAAGATAAAG GAATAGGATG GTAATATATT TGTNTGAAAT 120
TAAATTACTG TTTTNATTAA AAAATACTGC TTCATTGGGC TGATTTTGTA AAATGTAATG 180
AGTAAAATGA ATTACTGTAT TTNCCCTTTT ATGTCCACAG AATGAGAGTC ATATGTNGTN 240
ATATNCTAAA TNTNCATTAA ATATTCATGT CACCTTGAGT TGTCATGATA AGTATGTTTT 300
AAA 303

SEQ ID NO:761

LENGTH:373

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00836

SEQUENCE DESCRIPTION:

GATCTACTAT GTNATGTCAG GGCCTGCGTG GCAACTCATG CAGCAATTCC AGAACCCCTGA 60
CTTCCACANC GAAGTAGAGG AACAGGATGC CAGCACCCCTG CCTGTGTCTT GTGCCTGGAA 120
GAGTGGGATG AAACGCCACA GAGCAGCCTG TGCTTCGGCT AGTATTAATG TGTAGATAGC 180
ACTCTGGTAG CTGTAACTG CAAGTTTAGC TTGAATTAAG GGATTGGGGG GGACCATGTA 240
ACTTAATTAC TGCTAGNNNN GGAATGTCTT TGTAAGAGTA GGGTCGCCAT GATGCAGCCA 300
TATGGAAGNC TAGGGTATGG GTCACACTTT ATCTGTGTTC CTATGGAAAC TNATTNGNA 360
TATTNGNTT TGN 373

SEQ ID NO:762

LENGTH:406

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00837

SEQUENCE DESCRIPTION:

GATCTAGGGA GATGTGGAAG AAAGTGTGAC TACTATAGAA ATTGATGAAG AAACATATGA 60
AGAGATATAT AAATCAACGN AACGGAATAT TCCAATGCTC TTTGTCCGGG GAGATGGCGT 120
TGTCTGGTT GCCCCTCCAC TGAGAGTTGG CTGAAACAAA GAATTTGTCC TGTATGGAAA 180
NCGNNNNNNN GGTGTACAGT GGCCTCTCTA AAAGTACAAA ACATTCATAA GAGAAACCCG 240

CATACATTTT GATATTAAGA AATAATTCCG GGGATTCTTC CACTCCTGAA ATGAGTTGAT 300
TTGCAGATAA CTCACAACCT CTTAAGCTAA ATGGTATTTT CATTTTCTC AAGCTCTCCN 360
ATAANTATGG CCACCNNGG NNANNGNGTG GGGAAAAAA NAATTN 406

SEQ ID NO:763

LENGTH:120

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00839

SEQUENCE DESCRIPTION:

GATCCCCACG CCACAGCCCT TTTGTCTCTG CAAACTGCCT TCTTCGAAA GAAGAAGGTG 60
GGAGGNTGTN AATTGTTAGT TTCTGAGTTT TACCAAATAA AGTAGAATAT AAGACGNAAA 120

SEQ ID NO:764

LENGTH:115

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00840

SEQUENCE DESCRIPTION:

GATCTTGATG GTGTTTCTTT CCCCAAAAT TGACTTAGAT ATTAAAATTT GGTGCTTATA 60
AGAGAGAGTT AAAAAAAAT AGGATTGCTT CAATTAAAA TACAAAAGAG NCAAA 115

SEQ ID NO:765

LENGTH:113

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00841

SEQUENCE DESCRIPTION:

GATCCAGTGA CAGCAGGTGT CATGGGTCAA GCATAATCA TATATAGCAT TTTCAGGCAT 60
GTTCTGGTA GTTCTTTTGA GTCTGACATT CTAATAAAAT AATTTGTAGG AAA 113

SEQ ID NO:766

LENGTH:112

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00842

SEQUENCE DESCRIPTION:

GATCTTTGTG AGGATTAGGA ATTAGGTAA AAGAAATTAA GAACCATCTT CAAGCAAAAN 60
TTAAACTTTA TTTCTNCTTA ANCAATAAAT ACACCTGANT TAGTTTCCA AA 112

SEQ ID NO:767

LENGTH:112

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00843

SEQUENCE DESCRIPTION:

GATCAAAGAC CCAAAGGAAT GCAACANTTT ATCTNTTATC TACCTATNAC CTGCGAGCTG 60
 CCCACCACCC CCANGTTGTN GCGCCTTTCC AGACAGAACC AGTGATACATC TN 112

SEQ ID NO:768

LENGTH:130

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00844

SEQUENCE DESCRIPTION:

GATCCAAAAC TTAAATACAT CTATGAATTT CCTGGGGCTA TTGTGAGTAC TGTGTATGTA 60
 TTTAGCAAAT ATTTAAGACC TAGTAAGTGC TCAATAAATT GTAGCTGTGA TTGCTGTTGT 120
 NGTTTGTAAT 130

SEQ ID NO:769

LENGTH:111

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00845

SEQUENCE DESCRIPTION:

GATCGTGCCA CTGCTCTCCA GCCTGCATGA CGGGAGTNAG ACACCATCTC AAAAAATACA 60
 TATAATAATA TAAATAAAAA TATCTTTTNN GAAAATAATT TAATATNNCN N 111

SEQ ID NO:770

LENGTH:110

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00846

SEQUENCE DESCRIPTION:

GATCNAGTAN TGNAGGGGCT GTTAGGAGCT TCCTGCAAAT CCCTGAGAGG GCAGAAGATA 60
 GCTTCTGTGA ATTCATTATT CTTCCAATAA ATGTTGATTG AGTACCTAAA 110

SEQ ID NO:771

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00847

SEQUENCE DESCRIPTION:

GATCACCGNC CAGTAATGGG CTCAGAGCAG GTCTTCATCA TGCCTTGTC TTTTAACT 60
 GAGAAAGGAG ATTTTGTGAA AAGAGTACAA TTAAAGGAC ATTGTCAAA 109

SEQ ID NO:772

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00848

SEQUENCE DESCRIPTION:

GATCTTCTTC AATATGTGAA TTTGGGCTCA CAGAATCAAA GCCTATGCTT GGTTTAATGC 60
TTGCAATCTG AGCTCTTGAA CAAATAAAAT TAACTATTGT AGTGTGAAA 109

SEQ ID NO:773

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00849

SEQUENCE DESCRIPTION:

GATCAACAAG GTTTGCCACT GCTTGTATTA CCAGGGACTG GTTACAACCA TTATTTCTNT 60
TCATTTGCTT GGCTTATCTC ATATTAAAGT GAGTTTGGAG TTCTCCAAA 109

SEQ ID NO:774

LENGTH:110

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00850

SEQUENCE DESCRIPTION:

GATCCAGTTC TAACTTTGG GATATTTTTT TTCAATTTTG AAGAGAAAAT GGTGAAGCCA 60
TANGAAAAGT TACCCGAGGG AAAATAAATA CAGTGATATT CTTACGCAAA 110

SEQ ID NO:775

LENGTH:108

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00851

SEQUENCE DESCRIPTION:

GATCTGTGTG CTCTATCAC CAATCAGTTC AGACCTGGTT GATTTTGTAC TTTGGAAGTG 60
TACCTTGGAT GGTTTGTTT ATTAAGAG AAACCTGAAG TACTCAA 108

SEQ ID NO:776

LENGTH:108

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00852

SEQUENCE DESCRIPTION:

GATCACCATC TTAAATTTA CTTCAAATA AAAGCATGTA AGTNACTGTT TTTCAAGAAG 60
AAATGTGTTT CATAAAGGA TATTTATATC TCTNTNGCTT TGACTIONN 108

SEQ ID NO:777

LENGTH:106

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00853

SEQUENCE DESCRIPTION:

GATCCCCCTC GGAAGAGGGA CTCCAATGGG CATGTCCCCT CCGGAAATNC GGCCTCCTCC 60
CCCTGGAATG CNAGGNCCCC CTCCCCCGN AATNCGCCCA CCAAGN 106

SEQ ID NO:778

LENGTH:130

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00854

SEQUENCE DESCRIPTION:

GATCCCATCA TGAATTCATT GGAATTTGTG TTGCATGTAA GGCAATCTTT TCCNTGTTGT 60
AAATCTTCGG TTTTITAATG TACATATATT TTGAAAAATA TGAATAAACA TGAAATTTTA 120
AAAGCTGAAA 130

SEQ ID NO:779

LENGTH:104

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00855

SEQUENCE DESCRIPTION:

GATCATGGTG GGTCAGCTGT ACTGATTGTN ATCCTGACTT TGGCATTGGC AGCTCTTATA 60
TNCCGACGAA TATATCTGGC AAACNNATAC ATATNTAACT TTAN 104

SEQ ID NO:780

LENGTH:107

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00856

SEQUENCE DESCRIPTION:

GATCTTTTCA CAGTATCCAT TTATTATGTA ATNCTTNTNA GAAAAGAATC TTATAGTACA 60
TNTTANTATA TGCAACCAAT TAAAATGTAT AAATTAGTGT AAGCAAA 107

SEQ ID NO:781

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00857

SEQUENCE DESCRIPTION:

GATCAAAATG AAAGAAAATC ACAGAAATTA TCCTATGTGT ACTCCTCATC CCTCCTGCTG 60
TATATNTTCT NATTTTTTGC GTAATAAATN ATGTTAATTA CCAAATAAA 109

SEQ ID NO:782

LENGTH:125

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00858

SEQUENCE DESCRIPTION:

GATCTCCAAT GTTTGGGGA TGCTTTGAGT CTCAAAAAA ATTGATAATC AGAAAAGTAA 60
TTTTTGTGTTG TTTGTTTAAT GTATCCCTGT TCTGTTTTTA ATTAACTCC AAGTCTCATT 120
TTAAA 125

SEQ ID NO:783

LENGTH:103

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00859

SEQUENCE DESCRIPTION:

GATCGAGGTG ACAAATANTC AGTCCNTANG TCCCCACAAT GACCTCACCA NNATGGCTTT 60
GGGGAGCTCT TCACCCTAAA GATTCCGTCT GGTTCGTAA TGN 103

SEQ ID NO:784

LENGTH:102

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00860

SEQUENCE DESCRIPTION:

GATCTGGAGG CAAGATGCCA GGCCCCACAG GTGTTCTCAG GGCAGTCTT GGTGTCTGCT 60
TCTCAGATAC CAAGGACTGG AATTAAAACC TTTCCTGGGA AA 102

SEQ ID NO:785

LENGTH:99

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00861

SEQUENCE DESCRIPTION:

GATCACAGCC GAAGAGTGAA AGGTGCTGCA ATGAATGTGA GCTGTGGCCA CTGTGGATT 60
TTCGCAAGAA CATTAATAAA CTAAAACTT CATGTGAAA 99

SEQ ID NO:786

LENGTH:94

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00862

SEQUENCE DESCRIPTION:

GATCAAGTTA TTTTNAATTT GGTTCACACA TTGGAACAA GTCAGTCATT CAGATATGAT 60
TCAAAATGTCT ATAAACCGAA CTGATGTAAG TAAA 94

SEQ ID NO:787

LENGTH:102

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00863

SEQUENCE DESCRIPTION:

GATCTCTTCT TCTCCCTGTG GCCCCTGCGC TGTGCCCCG TCCCCGTCAC CCCGCCGNN 60
ACTGAAATNT ATAATCTGAC TTCCTGTACA GAAACCTGCA AA 102

SEQ ID NO:788

LENGTH:93

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00864

SEQUENCE DESCRIPTION:

GATCTTGTTA GCAATGCTGT TTTTNCCTGT AGTCGGGTGA GAGTTGGCTC TACGCGAGGT 60
TTGTTAATAA AAGTTTGTTA AAAGTTTAAT AAA 93

SEQ ID NO:789

LENGTH:100

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00865

SEQUENCE DESCRIPTION:

GATCTTCAAG TGAACATCTC TTGCCATCAC CTAGCTGCCT GCACCTGCCC TTCAGGGAGA 60
TGGGGGTCAT TAAAGGAAAC TGAACATTGA ACCCTTTAAA 100

SEQ ID NO:790

LENGTH:92

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00866

SEQUENCE DESCRIPTION:

GATCAGAATT TAAAATGTGT GATTCTTTTT CTTCTGTAA GTATGTATTG CTATGATAAA 60
TAAAAAATGG CAGGACCATT NTTTTATNA AA 92

SEQ ID NO:791

LENGTH:93

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00867

SEQUENCE DESCRIPTION:

GATCTCCAAC CAGGCCAGAG AAGATTCTCA CAGAAGGTTT TGAACCTCTAA GAAATAAATT 60
GGTTTGGTAA TAAATGGCTT CTGGTCAGAT AAA 93

SEQ ID NO:792

LENGTH:114

2153480

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00868

SEQUENCE DESCRIPTION:

GATCTGTAT CTTGTATAA CGGATGTNAT TTGTACGAAG GGCAGTTCGT AAACAGCACT 60
TGTNCTTTTA ATAAAAGAAT GTTTTCGAAA AAAAAAAAAA AAANCCCNAG GAAA 114

SEQ ID NO:793

LENGTH:90

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00869

SEQUENCE DESCRIPTION:

GATCTGTTTT GTACTTTTTA TACTGTTGGA TACTTATAAT CAAAACTTT ACTAGGGTAT 60
TGAATAAATC TAGTCTTACT AGAAAATAAA 90

SEQ ID NO:794

LENGTH:88

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00870

SEQUENCE DESCRIPTION:

GATCCATTTC ATAAAGTATG ATTTGCCCAA ACCTGTACCA TTTCCGTATT TCTCCTGTAG 60
AAGTAAGAAA TAAATTCCT TAAATAAA 88

SEQ ID NO:795

LENGTH:89

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00871

SEQUENCE DESCRIPTION:

GATCTGGCGC TTGGGGGTAA GTGGNATGAT TTGCTAATAT TGAGNATCTG TTGTATCAAA 60
CATAATAAAC TTTTTTTTGA GATGTGAAA 89

SEQ ID NO:796

LENGTH:89

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00872

SEQUENCE DESCRIPTION:

GATCAGGGTG TCTCCTTGTC CTTCTNAGAT GTGGAGAAGA GGCTGCTGGC TACCCTAAAA 60
NTTGAAATAA AAGATTTTGG CCTTTGAAA 89

SEQ ID NO:797

LENGTH:86

00493

2153480

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00873

SEQUENCE DESCRIPTION:

GATCCATTGA GCCCAGCAGT CCAACCTGGG CAAAATAAGT GAGAGACCCT GTATCTGAAA 60
GTAATAATAA AAATAAAAAA TATAAA 86

SEQ ID NO:798

LENGTH:86

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00874

SEQUENCE DESCRIPTION:

GATCCTTTT GATAATCTCA TTCCTAGAAA TTAACTTA ATGAAATCCC TAATAAAACT 60
CAGTGTGTG TTATTGTGC CTCAAA 86

SEQ ID NO:799

LENGTH:87

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00875

SEQUENCE DESCRIPTION:

GATCGAACAT TTCACCTCTC ATATTAAGTC TGGCAATGAT GACTATATGT ATTCCTGCCT 60
AAATAAATCA TCTATTAATC ATAAAA 87

SEQ ID NO:800

LENGTH:86

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00876

SEQUENCE DESCRIPTION:

GATCTCCGAG TCAGGACGGT CGGCCAGACC CACGGGGTAA CGGGTCTAAT CGTGTAGGAA 60
TAAAGCTGTA TTCCAGTGCT TCCAAA 86

SEQ ID NO:801

LENGTH:84

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00877

SEQUENCE DESCRIPTION:

GATCCCCGCG ATACTTCAAC GCCTTCTGAC TTCCAGGTGA TGA CTGGGCC CCCAATAAAT 60
CCCGTCTTTG GGTCTCTCTG CAAA 84

SEQ ID NO:802

LENGTH:84

00494

2153480

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00878

SEQUENCE DESCRIPTION:

GATCCCTCAA AACCTCACTA ACTGGAAGGA TGATTTTGTC TCAGTTTGTA CTCCTAAATA 60
AAAAGTAAAC ATGACACCTC TAAA 84

SEQ ID NO:803

LENGTH:88

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00879

SEQUENCE DESCRIPTION:

GATCTGTGAA GAAATGAAAT AAAATGGTAT TTAGTAAGAA ATCTCTATTT TAAGAAAAAA 60
AGTAAAACCT GTTATAAACA CATGCAAA 88

SEQ ID NO:804

LENGTH:82

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00880

SEQUENCE DESCRIPTION:

GATCGTGCCA TTGTGATATG AATATGCCTT ATATGCTGAT ATGAATATGC CTTAAAATAA 60
AGTGTTCCCC ACCCCTGCCA AA 82

SEQ ID NO:805

LENGTH:81

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00882

SEQUENCE DESCRIPTION:

GATCTTAAGT CATACATTTN AATTGTNTAG AGGTTGTTCA ACTGAAGGAA TAAATGTCTA 60
TNAANCTAAA ACAAATGGAA A 81

SEQ ID NO:806

LENGTH:78

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00883

SEQUENCE DESCRIPTION:

GATCAAGTTT GTACATAACA CTAGTGGCAT TTCTTATCAA AAGGATTGGA TAATAAAAAT 60
AAGTTTCTAC TGGGTAAA 78

SEQ ID NO:807

LENGTH:78

00495

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00884

SEQUENCE DESCRIPTION:

GATCCCCCA GCAAGGATAN CATTCAAAGG AGCTCACATT TATGGAATGG ATGAATCAAT 60
AAATTAATTC ACTTTAAA 78

SEQ ID NO:808

LENGTH:77

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00885

SEQUENCE DESCRIPTION:

GATCCCATTT CTGATGGATG TGTCACACCT TTTCTGTCAA AATAAAATGT CTTGGAGGTT 60
ATGACTCCTT GGTGAAA 77

SEQ ID NO:809

LENGTH:77

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00886

SEQUENCE DESCRIPTION:

GATCTGTGTT AATCTGAGTA ACTTATTGCC TAGCCTATAA ATAAATTCCA AAATATCCAA 60
TTCATTCTT CTGAAA 77

SEQ ID NO:810

LENGTH:75

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00887

SEQUENCE DESCRIPTION:

GATCATCCTT CCTGGCAAAT AAATCCCGT TTCTATCCAA AAGAGCAATA AAAAGTTTTC 60
AGTGAAATGT GCAAA 75

SEQ ID NO:811

LENGTH:76

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00889

SEQUENCE DESCRIPTION:

GATCTGAAAG CCTGAGTGTG TGTACGTGCG CGCGTGGTG AAGGCCCTGC CACGATTAAA 60
GACTGANACC GGCAAA 76

SEQ ID NO:812

LENGTH:129

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00890

SEQUENCE DESCRIPTION:

GATCTTTAAT ACAATATAGA AATTGTGTAA TAGTTATTAT AAATGTTAAT ACACAACTTT 60
CAGGTAATTT TAACTGATTA TTTCTTTTGC TCTTTTAACT TAAGTTATTA AAGTTTAAAA 120
GTTCTGTAAT 129

SEQ ID NO:813

LENGTH:74

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00891

SEQUENCE DESCRIPTION:

GATCTGGTCT CGGTGGTCCT TCCCCGCAGG CAGGTGTCAG GACCGGCCTA ATAAACATGT 60
GTGGCCTCCT CAAA 74

SEQ ID NO:814

LENGTH:82

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00892

SEQUENCE DESCRIPTION:

GATCCAAATC CCATTACAGT TGTATAAAGA AATAAAATTT TGTACTNATA TTATTAATAAA 60
TCACATTTTT AATATTTGTA AA 82

SEQ ID NO:815

LENGTH:72

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00894

SEQUENCE DESCRIPTION:

GATCCCCAGA GACCCCATTT GCCTCTCAAC ACTCAGACCT TCAACTGTTT TTNAATAAAT 60
CTACTTTTTA AA 72

SEQ ID NO:816

LENGTH:72

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00895

SEQUENCE DESCRIPTION:

GATCCTACAC CCNGAGCCTC AGAGCACTGC TACTTTTTAA AATACTTCTT TCTCTTAAAA 60
GTCTTTACCA AA 72

SEQ ID NO:817

2153480

LENGTH:71

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00896

SEQUENCE DESCRIPTION:

GATCAGATGT TAAGACTGAC ATTTCCAAGG TTGGCTACTA TGTAATAA AAATTACACA 60
AATTGTGCAA A 71

SEQ ID NO:818

LENGTH:71

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00897

SEQUENCE DESCRIPTION:

GATCTGAAGT AATTGTGCTG TATTTATGTT TATTCACCAG TCTTTGATTA AATAAAAAGG 60
AAAACCAGAA A 71

SEQ ID NO:819

LENGTH:84

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00898

SEQUENCE DESCRIPTION:

GATCTAGCTC TCTGATTCCA TACATTCCAG ACTTCTCAGT GGATTGTAA TAACTATAA 60
ATAAAAAATAG CTCTCATTTA TAAA 84

SEQ ID NO:820

LENGTH:73

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00900

SEQUENCE DESCRIPTION:

GATCATGTCT TTTCCATGTG TACCTGTAAT ATTTTCCAT CATATCTCAA AGTAAAGTCA 60
TTAACATCAG AAA 73

SEQ ID NO:821

LENGTH:69

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00903

SEQUENCE DESCRIPTION:

GATCTGATTA TTTACTTTGT TTATTGTCTA TATGCCTTTT AAAAAAATAA ACTTGTTATG 60
CAAAAATAAA 69

SEQ ID NO:822

00498

LENGTH:69

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00904

SEQUENCE DESCRIPTION:

GATCCAGTTG TAGCTGCCAT CAGATGCCGG AGACTCGCCC NTCAATAAAA AAATCTCTTC 60
TAGCTGAAA 69

SEQ ID NO:823

LENGTH:72

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00905

SEQUENCE DESCRIPTION:

GATCACTGTA AATGGTAATC AGTTGGAATT CTCCTAAATG TCTCCAGAC ACTAGTAAAA 60
AACGACCTGA AA 72

SEQ ID NO:824

LENGTH:68

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00906

SEQUENCE DESCRIPTION:

GATCTTTCTA CCTGCCTTTC CATGTCATGA GAGGAAGAAA CAAGAATGAC AAGTGTATGA 60
CTNCCAAA 68

SEQ ID NO:825

LENGTH:67

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00908

SEQUENCE DESCRIPTION:

GATCACGTAC CTGTGCAGAA ACCGCCTCTG TGGCTGCATT TGAAATAAAA CCCGACCCAG 60
CAGCAAA 67

SEQ ID NO:826

LENGTH:342

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00910

SEQUENCE DESCRIPTION:

GATCATATTT TATGAACAGA AAGACTCAGG ACATATTAAA AAATAAACTG AACTAAAACA 60
ACTTTTGCCC CTGACTGATA GCATTTCAGA ATGTGTCTTT TGAAGGGCTA TGATACCATT 120
TATTAAATAG TGTTTTATTT TAAAAACAAA ATAATTCCAA GAAGTTTTTA TAGTTATTCA 180
GGGCACTATA TTACAAATAT TACTNNGTTA TTACACAAAA AGTGATAAGA GTAACATTG 240

CTATACTGAT GNTTGTNTAC TCAAAAACCT CNGNTNAACN GTATGTAATC TNAGTTCACT 300
GCACTTAAGT TCACCNAACA TNNATNAATG TCAATGNAGA AA 342

SEQ ID NO:827

LENGTH:72

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00911

SEQUENCE DESCRIPTION:

GATCTAAGAA GTTGTGAATG TTGTTAATCA TTTAGCCGTT GCAATAAATG TAGAGGAAAT 60
GCAGTGTGCA AA 72

SEQ ID NO:828

LENGTH:65

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00912

SEQUENCE DESCRIPTION:

GATCACCTGA GGCCATGAGT TTNAGACCAG TCCTGGTAAC ATAGCAAGAC CTCCATCTCT 60
ACAAA 65

SEQ ID NO:829

LENGTH:65

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00913

SEQUENCE DESCRIPTION:

GATCCTAGAC AGCGCCTTAT CTATGATTGA GTGTCCGTGT AAATAAATTC CTACTTAGAC 60
TTAAA 65

SEQ ID NO:830

LENGTH:65

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00914

SEQUENCE DESCRIPTION:

GATCTGGGAA CTTTTNCTG TACAAATCTG TTAAAAAAA AAAAAAGGNA CCNCATTGAT 60
TTAAA 65

SEQ ID NO:831

LENGTH:63

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00915

SEQUENCE DESCRIPTION:

GATCCAAATT AAAACCTGGT AGAATCTAAT ACATTGACTG CAATTAAAAAT GTTGCCTGG 60
AAA 63

SEQ ID NO:832

LENGTH:68

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00917

SEQUENCE DESCRIPTION:

GATCCAGTTC TAAGTGTAT CTTTATNAT NAAGACAATA AAATCTTGAG TTTATGCTTC 60
ACTTNAAT 68

SEQ ID NO:833

LENGTH:63

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00918

SEQUENCE DESCRIPTION:

GATCCACGGT TGTNACCATG TATTACCACA AATTAAACAA TAAAAAATTG TTTAAGAGT 60
AAA 63

SEQ ID NO:834

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00919

SEQUENCE DESCRIPTION:

GATCTACTGT CATTTGNATG CAATTCCTG TTACCTTGAA AAAATAAAAA TGTTAACAGG 60
AATGCAGTGT GCTCATTCTC CCNAAATAGT AAANCCCACT GTATACAAA 109

SEQ ID NO:835

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00920

SEQUENCE DESCRIPTION:

GATCCAATTA CACACATTG TTCACAACCTC AACACAAATT CCTATTAAAT ATTAAAAGTA 60
AA 62

SEQ ID NO:836

LENGTH:61

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00922

SEQUENCE DESCRIPTION:

GATCTTAAAC ATAGGAAAAC CATACGTGTT CATGATAATA AAATGCTTTC TATGAAATAA 60
A 61

SEQ ID NO:837

LENGTH:56

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00924

SEQUENCE DESCRIPTION:

GATCATACCA CTGCTCTCCA GCCTGGCTAT CAGAGTGAGA CTCTGTCTCA CAGAAA 56

SEQ ID NO:838

LENGTH:56

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00925

SEQUENCE DESCRIPTION:

GATCAGACAC TTAACCTTA TAANTTAAAG TCAATAAAGC ACCTTTTAA AGGAAA 56

SEQ ID NO:839

LENGTH:57

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00926

SEQUENCE DESCRIPTION:

GATCAAAGTG AAACAATGTT TGGATGCAAC GCAGAATAAA AGAATATAAG AAATAAA 57

SEQ ID NO:840

LENGTH:52

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00929

SEQUENCE DESCRIPTION:

GATCTAATTA AAAGACCTTC TGCACAGCAA AAGAACTAA CAACAGAGTA AA 52

SEQ ID NO:841

LENGTH:52

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00930

SEQUENCE DESCRIPTION:

GATCCCGGCA GAAGCTATGA AAGGGAATAA AGAGAAAAGA AGTACCCAGA AA 52

SEQ ID NO:842

LENGTH:52

TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00931
SEQUENCE DESCRIPTION:
GATCTTTTAG TTTCAACTCA GCTTTTACAA TAAAANGGAT TTGTATTGCA AA 52

SEQ ID NO:843
LENGTH:58
TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00932
SEQUENCE DESCRIPTION:
GATCTCTTTT CAGAAGTGTC TATAGAACAA TAAAAATCTT TNACTTCTGA CCTTGAAA 58

SEQ ID NO:844
LENGTH:53
TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00934
SEQUENCE DESCRIPTION:
GATCCTAAAT CATGACTTAC CTGCTAATAA AAATCATTG GAAAAGTGAG AAA 53

SEQ ID NO:845
LENGTH:52
TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00935
SEQUENCE DESCRIPTION:
GATCAAGCTG TAAAAAACN AAAAAATTAA TAAAAATTC GAGAAATANA AA 52

SEQ ID NO:846
LENGTH:51
TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00936
SEQUENCE DESCRIPTION:
GATCAGCATT GTGACTTGGA GATAATAAAA TTAGACTAT AAATTTGGAA A 51

SEQ ID NO:847
LENGTH:62
TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS00937
SEQUENCE DESCRIPTION:
GATCTGAGGT AAATTTGAA GTAAAATAAA AGCTGTGTTT GAGCATCATT TGTATTTCGA 60

AA

62

SEQ ID NO:848

LENGTH:59

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00938

SEQUENCE DESCRIPTION:

GATCCTCCCT CCCCTAATTA AAGTCTCTTT TTGCCCCTTT GGGCTGNCAT GAGGTCAAA 59

SEQ ID NO:849

LENGTH:71

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00955

SEQUENCE DESCRIPTION:

GATCAGAATT TTAAATNAAA GGTTTTTCTT TTAAATNATT TGTATTACTT TATTAAGAACT 60
CTGATATTAA A 71

SEQ ID NO:850

LENGTH:661

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00972

SEQUENCE DESCRIPTION:

GATCCGGTTC TGGGACAGCA GGGGGCCCCA CTGCACCCAG GTCATCCCTG TGCAGGGCCG 60
GGTCACCTCC CTGAGCCTCA GCCACGACCA ACTGCACCTG CTCAGCTGTT CCCGAGACAA 120
CACACTCAAG GTCATCGACC TGCCTGTCAG CAACATCCGC CAGGTGTTCA GGGCCGATGG 180
CTTCAAGTGT GGTTCCTGACT GGACCAAAGC TGTGTTGAGC CCGGACAGAA GCTATGCACT 240
GGCAGGCTCC TGTNATGGGG CCCTTTACAT CTGGGATGTG GACACCGGGA AACTGGAGAG 300
CAGACTACAG GGACCCCAT TGCCTGCCGT CAACGCCGTG GCCTGGTGCT ACTCCGGGAG 360
CCACATGGTG AGCGTGGACC AGGGCAAGGA AGGTTGTGCT TTTGGCAGTA GGGCCACGAC 420
CTGCCTGCTT GGGNTGGAGN TTTTNCCTG AAGCTNAAAG TTTCTTNGG GGCAATGAAG 480
GGGTTTGGGG TTTGGGATTN GAGNTTNGNC TTGGGATTA ATTGGGNAAG AAGGCTTGGA 540
AAGACCTTGN CTTTTTNTT TAAAANTNAA GTATTGGTTT GGGGGNTTAA GGTAATTTT 600
TTTTNGAATT TTAANTTAT NTCTAAATTT TTTCCAAAT TTTGAAAAAT TTTTTTTNAA 660
A 661

SEQ ID NO:851

LENGTH:641

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00973

SEQUENCE DESCRIPTION:

GATCTTGGAT GTCTATTATA GGAGAAGTAT GTCCTGCCAA TGTACAAGAA GGCAGCATTG 60

TAGGATTAAC ATTCTTGTCT ACTGTATATT ATCTTGAAG GCTCTTGTTA ATATGTTACA 120
 CTTAATATTC TCCACAGTTA CCTTTAGAGA GAATTTATGA GAAGTTAGTT TCTGATGCAG 180
 AGGTTTTTAG GCTGTGATTT CATCAAAAGT CCTAATAGCA TTCTACCTCA AAGGGACACT 240
 TAGNATGCCT AAAATTTATT CACTTAGTTT TCCTTTTTTA TTTGAAAAAA TACATGACAT 300
 GTAATCTTTT TTTCTTGAAT TCTTTCTCAG ATTTTAAAGT ACTATATTAA AGAAAAAAAT 360
 TAATGTCTAA AGGCCTAGCA TTCCTTGCA GACCCCTATA CTAACCATGG TAATGGGGGA 420
 GAGGGGTGGG GCAGNTNNGT AGGGGNACCA GGTTCAGGC CTCAAGCTTC CCAAAGCCAT 480
 TTTTNTAAA TGGGAAATCC NTNAANTTNT GGAACCCGCT TTGNTATNGG NGCCCTTTT 540
 TTTAAATTC CNGGCCTTTT TTTNNTGGT AATGGGGGTT NCTGTTTNGG GTTTAACCT 600
 NANCCTGGNC CGGGGGGGTT TAAAGGAATG CTGCTGCAA A 641

SEQ ID NO:852

LENGTH:627

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00974

SEQUENCE DESCRIPTION:

GATCTGCTNC AGTGCTCTGA GCCCTAGGAT TCATCTNTCT TTTCACCGTA GNGCGCNNGA 60
 CTGGCATTGT ATTAGCAAAC TCATCACTAG ACATCGTACT ACACGACACG TACTACGTTG 120
 TAGNTCACTT CCACTATGTC CTATCAATAG GAGCTGTATT TGCCATCATA GGAGGCAACA 180
 TTCCTGATT TCCCTATTTC TCAGGCTACA CCCTAGACCA AACCTACGNC AAAATCCATT 240
 TCACTATCAT ATTCATCGGC GTAAATCTAA CTTTNTCCC ACAACACTTT CTCGGCCTAT 300
 CCGGAATGCC CCGACGTTAC TCGGACTACC CCGATGCATA CACCACATGA AACATCCTAT 360
 CATCTGTAGG CTCATTCACT TCTCTAACAG CAGTAATATT ANATAATTTT CATGATTTGA 420
 GAAGCCTTCG GTTTCGAAGC GAAAAGTCCT AAATAGGTAG GANGAACCT TCCATTAAAC 480
 CTGGAGTGAC TATATGGNTT GCCCNTACCC TTACCANACA TTCNGAGGAN CCCGTATACA 540
 TAAAATTNTN GNNAAAAAAN GGANGGNTTC GNACCCCCCA AAGGTTGGTT TNANGNCAAC 600
 CCCCNTGGGC TCNATGGTTT TTTTAAA 627

SEQ ID NO:853

LENGTH:617

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00976

SEQUENCE DESCRIPTION:

GATCAGANTG CCCCTCCACT CATGAGACTC TTCATTTTGT CCACTTTGAC AGGAAAAGTG 60
 GGAATGTATG CAGAGCTCTC AAAAGAAACA AAAAAGGCCA AAACGGTGCC TTCAGCCACA 120
 TCCTCTGAAT TGGCCCTGAC TTGGACTAAA NCCNCTAATG CAAAATCCCT TGACAAAAGC 180
 GCATAGGTTA TTTCAAACCA GCATTGTTTT TTATGTAACC TGTTTTACCG CATCTTCTCA 240
 GCAGCTTCTG ACCACTGCTC AATTTTTTCC TTTACAGCCA TTGTTCTGGT GGACAAATAA 300
 CCTAGGTACT CCAATCCTG GCAGGAAAAA TATACAGCAT TATGAAACAG CACTCAGTAA 360
 TCCTAAAATG GATTTTCCAA AGCTGGTTAC ACATGNCCTG CAAAGTCTTA TTTAAATTTA 420
 AAAGGCCTTT CTCATTTACC AGGGGTTTAG GTCAACGNG GCAAACCCCT GGGGGAATTT 480
 AAATTGGGAA GGTANTTNC CTTTNGTAAA TTCATAGGNN CCAAANGGCN GGGNAGTTAA 540
 TTTTCCATN GGGTTGGTGG CNCCCGGGNT TCATTGGTNT TNGGCCCCAN GGAATTTAAT 600

TTTTTTAAAN CCTTAAA

617

SEQ ID NO:854

LENGTH:602

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00977

SEQUENCE DESCRIPTION:

GATCCCGTGC GCGCGCTGC CCGAGGGGAG CAAGGACAGC TTTGCAGTTC TCCTGGAGTT 60
 CGCTGAGGAG CAGCTGCGAG CCGACCATGT CTTCATTTGC TTCCACAAGA ACCGCGAGGA 120
 CAGAGCCGCC TTGCTCCGAA CCTTCAGCTT TTTGGGCTTT GAGATTGTNA GACCGGGGCA 180
 TCCCTTGTC CCCAAGAGAC CCGACGCTTG CTTCATGGCC TACACGTTG AGAGAGAGTC 240
 TTCGGGAGAG GAGGAGGAGT AGGGCCGCCT CGGGGCTGGG CATCCGGCCC CTGGGGCCAC 300
 CCCTTTTNA CCGGGTGGGT AGGAACCGTA GACTCGCTCA TCTCGCCTGG NTTGTCCGC 360
 ATGTTGTAAT CGTGCAAATA AACGNTCACT TCCGAATTAA GCGGTNTATT TNTGAANGT 420
 TTAATAATTG TGTTTTNTGA ATACTGAAGT ATTTGGCTTT AAATTCTTAA NTTAAAAATT 480
 TAATNTTTTA CTTTTTAAAT TGCTGGGTTT AAGATNGTTN AAGATTATCC TTGNAACTTT 540
 NNGGGGGANG TTNTTATTTT NGAGTCTTTT NGGAANAGNC TTNAGGCTTT TNNACTTNGA 600
 AN 602

SEQ ID NO:855

LENGTH:595

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00978

SEQUENCE DESCRIPTION:

GATCCCAGGG CTCCTGCCA TTTTAGTGTC TTGGTGTAGT GTAACCATT AGTGGTTGGT 60
 GGCAACAATT TTATGTACAG GTGTATATAC CTCTATATTA TATATCGACA TACATATATA 120
 TTTTNGGGGG GGGGCGGACA GGAGATGGGT GCAACTCCCT CCCATCCTAC TCTCACAGAA 180
 GGGCCTGGAT GCAAGGTTAC CCTTGAGCTG TGTGCCACAG TCTGGTGCCC AGTCTGGCAT 240
 GCAGCTACCC AGGCCACCC ATCACGTGTG ATTGACATGT AGGTACCCTG CCACGGCCTA 300
 TGCCACCTG CCCTGCTTCC TGGCTCCTTA TCAGTGCCAT GAGGGCAGAG GTGCTACCTG 360
 GCCTTCCTGC CAGGAGCTTT NCACCCACTN ACATTCCGTC CCCGCGGCTT AACTGNAGCA 420
 AGCGTGGNCC TAGGACAGNA GGAGCTTCGG GCCNGTTN ACCTTGCGGT GGGGCTNANG 480
 GGTGGCATT TCTTGCTGG GGGCACTGGG TTNAAATTTT GGGNTGATNA TTGGGGNGAG 540
 GGGTGGGGTA ACAAACCAN TTTTGGNNAA GNTTGGGANG NTTTTGNCTT TAAA 595

SEQ ID NO:856

LENGTH:581

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00979

SEQUENCE DESCRIPTION:

GATCTGGAAT TGCAGCCAC ATAAACATAA AGGAGGATGT CCCTGGTCTG TTCCATCCCC 60
 ACGGATGGTG TTGCTGCTGG GCAACAGTGT TGGCTTCTTT NAAGTACCCC CTTTCTCCT 120

CACCCACCTC CAAACTGACT AGCACTCAGA GGGACTTATG ATAAAGGTTT AGCTCCAGGG 180
 GTAGTACCTG AGTGTGTGCC ATGCCCTTC AGACCAGCTG CTTCCATCAG AATTCCAGGG 240
 TCACAGCCCC AACAGAAGCA GCAGTGCCTC TGTAGGAGGG GTGCTGGGCT CTGGNCTTCT 300
 NATGCAGAGA GGTCCGGGAC AGGGTCAGTA TCGTGGGCAT GTNTATAGCT TCCCAAGTTC 360
 TTTTACAAGT CCCNTGCTGG GACTCCCTGA NTTTACTTTT GGTNGGNTTC CTAGGTNCTA 420
 ATTGGTTTAA CAACTTACA NTTTNTAGG AATTGANTT ANGATTANCT TGNTTTAATT 480
 TAATTGTAGA NTTTNGGGGC CTTTTTGGN CTCAAATTTT NCCATTACAA GGNNTTATTN 540
 GGGAAANAAA GNGGTTTNA TNAATCCT TGGCCAGGAA A 581

SEQ ID NO:857

LENGTH:569

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00980

SEQUENCE DESCRIPTION:

GATCTAAATC AGACAGGAGT TGGTCTACAT AGTAGTAATC CATTGTTGGA ATGGAACCTT 60
 TGCTATAGTA GTGACAAAGT GAAAGGAAAT TTAGGAGGCA TAGGCCATTT CAGGCAGCAT 120
 AAGTAATCTC CTGTCTTTG GCAGAAGCTC CTTTAGATTG GGATAGATTG CAAATAAAGA 180
 ATCTAGAAAT AGGAGAAGAT TTAATTATGA GGCCTTGAAC ACGGATTATC CCCAAACCTT 240
 TGTCATTTCC CCCAGTGAGC TCTGATTCTT AGACTGCTTT GAAAATGCTG TATTCATTTN 300
 GCTAACTTAG TATTTGGGGT ACCCTGCTCT TNTGGCTGTN CTTTTTTTGG AGCCCTTCTC 360
 AGTCAAGTCT GCCGGATGTC TTTTTTACC TACCCCTCAG TTTTCCTTAA AACGGGNACA 420
 CAANCTCTAG NGNGGTGTTA NGANTAATNG TTACTIONGGT TANTGGGGTA NNTNNTGGGG 480
 TNTNGGTTTG GGGCTAGGCA TTGTGGTAGG TTTTNAANAA TTAGNGGGTT GGNCCCCNTT 540
 NGNTGGGGTG NTTTCANGGT NGAATNAAN 569

SEQ ID NO:858

LENGTH:566

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00981

SEQUENCE DESCRIPTION:

GATCCCCACC NGGCTCTCC TGGAACCTCT AACCTGCTGT GGAAGGAATT GGCCATGACC 60
 TTCACCTCTG GAGAGTAGGG TCTATGGCGA GGGAAAAGGG NNTTCACCAT GATAACCTAG 120
 TGCTCCATA GAGGGGTTTG GAAAAATTCC AGTCCGATTT CTTTGTGTGT CAGCTGACTT 180
 CCTTAGCTGA TTGTCCACAC TTGCACCTCT CCACCTTTGG CACTAGAACT CCTGAGACAC 240
 CACTTCTCAT GCTTCTCCCT CCCTACCAGC GGTCAAGGCT TTGGAGCCAC TCTTTTGTA 300
 CTCCAGATTA TTAAAGAGA AAAGTACAAG ACAGAAATCT TCTAGCACTT TGTAACACA 360
 GTTGATTAAC CCTCTGGGN GTATTTTGTG GGCTTTATAT AAAANCANGG TTTTTTAATT 420
 NGTAAAGTNT AAGTGCCATT AGGAANATGC ACCAGGGCAT ATTTTGTGTT NAAGGTGGTT 480
 TTTTCAATGG TTTTNCAGGN TTNCATTTTC AAAAAAANGG TTTTTTAAT GGAGGTTGTT 540
 NTTNAAANNT TCNTGANTGG TGGAAA 566

SEQ ID NO:859

LENGTH:556

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00982

SEQUENCE DESCRIPTION:

GATCTACAAT TACTAATTAA AGCTGTGAAT CTNTTCCCTG CTGGAACAAA TTCAAGATGG 60
 GAAGTTATTG CTAATTACAT GAACATACAT TCTTCCTCTG GAGTCAAAAG AACTGCCAAA 120
 GATGTTATTG GCAAAGCAAA GAGTCTCCAA AAACCTTGACC CTCATCAAAA AGATGACATA 180
 AATAAAAAGG CATTGATAA GTTCAAAAAA GAACATGGNG TGGTACCTCA AGCAGACAAC 240
 GCAACGCCCT CAGAACGATT TGANGGTCCA TATACAGACT TCACCCCTTN GACAACAGAA 300
 GNACAGAAGC TTTTNGAACA AGCTTTGAAT ACATACCCAG TAAATACANC TGAAAGATGG 360
 GNANAAATAG CAGTAGCGGT GCCTGGCAGG NCAAGGAGG GNCTGCATNN ANCCGGTTNC 420
 AGGGGACTTT GTCGNGTGG GTAAAGCCAA AGGAAGCTTG TTCCAGGTCN ANGTGCTGGA 480
 TGCAAGTTGG GGCNTGGNAT TNNCNAATTT TGTTGGGGT GTTCCTTTT TTANTAAACC 540
 TGNANTTCTT TTTAAA 556

SEQ ID NO:860

LENGTH:555

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00983

SEQUENCE DESCRIPTION:

GATCTGGATT ATTTGTCTAA GTGAGAGATT GCGAATATCA AAATATCTGT CTCACTTCTT 60
 CTGTGAATNA CACAGAGTAG AAATAAATTC ACTTTAAAAA TATGACTGAA TTTTGAAAAT 120
 CAAGACTGAA TCTCACATAG CTGCAGACAG GAACTAAGCC AGCCTCTTTG TATGTGGTAA 180
 CAAGTACAGT ATAAGANTGA AAGATTTACC ATCCTTGAAA GCTCTAATGA AAATCAAATC 240
 CAGCAATATA TATTCAACTG TGTACAGGAT TTAAGAACTT ATTTTATGAA GGAGTAATAG 300
 TGTGTAGATA TAGATTCTGA AGTCTTTAAA CGTGCCTTAA TAAATNAAGT TCNCTGGCAT 360
 TGAGNTGANN ACCAGGTGAC CNTTGGGGNC AAAAACCNC ACAAGTGATT NGCACACCAG 420
 TATACNTTCA CCANTATACT NTNTGCACAC ACANCNTTGT TTTNGGTTCA GGGTTTTGCA 480
 AATNGGTCCN ATGTATTGGC ACTGGCGTCT TTGNATTGTG TAAGTGGNTA TTTTNTGAGG 540
 NTAGCGTGGT NNCNN 555

SEQ ID NO:861

LENGTH:554

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00984

SEQUENCE DESCRIPTION:

GATCCATGTC TCAGCCTCCA CCCC GCCACA CCTGTCTGTG CAGCCACCG GCCTTACCTT 60
 CTACCCTGCC GTGGATGTCC AGGCCTTTGC CGTCCTCCCC AACTCCTCCC TGGCTTCCCT 120
 CTTCTGATT GGCATGGTAA GCAGTTCTGT GGTGGACAG ATGAGGAGCC CCAGACAGTC 180
 CCAACAGCAC TGTCTTTGGA GTCAGGAGAC CATGTGAATC CTGTCTGGAT TCAAACCTGG 240
 ACTGTGTAC TCCGGAGCCT GAGGCTTGAG TCACTGTACT CAATGGTGCC GACTCCTGGA 300
 GGTATTCATT CACCCAGCCA TTCACTAGTG CGTTTGTTA CTTATTCATT CAATTATTCA 360
 TTCAGTCAAT TTCTCATCA TTCANTTATT CATTCCATGT TGGCTTGAAA TATGTGTACT 420

GTNCCAATTN ATCCATTTAT ATCTTTAGTC ATTCAATTAT GCATTNGTGG TATTTGTTCA 480
 TTNATTCANT TNTTAATTTN ATTNAGTTAN TNNNTNGGTT GGTGNCTTGG NGTANNGTNA 540
 TACATTTGNG GAAA 554

SEQ ID NO:862

LENGTH:549

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00985

SEQUENCE DESCRIPTION:

GATCCTATGG TTCAGGAGGC CAGAAATTC CACCTCTAGG AGGTGGTGGT GGCATAGGTT 60
 ATGAAGCTAA TCCTGGCGTT CCACCAGCAA CCATGAGTGG TTCCATGATG GGAAGTGACA 120
 TGCCTACTGA GCGCTTTGGG CAGGGAGGTG CGGGNCTGTG GGTGGCAGGG TCCTAGAGGA 180
 ATGGGNCCTGG AACTCCANCA GGAATATGGT AGAGGGAGAT AAGAGTACGA AGNCCAAACA 240
 AAAAACCCCG ATTTTAGATG TGATATTTAG GCTTTCATTC CAGTTTTGTT TTGTTTTTTT 300
 GTTTAGATAC CAATCTTTTA AATCNTTGCA TTTTAGNAAG AAGCTATCTT TTAATGGTTG 360
 TAGCAGTTAT TGACCTAATA TTTGAAATGG CTGTTGGCAG TAAATTATGA ATCAGTTTTT 420
 GACCAGGNGA TTTTTTNCN TNTATTCCTT ANTTTCCTGT TNCTGATATN CCCCCAAGTA 480
 TGCAGTTNCT NNNCNCNTAA TTCCANGGNN CCATTTTTTT TTCNGGGTTC AANAATNGAA 540
 TNGNTTAAA 549

SEQ ID NO:863

LENGTH:543

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00986

SEQUENCE DESCRIPTION:

GATCAGCAGT CTTCTGCTGC CTTCTTAATG TTTCACCTAA GTTCCCATAG TTGCTCTCAA 60
 AAAGTTTCTT GGCCCTCGTG GGCCAGTNTG GAGGGGCTGT ATCATCATTC ATNAGGAGCG 120
 TCACTTGGTG GTTTAGGGGG AAATAATCTA TTCTNAAGAT TGAAGAGAGT GCAGGATTTG 180
 GGGGGTTGAC TCTACATCCT TCAGTATCAG GGCTTATCTC CTTGTNTTAC CTCCTAGGAG 240
 ACCCTCCTGT TCTTAACTGT GGGCGATGAG AAAGGTGGTG GACTCTTCTT ACTGGCAGGG 300
 CCACCTGCGT CTGTGGAGAC CCTGGGGCCC AGGGTGGCTG AGGTCCTGGA AGGCAAAGGA 360
 GCAGGGAAGA AAAGGCCGTT TTTCAGGGCA AGGCCACCAA GATGAGCCGG CGGATGGAGG 420
 GCGCAGGCGG TTCTCCAGGN CTACATCAGC AACGNAGAGT NCTAAGNANT TANGCCTTTA 480
 GGGCACTTAN CTNCTGGTTT CCACAGGAAT CTTTNGTCA ATNAAATTAG TTTGCCTCAG 540
 AAA 543

SEQ ID NO:864

LENGTH:538

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00987

SEQUENCE DESCRIPTION:

GATCATTTCT ATAAAAGAAA TGGTCATTTT ACTTAGATGC CAGTCTACTT TATAAAGACA 60

AATGGATTAT AGACTTAAAA ATAGTCATTT TTCTTATTCA TAAATCTGAC AGGCATAAAC 120
 CCAAAATCAAA GATAATTTGG TGCCCATTTAT GAATTTGAAG TTAAGTGATA GCTCACTTGT 180
 AAAGTGACTA CCTTAATGTG TATAGAGACC CCAGTCTACT ATTATTTGGG AAAATTGTTT 240
 AGGTTATATG GGAAAAGTAG CTCTTTAAAA ATCATATTGC CCAACAGAAA CCTTAGGCTG 300
 AATTTACAGG TATGATAATT TTTGTAATTA ATTTCTTAG AATTGTGCAG GCTGGGATGG 360
 GGATAATGNC ATACTCTTTT ACACGTGTACC AGCAGCATTT ATTNCCCTNG GACCTTTTAA 420
 CCNTTTTAGG GGTTAGGGTN CTNGGGGAAC CAACCTTAAT TNGGNCATCC TCCATTTTNC 480
 TTNTNTNCCN NNNNCCCNNT TTTTTTTTG GNCCCCNTN GGNCCCCCTA AACNACCN 538

SEQ ID NO:865

LENGTH:533

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00988

SEQUENCE DESCRIPTION:

GATCAAACT ATANGTGGCT ATGGCGGATA TGATTATACT GGTATAACT ATGGGAACTA 60
 TGGATATGGA CAGGGATATG CAGACTACAG TGGCCAACAG AGCACTTATG GCAAGGCATC 120
 TCGAGGGGGT GGCAATCACC AAAACAATTC CCAGCCTTTC CACATTGGCT TTCCCATGTA 180
 GTCCTTAGTG TGTCTGCTNC TCCTCTCTCT CCTCATCACA GTTCCCAGCC CCCACCTTCA 240
 ACTGAACTCA AAAAAATCTT CAACTTCATA CAGTAGTCAC ATTGTTAGTA ATAACACTGG 300
 GCATTTTTAT TTTGATANAN TAGACCGTTT AAATTTTGA GATTCTACCT TATATTTTTT 360
 GAATTATATA CTAAAGCANA TAAGTAGGTG NTGTAATGTC CATTGGGGNC CAAGNTTTTT 420
 AGGTGTAAAT GGNAAAAGG TANCAAATTT NAANCTCAAG TAAACACCCT GTAGGCTTTC 480
 CCCATGGNTT GGGGNATNTC CGGATTAAGG NCAGGGTTTT CCNTTTTCTN AAA 533

SEQ ID NO:866

LENGTH:532

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00989

SEQUENCE DESCRIPTION:

GATCTGAAGT GGTGGATTCC TTGTTTTTGC TAGTATCTCA TTTAGAGTTG AGATGGACCT 60
 TAAAACTCAT CTGTTTTAAC TCACTTTTAA ATAGATGAGT TAACTTAAT TTAATAAGG 120
 ANNNNCAGTT AGAGCCTGGA ACTTCAACCA TTATCACTC CCCATGCCCT GTTCCCCCCC 180
 ACTTCGAAAT TAAATGCGGT TAGCATCATA TAGTTCATTT TCCCCCTCCA TGCTGCTGTG 240
 TGATTCTTGA CCTTGGGTAT GAGTTTTTCA TCCTTCATGC AGGGTTCTGT CAGTTCATGG 300
 TATAGTGATT CAGTGTTAAA ATGGTGGTGT CTCAGCTGTG CTGTGCACAT TTCCAACCTT 360
 GTCAAATTAA TAGTCCTGAG CAAGCAAGAA AAAGAGGTAA TAACATACCC ATTTCTTTT 420
 ATGGANTATA AGCTTAATAA TATTTTTTTC NATGNCCTA TTTTACCT GNGCAAATTN 480
 GTATGGNCTC ACATGGTTAA CCCCAATNAA TTANTCTTGG NCAATTTTAA AA 532

SEQ ID NO:867

LENGTH:528

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00990

SEQUENCE DESCRIPTION:

GATCGCAAAT NCACCTAAAC AATACATTTA CAAAGCCATC TTTACATGCA TTAAACGAGG 60
GCTACAACAA TATTGTTTTA CAAATACTAG CACTTTTTTC CTGTTATGTA CTTAGTGTTA 120
GAGGGTCAAA ATAATCTTTC TGCTTAGCAT CTCTTAAACC ATACCTGCAA ATATAGCAGG 180
ATTNTTACAT TTACAGTACT TTAATACTTG TATAANCTAT GCAGAAATTT TTAATAAAGT 240
GTAATATATT TNATAAGCTA ATAAGACTGA ATGGGTAAAG GTTTTTNGCA TGCGTTAGTA 300
TACTTGCAGA TACTGAAACA TTTTGGTAAT CTTTCTTACT AAAGGATGTG AATGTTTAAT 360
GTACCTTCTC TGTTTCTACT CTGTAGTCCA ATGGGAATTC AGTAATGNCA TTTTGNCATG 420
TCAACCTGGG GACCATAAAN TTGGTCCTGG TCCAGGCCCT CATNTCCTAT ATCCAGTATG 480
CAATNTTATN TNNTNTNCCT GGTNAATNAA CCCCTCCGGG NTTTTAAA 528

SEQ ID NO:868

LENGTH:526

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00991

SEQUENCE DESCRIPTION:

GATCTTTCCT CAGTATGTGC TGATGTTTGG GTTGCTTGTG GAATCACAGA CACTCCTAGA 60
GGAGAATGCT GTTCAAGGAA CAGAACGTAC TCTTGGATTA AATATAGCAC CTTTNATTAA 120
CCAGTTTCAG GTACCTATAC GTGTATTTTT GGACCTATCC TCATTGCCCT GTATACCTTT 180
AAGCAAGCCA GTGGAAGTCT TAAGACTAGA TTTAATGACT CCGTATTTGA ACACCTCTAA 240
CAGAGANGTA AAGGTATACG TTTGTAAATC TGGAAAGACTG ACTGCTATTC CATTNGGTA 300
TCATATGTAC CTTGATGAAG GGGATTAGGT TGGATACTTC ANGTGAGGCC TCCCNCTGGA 360
AACAAGCTGC AGTTGTTTTA GNTANTCCCA TCCNGGTTGA NATTGGGNGN GGNCCCTGNN 420
CCTAGCATTN CGCATCACNA AGGCAATGTC NGCNTCACAG TTANGGCATT GNGGGGCCGT 480
TTNCCATGN GNACTGGGTT ATTGGGGNCT NACCAGGTCC AANTTN 526

SEQ ID NO:869

LENGTH:526

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00992

SEQUENCE DESCRIPTION:

GATCTGTTG CTTCTGCAGG CCATTTTCTG AAAACCCCTG TTAGGAAGGT TGGATTGGC 60
GTGACTTGCT TGAGCAAGAG TCCTGGGGAG AGATTTTNG GTTTAATTTA ACGGTATATC 120
CAGAGCTAAC AGTGAAGTCA CTCGTCTAGT TCTGCAAGTC AGATGTACAC TTAGAGTCTC 180
TCTGTGAAGG GTTTGGGTCT GAGCTGTATA GTATGTCAAA CTGCCAGTAA GCCAGCCCT 240
CACCNTCTGA TAGATATTCC TTTAATGCAC CAGACTTCAT GTTTGATAAA TGATTAATGG 300
TTGAAATTGT TTCTCTTCTT TTGTGTTTTC CCAGTTAATA GATGGTCACT GTTCCACAA 360
TGTTTTATAC TTTCCAGCTT TTNGTAACTN AACCTATAAT TACTTNAATT TTAATTTTT 420
TTAAAGCTTN GTTGGTGNC CTAATGNAA GGTNTTTTC CAGTGCATNA ATGGTTTTT 480
NTGGNGCTC TGNNAATGN CCNTCCCAAT TGTGGGTTGG GTTTTN 526

SEQ ID NO:870

LENGTH:520

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00993

SEQUENCE DESCRIPTION:

```
GATCAGGACG GCTGGATTCA GGTGTCGTAC GAACAGTACC TGTCCATGGT CTTCAGTATC 60
GTATGACCCT GGCCTCTCGT GAAGAGCAGC ACAACATGGA AAGAGCCAAA ATGTCACAGT 120
TCCTATCTGT GAGGGAATGG AGCACAGGTG CAGTTAGATG CTGTTCTTCC TTTAGATTTT 180
GTCACGTGGG GACCCAGCTG TACATATGTG GATAAGCTGA TTAATGGTTT TGCAACTGTA 240
ATAGTAGCTG TATCGTTCTA ATGCAGACAT TGGATTGGT GACTGTCTCA TTGTGCCATG 300
AGGTAAATGT AATGTTTCAG GCATTCTGCT TGCAAAAAA TCTATCATGT GCTTTTCTAG 360
ATGTCTCTGG CTCTATAGTG CAAATGCTTT TATTAGCCAA TAGGAATNTT AAAATACCAT 420
GGACCTTACA CAAAAGGCTT TCATGNCCTT ACTTTNTNAA AAGGGGTTAT TGTATTCATT 480
GGATATGTGC CGTAGCAATN NNGGGNTGTT AGCGGNTAAA 520
```

SEQ ID NO:871

LENGTH:517

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00994

SEQUENCE DESCRIPTION:

```
GATCTCCGTG GCTTTGGGTT AAAAGACACA CTTGTCCACA TAGGTTTAGA GATAAGAGTT 60
GGCTGGTCAA CTTGAGCATG TTAGTGACAG AGGGGGTATT GGGGTTATTT TCTGGTAGGA 120
ATAGCATGTC ACTAAAGCAG GCCTTTTGAT ATTAAATTTT TNAAAAAGCA AAATTATAGA 180
AGTTTAGATT TTAATCAAAT TTGTAGGGTT TCTAGGTAAT TTTTACAGAN TTGCTTGTTT 240
GCTTCAACTG TCTCCTACCT CTGCTCTTGG AGGAGATGGG NACAGGGCTG GAGTCAAAAC 300
ACTTGNANTT TTGTATCTTG ATGTCTTTGT TAAGACTGCT GAAGATTTAT TTTTTCNN 360
TTATAATANG GGGNTAANCC CCACCTTNAT TCCTCAATT CACCTACCA TTTTCNNGGG 420
TTCTTNGTGT TGGGCTTGTG GCAGGNCCAG CTTNTGGGTT TTCCTTTTNN CCATGCCAAN 480
NTTNTNAATT NCCCATGTAC CAGTTTGNTN CAAAGGN 517
```

SEQ ID NO:872

LENGTH:517

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00995

SEQUENCE DESCRIPTION:

```
GATCAGAAAT ACAGATTTTG ATAGCAAAGC GACGTTAGNT NGANGCTCTT GTGAGGAAAG 60
TCATTGGCTT TATCCTCTTT AGAGTTAGAC TGTTGGGGTG GGTATAAAAG ATGGGGTCTG 120
TAAAACTTTT CTTTCTTAGA AATTATTTT CTAGTTCTGT AGAAATGGTT GTATTAGATG 180
TTCTCTATCA TTTAATAATA TACTGTGGA CTAAAAGATA TAAGTNCTGT ATAAANNCNN 240
CCAATTATGT TAAACTAGCA TATCTGCCTT TATTGTGTTT GTCATTAGCC TGAGTAGAAA 300
GGCCTTTAAA ATTTTTTTAG AAAGCATTG AATGCATTTT GTTTGGTATT GTATTTATTC 360
AATAAAGTAT TTAATTAGTG CTAAGTGTGA ACTGGACCCT GTTGCTAAGC CCCAGCAAGC 420
AATCCTAGGT AGGGTTTAAT CCCAGTAAA ATTGCCATAT TGCACATGGT CTTAATGGAN 480
```

GTTTGAATCT TAAATAAATT GGATATTCAC TTTTAAA

517

SEQ ID NO:873

LENGTH:515

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00996

SEQUENCE DESCRIPTION:

GATCTGCGAA AGACCAACTT TTAGGCAGTG ATACTTTTCT CCCATTCCCT GGGGTGGGG 60
GAGTATGCAG TTGGTGCTTT CTGTAATTCC CTTGTNCTGT TTTGTTTCTG TAAGCTTTTC 120
CCCTGGTGTC ATGGAAAGGA CTTCTTAAAT AACCACATTG TGGGTGGCTG TATCCAAAGT 180
TTAAATAAATT GGCCAGAAGT GCAGAGTATC CTTTCCTGGA TTCGTGTCAG AAAAGGGCTC 240
CTTGCCACAA CTGAACCTTAC TGTATAAAAA CCTGGCTAGG GAGATTTAAT TTTACTAAAA 300
TTACAGTTTA ATGTTACCGT CTAGCCACAA ATCAAGCAGC AAAAGCTATT TTGATGATGA 360
AAGGGGGTCC CGTTGAGCTG GCCATCTAGT GCAGTGTGCT CTCAGATNCC ATGTTTGTG 420
ATTGTGTGCT TCACAAGNCC NTCTCTGGTG CTTGAATTGG ATTTGAATTC TTGGTNAGAA 480
GNCTCAGCAT CTCCTGGGG TNGGCTGGG CCAAA 515

SEQ ID NO:874

LENGTH:514

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00997

SEQUENCE DESCRIPTION:

GATCAGNNA TNAAGTGCAG CAATATCATG AATTCTCAGA AGCCCTTTCA GGGAGCCAGT 60
NAGTCATACA GTATCCACAG TTGAGTCACT TAAAGATGTC AGTATACGAA ACATTATTCA 120
CAATCCTTGG GCAATCTCAT TTTTTTTTCC TTCTCCCTC CTCCCCTGCC CCCCATACAT 180
TTNTATCCTT GAGTTAGTTT TGGNGGGGCA GGAAGTACTT AACATCTCAG AAGCTAGATT 240
GGGAAACATG CTCAGCTATA AGAACTGAGC TTTAAATTTT GAGTTTAAAA ATGTACATCA 300
GGAGCAGNTG GGGAGGGTCT TTTTTTNAA AAAAATCTTT CCAATTTTGG GTTTTCTNTG 360
CCATATGGCC GTTTTGTAAT TNCTTTNGGG GTTTTNNATT NTTTTNGAAA GTGGNTGAAA 420
TCTTGTNTG GGNTTTTTTT CCCCAGAAACA TTTNNAATAT AACCCNGTTT ATTTTNNAT 480
GNAAATTAAT CCTNTTTTGG GTAAAAAGGT TAAA 514

SEQ ID NO:875

LENGTH:513

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00998

SEQUENCE DESCRIPTION:

GATCTTCTAT TAAANTGATT CCTCTTTATT AGAGAAGGAA AATTTAGTTG CTATACATCT 60
TATATTTNCA CAGTTTATTA AAGTCAGTNC CCTAAAGGTA CCTNCTTNC TTTGTGGCAT 120
ATATGGCATC TNCTGTCTTC AGATTTNCTT ACACCTTTGT GATTATAAT GTTAGTGATT 180
GGTGCCCTAT TCTCTGAGGA AAGATGGAGG GTTCATAAAG CAATGCCCTA TCCACAGCAG 240
ATTNCTTGT ATATTAAGTT AAACAGAATT CTGTAAATTA TTATGAAGGG TTCAAGCTCT 300

TTAGGGGGAG TTTTTTTTC TTGTTGGTA ACAAATTGGT TGCAATCTNT TATATTTTCG 360
 AATTGGNTTA GATATTACAG TCTACTTATT TTTNCANGNG TAAATTAATT GTNTAAGGTT 420
 TGGGTTNGGT ATAAATGGNT AAAATATTAA TATNGTGGGG GGTAAAATTT GATTNGGNGT 480
 TTTTTTTTTT NAAGGCCNNN GGNTTTANGG AAN 513

SEQ ID NO:876

LENGTH:510

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00999

SEQUENCE DESCRIPTION:

GATCAGTATG AGANGCAATA CCTAATCCTA TGTGCTATT GTATTTTNC CTAGTTGGTG 60
 TGCCTGCTCA GAAAAACATA TACTGTATGT GTATACATAC CTGTGTATAT ATAAAAGGTC 120
 AATTATATA TNTNCCTATA GGAAATGGA GTAACAAGTT CCCTATCTCC CATATTATT 180
 TGTCCATAGT AAAATGGCCA CATTGATGAT AATTTCTAGA ACTAGTTTCT GAGATTGTCA 240
 GCCCTTTGTC TAAATAATG GCAGTATTAA TGATTGACTT CTGTCACTGC CATAGTTACC 300
 TGGATTGTCA GCCTNGGTAG CCTTTGTCTA AAGTCCTAAA GAGTTCCAAA AAAAATGTGT 360
 TGAAATAATT GCTAAATAGT GGTGGGTGAT TCTTNCAGTA GGNATTGTGA ATAATTCNT 420
 GGCAAANAAG GTTATTNCCT GCTATTGGTA TTGGATNATT NGNCTTNTAT NCNGGTATTT 480
 TNNAAGGC AGGNNTATAN GGNTNNCCN 510

SEQ ID NO:877

LENGTH:504

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01000

SEQUENCE DESCRIPTION:

GATCTTCCAT CCTCAAATGA CTCTTTTTC TTTATATGTT AACATATATA AAATGGCAAC 60
 TGATAGTCAA TTTTGATTTT TATTCAGGAA CTATCTGAAA TCTGCTCAGA GCCTATGTGC 120
 ATAGATGAAA CTTTTTTTAA AAAAAAGTTA TTAAACAGTA ATCTATTTAC TAATTATAGT 180
 ACCTATCTTT AAAGTATAGT ACATTTTACA TATGTAAATG GTATGTTTCA ATAATTTAAG 240
 ACCTCTGAAA CANTCTACAT ATACTTATTA CCCAGTACAG TTTTTCCTCC CTGAAAAGC 300
 TGTGTATAAN ATTTATGGTG GATAACCTTT TATGGTTTCC CTTTCCAAAG GCCCAGGGTG 360
 GGAGGGGGGA TTAAGGGGGC CTAAGGTNTA TGCCTCCNNG GTTTAAANT TAAATNCCCT 420
 CNNGGTATTT AAATTANNTT TTNCCNANGG TTTNTNGGGG GANTGGGGGG GTTANANTT 480
 GCCTTNTTNN GGGGTTTGGG GAAA 504

SEQ ID NO:878

LENGTH:500

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01001

SEQUENCE DESCRIPTION:

GATCTGGGCT CTGAGCACAA GTCAGGAAAC ACCAACATAT TCACACTCTC CCAGTAGGTT 60
 CCTCAGTCCG ATGGTGAATG GCTATTCGTA AATGGCTGGT CTGGCTCTTT GGTGTTGGAG 120

CCTTTCCAAT AGCCCCATGA AAAGAAGCAT CACCCAAGGA TATTGTAAAA AGGATGTAAC 180
 AAGGAGATAG GGTAGACATT GTACTCAGTG GGCCTTGGGG CCTAGCCCAG CTCTGAGCAG 240
 AGGACTGTGG CATTCACGTG CCTTGAGTGT TTCACCTTCT TGGATAACAC ACGGGCCTTC 300
 TCTTCTGGAT TTCATCAGAG ATTACAGCCA GATGGGGGCT GAAGACCATC CTCTTTGACC 360
 ACAGAGGGTG TGAAGTGTGG GAATTCCTCC CAATTTATGG TTTCNAGGA AAATCTTAGT 420
 TCCTTTTATT TATAGGAATG CATGNCNTTT TGGTGTAAAG GAAACCCAAG GGGNANTTAA 480
 NGGGACCANT CCTANTNAAA 500

SEQ ID NO:879

LENGTH:500

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01002

SEQUENCE DESCRIPTION:

GATCTCCAGC CTCCCAGAAG CCTGCTGTGC TTTGCTCCCA CAGCTTTCTG CCCATTGTTT 60
 CTTACTAGTT TCTTGAATTG TNCTTGTGGA CTTTNCCTCA GGGATACATT GGCCTGCAGG 120
 TCCCAGTTCA CATGTAGTCC CCTGCTCACC ATTGGAGAAT CAGCTCACTG CTCTCTAGAA 180
 ACGTGGCGTT GGTGAACGGA CCATGCTTCC GTAGCTCTGA CCTGGGCAGC TTGGACCTGG 240
 TCATCCTCTA CTGCCATACC TTTCCCTGGG GGCTTGAACA CAGAACAGGG AGATGGACAA 300
 CCACTTCAAA GAAAGACCCA CCGAATGCAG TTTCTGCTTG ANTGACTGGG NCTGCAGTTC 360
 CNTTNTCCTG GGACTTAGAG GTGGNCAGAT NTANGGCCCC TTTACTCATC CANCTTNGTN 420
 TTCAACTGGN ACTNCCNAAT NANTNAAAGA GCCTNAAATT TTAAACTNGN TGTGGATNGG 480
 GNATATGGGA NTAGGGTTGN 500

SEQ ID NO:880

LENGTH:500

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01003

SEQUENCE DESCRIPTION:

GATCGTCAGC AAGTACTGTA NCTGTAAAGG AAAATCTCTC TCTCTGGAGA ACCCACACAA 60
 ACCATTGACC TGAGTGCGCA TGACAGCCAC TGGNNATNTT TTCTATGATT GAAAATCTGC 120
 CATCGCTGAC TGTTGGCCAG TTTCAAAGGG ACCCATTGTA TACAGGGTGC AAATGTATTA 180
 TACGGATGTT TCCTTTTGTA CACTTCATTT TTACAAGTTT TGCTACTCAC AAGCTTTATG 240
 TAGTGGAGGA TAGAGGTATT TTTGGTCTTT AGAAGCTTGT CGGGGTGAGG GCTGCTAACT 300
 TACACTTCAG AGGCCTGTGT CCCAAAGGCC TGGCTGCGTT TGCCGTGCTG TGCAGGAGCC 360
 TGTGTACACA GGCAGGTGTT CGCCTGCCCG AGCGCGAGTA GCTCTTTGTG TAGTNGGTGA 420
 AAATGCTTGC AGGCATCTGT TTAATTAAAA ATTNCCTGCT GTTAAAGNCA GGGGTAAAAA 480
 ATNTCCACAA TTTANGGAAA 500

SEQ ID NO:881

LENGTH:498

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01004

SEQUENCE DESCRIPTION:

GATCAGGATT CAGANGTGGG CATCTTCCCC GCAGACTNCC CTA CTGAGGCC ACCTAGCACT 60
 GCCACGAACC GGTGGGCTA GGAAGAAGT AAAATATTTT GCAGAGTCTG ATGAAGAAGA 120
 AGATGATGTT GATTTTGCAA TGNNTAATT AAGTGCCCAA AGAGCAGAAA CATTTTTCAG 180
 CAAATATCTT GTGTGTCCT TTTGTCTCT CTGTCTCAGA CTTTGTGACA TCTGGCTTAT 240
 TTTAATGTGA TGATGTAATT GACGGTTTTT TATTATTGTG GTAGGGCCTT TTAACATTTT 300
 GTTCTTACAC ATACAGTTTT ATGCTCTTTT TTTACTCATT GAAAATGTCA CGTACTGTCT 360
 GATTTGGCTT NGTAGGAATT GTTATAGGN CTGCCCCTGC ATTAGGCACA GGATTTTAA 420
 ATGTCCATG GGTNCCANC CTACCAGACC CTGCTTTTTT NGNNAATNGG AATTTTNAAC 480
 CATTNANAAA TNGGAAAA 498

SEQ ID NO:882

LENGTH:494

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01005

SEQUENCE DESCRIPTION:

GATCTTACTC CACGNATACT TTTTGGTNTG TGAAGGCATC GGTAAAGGGC ACAAAGACAG 60
 CCATGGGGAC ATTTATGTAA ATACGTCTCT AATTGCCACA CTGCAGCTGA ACAGTGTGTA 120
 GTATTTCCC AGTCAGCTTT GCCATACTGA CGTCAATCAT TTGAGAGAAA TTATTCAGAT 180
 TTNATTTTGT TATCTGTGGT AACAAAACAT TAACCAAAG ATTTTNTGTC CAGAAGCCTC 240
 CCCGNCCCC CAAGCTATTT GCTCACATTA ACANATTAAA GTGCCTGAAG CATAATTCAT 300
 TCTTTACCTG TATACTAAAA ACCCTGTTGT ATTGGTTTTT TTTNTAATAA GCCTTTTAC 360
 CTCTGTGTAA ANANATATAT ATACCAGGTG TATGATGGTN CATTTTGGGT CTTNANCTTT 420
 TTTTAATGG TTTCTAATNT GTNTGNCCNA ATGTTGGCNT TGNTTTTANA NTTGTNCCGG 480
 GGTNNATTTT TANN 494

SEQ ID NO:883

LENGTH:493

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01006

SEQUENCE DESCRIPTION:

GATCTTGATG CTGTGGAAGT AGTTTGAGGA ACATCCTATG AGTTTNCCTA GAATGTATAA 60
 AGGTTGTAGC CCATCCAAC TCAAAGAAAA AAATGACCAC ATACTTTGCA ATCAGGCTGA 120
 AATGTGGCAT GCTTTTCTAA TTCCAAC TTTTATAAGT AAAAAAGTGT TTGCTTATTC 180
 CACCACTCT ACTGTGACAT ACTCGAGTAT AAAGACATGT AGCAATAACG GGGAGTGGGG 240
 GGGGAGTCTC ACAGTGCTT TGGGAAGGCC CGAAGTGGC TTAAATCTTC CTCAACCAAA 300
 TAAGTATTTT ATTAGTGCTT GAGAGAATCT GGAATGTAGG NTGGGTTCAA CTGCACAAAN 360
 GGGAAANGNT TTTTACCACT NTTTTATAT AGNTATAAAG TGNAGCAACC GCCTTAGTGC 420
 CTGAATATGT AGTCCATGAN TATGCCTTGT NTAATTTCCA GAAATTCAN ACCTGTACT 480
 GTTTTTTTC CCN 493

SEQ ID NO:884

LENGTH:492

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01007

SEQUENCE DESCRIPTION:

```
GATCAGCACT GCCAGTGGAG ATGGGCGTCA CTACTGCTAC CCTCATTTC CCTGCGCTGT 60
GGACACTGAG AACATCCGCC GTGTGTTCAA CGACTGCCGT GACATCATT AGCGCATGCA 120
CCNNNGTCAG TACGAGCTGN NCTAAGAAGG GAACCCCAA ATTTANTTAA AGCCTTAAGC 180
ACAATTAATT AAAAGTGAAA CGTAATTGTA CAAGCAGTTA ATCACCACC ATAGGGCATG 240
ATTAACAANG CAACCTTTCC CTTCCCCGA GTGATTTTGC GAAACCCNCT TTTCCCTTC 300
AGCTTGCTTA GGATGTTCCA ATTTAGGAA AGCTTAAGGC GGCCTACAGA AAAGGGANAA 360
ANGGGCCACA AAAGTTTCCT TTAACTTTT NAGTAAAAAT TAANTTAAAN CAGCAGCAGC 420
AACCANTTTA AATTGGATT AANGGGTCN AATTGGAATT NAATTTTTTG GNTTNNNCG 480
GGNTTTNAAA AN 492
```

SEQ ID NO:885

LENGTH:490

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01009

SEQUENCE DESCRIPTION:

```
GATCGAGTTT NATGCATCAC AGTTAACATG TCAGCTGGCC CTCCAGGCC CCGCCCCAT 60
CCCGTCCACG TTGCTGTGTC GTGAGGTGCA GCGGGTCACC CTGTGGCCCG TCCTGTGACC 120
CATATTTAGC CGTGTGTTGG ACTCCGTGTC TTCAATGGTT TGTTAGTTGC CATTACAAC 180
TTGTCTGGGT AGAGTTTTTG AGTTTTNCA GTTCAGTATC CCTCTGTCTA TTCACACTTC 240
GTGTTAGTGG TAACTCAGTT TGTCTTTAAA TAGTTACAGA AGGGATACGT CATTGTGTA 300
TGCTTTTGTG AAGTGAGTTA AACGAGCTTT CTGTATTTA ATGCTTTAGT GTTTCAGTTT 360
TATAAGTGAA GATTTTATTT TAAAAACCAG TGGGAAAGAG TGGGGGGTTT CTTTTATGT 420
CTGGGTCATT CAGGCAGTAC ATCTGNTTTA AAGCTGAATG TAGGACANTT AATGAAATCC 480
ANATCTGAAA 490
```

SEQ ID NO:886

LENGTH:487

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01010

SEQUENCE DESCRIPTION:

```
GATCAGCTAT ATACTATTTA TATACAAGTN ATAATACAGA TTTGTAACAT TAGTTTTAAA 60
AAGGGAAAGT TTTGCTCTGT ATATTNNTT ACCTTTTACA GAATAAAGA NTTACATATG 120
AAAAACCCTC TAANCCATGG CACTTGATGT GATGTGGCAG GAGGGCAGTG GTGGAGCTGG 180
ACCTGCCTGC TGCAGTCACG TGTAACAGG ATTATTATTA GTGTTTTATG CATGTAATGG 240
ACTATGCACA CTTTAAATTT TGTGAGATTC ACACATGCCA CTATGAGCTT TCAGACTCCA 300
GCTGTGAAGA GACTCTGTTT GCTTGTGTTT GTTTGTTTGC AGTCTCTCTC TGCCATGGCC 360
TTGGCAGGCT GCTGGAAGGC AGCTTGTGGN NGGCCGTTGG NTCCGNCCAC TCANTNCTTC 420
TGGNGCACTG GTTNTNCTT TANAGTTANG GTNCCATGNN NCAAGGGGGG TTCCNANGNG 480
GAGGNCN 487
```

SEQ ID NO:887

LENGTH:485

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01011

SEQUENCE DESCRIPTION:

GATCGCAAAT AACTAAATG TGGAGTGTAG GAACCAAAAT GAAACCTGCT GTATGGAAAC 60
TACTTTCAC TATGGTTCAT TGGTTTTGT ACCAATATTT TTTATGCACT TCAGTGCAAG 120
TNTGTGCACT TAACCTTACT TTATGAGTAA GCTAAATAAC CCAAATTACA TTTNTTTAAA 180
CCTGTTTTAC TACTATGGCA CTTTGATAAA ATGGTCAGGA ACCAACTTTA CTGGCAAAAG 240
GGTCCATGTA CCACCATGTG CTGGAGCATC TGTTCTACAT GTGGATATCT ATGANTGGTA 300
ATGTTTTCTT TCATGTAAAG GCCTATTCAG AGTTTCAGAA TTTTAAATG CCAAATATTT 360
TCATGGGTCA TTTGCATGTA GTAAGCCAGA AAATATTCAA NGGGATTTTG GAAAACCAAT 420
TGGTATTTAA CCAGCCTCAA ATTGTGCAAC CATGGTTGTA TAATAANGGA TTTGGAACCC 480
GAAA 485

SEQ ID NO:888

LENGTH:485

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01012

SEQUENCE DESCRIPTION:

GATCTAATGN CATATTCCAA AAGCTCAACA GCAACACCCA GGTAGTTTTG CTGTCAGCCA 60
CAATGCCTTC TGATGTGCTT GAGGTGACCA AGAAGTTCAT GAGGGACCCC ATTCGGATTC 120
TTGTCAAGAA GGAAGAGTTG ACCCTGGAGG GTATCCGCCA GTTCTACATC AACGTGGAAC 180
GAGAGGAGTG GAAGCTGGAC AACTATGTN ACTTGATGA AACCTGACC ATCACCAGG 240
CAGTCATCTT CATCAACACC CGGAGGNAGG TGGACTGGCT CACCGAGAAG ATGCATGCTC 300
GAGATTTTAC TGTATCCGCC ATGCATGGAG ATATGGACCA AANGGAACGA GACGTGATTN 360
TNTGGNANTT TCGTCTNGC TCTAGCAGAG TTTTGATTTC CANTGACCTT TTGGNCAGAG 420
GAATTNTTGT TTNNGAAGGT TTTTTTTAG TCATCANNCT NTTGTCCTTT CAACTATCAG 480
GGGTN 485

SEQ ID NO:889

LENGTH:492

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01013

SEQUENCE DESCRIPTION:

GATCGCAACG CCAAAGGTGA AGAACCANCT CAAGGAGACC ACTGAGGCAG CCTGCAGATA 60
CGGAGCCTTT GGCCTGCCCA TNACCGTGGC CCATGTGGAT GGCCAAACCC ACATGTAATT 120
TGGNTCTAAC CGGATGGAGC TGCTGGCGCA CCTNCTGGNA GANAAGTGGA TGGNCCCTAT 180
ACCTCCAGCC GTGAATGCNA GATTTTAAGA TTGCCCGGAG GAAGCAAACCT TTTCGTATAA 240
AAAAAGCAGG CCATCTGCTT AACNTTGGN TCCACCATAA GGCCTGGGA CTNGGATTTT 300
TNTATCTGAT AGAGGTATTT NTTGTGGCCC TGGGAGCTGT CTGNTTTTCC CCTACCCCCA 360

AGGNTGCCAG GAAGACGTCC ACCATTAGCC ATGTGGNAAC CTTTACTTCT ATGCTTACAA 420
GTGCCTTTNA GNGAGCCCCA ATTCTGGTTT TNCCACAAAA TAAACCTAAT GCNNTCAGGG 480
AAAACNNTTA AA 492

SEQ ID NO:890

LENGTH:478

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01015

SEQUENCE DESCRIPTION:

GATCTTGCTT CCAGGCAGCA GCTTGAATTC CCGAATCTNC CTGCAAGCNG CATACAAATG 60
CAGCGTGAGA ATCCATACAC GTAATCCATA TTCACCTTCC CATCCATCCC GCAGAAGAGG 120
CATGGTGACA CCCAGGCTAC TGTCCATGCT TGAGAGGACG TATTTGAAGG TTCTGTTACT 180
ACAAGTTGGG AATATTCACG GGCCATGCCT GAATACCCGG NCTGTANCTC ACACNGTGGT 240
CTGTGTAAGG GGNATACCTN GGGGCGGCCT GGTTTAATCN TGATTAATAT CTGAAAGCNT 300
GGGTNNNTG GGGAAATGNA GGGTTTTCTT AATGCCATTA AATTTTTTTT TAGGCNGTAA 360
AAATTAAAT NCATTTTNTT ATCCAGCAGG CCTCTTTTAT ACCTTTATNG GGAATCTNC 420
CATACTTACT TTCCGGCCAN NTTTTCAATA ATNAAATTTA TTTTGGAAN TTTTAAA 478

SEQ ID NO:891

LENGTH:474

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01016

SEQUENCE DESCRIPTION:

GATCTTACAC TCTGCTTTTG TCCAAATAAA ATGCAATAGT ATCAATATCA ATTTCAGAAA 60
AATGGACTGA ATATGCTTTT TTGGTGATGA AATCTCATGT ACGATATTTA TAGTGATGTG 120
CTTTTATTN CTCATGAGAT ACTAAATATT AATTGTGTG TACATTTGTN CTTAGCATAT 180
ATTAAAGTTT TGAACCAAAT GTGTTAAAGC TTACGCTTTG CCATGTAAAT TTCCAGAAG 240
TTGTTGAGCT CAAATGTATC CTACATCCAG CTGTAGAAAT TTGTCAGAAA TTGTTTAAAT 300
TTTGATATA ATTGTACTGT TTAATTCTAG CCATTGCGCT GAACAGTATT TGAGTTACCA 360
TATAATATGG CTTTACACAA NGGNAATGTG TGGCTTTTGT TTTGGTATTT TTTCCAGTAT 420
AGGAAGTTCC CTGTGGCCTT ATTTAAATA AAGGTTATTA GGTAAACTG GAAA 474

SEQ ID NO:892

LENGTH:473

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01017

SEQUENCE DESCRIPTION:

GATCACAGCT CACTGCAGGT TCAGCCTTCT GAGTTCAAGC AATCCTTCTG TCTCAGTCTC 60
CTCAGTAGCT GGGGCTTTAG GTGGGCACTG CCACACCGTA CTAATTTTNG TATTTTTTGT 120
AGAGACGAGG TCCCACCATG TTGCCAGGC TGGTGCAAA CTCCTGGGCT CAGTCAGTCC 180
CCCCATCTCA CCCTCCCCAA GTGCTGGAAT TACAGGCGTG ANTTACTGTG CCCAGCCTTA 240
CGGACATCCT TTTGAATTAT CTTTTTCACT CATAGAATAT GAATACATTT ATTTAGACTT 300

TTTCTAGAAC TTTCTGTTT TCATGTCTTT GNTTCACCTG GAATTGGGTT TAACACCCTT 360
 TTATAAAGTT TGTGGTTTGN AAAATTTCCA TTGGGGCCAT CAATACGGAA ATATATTTGG 420
 TAANATTNGG GGGTTCNATT TTTAATTAA AATGGCAAAT GANNGGCAGG AAA 473

SEQ ID NO:893

LENGTH:473

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01018

SEQUENCE DESCRIPTION:

GATCGGGTTG AGGATTGGGG CTAGCTCGAT NACANTAAGG CCCCAACATC GNGGGACCTG 60
 CTGTGGCGCG GATTCTTAGG AACGCTGTTC TAGCCGGCCC CCTCTCCAGG GGTGCGCGTG 120
 GCCGGCATT A TTTCTAGTT CTTCTTGTA CCCTGAGGTG CCAGCGCGGG GAGTGAGGAG 180
 GGGTCAGGG GCTAAGGATG CAACCTCTGA CGTCTGCGC CTTCTAGGA GAGTCTTACA 240
 TGTNTTGAGA TTTACAAGC AATGCGAGTT GTAAAATACC AGCTCTACAN GAAGCTAGGC 300
 TCTGTGACGG CATAGTTTTC AGTAGCTNTA TCACAATATT CACAATGGAG AATTATATGA 360
 CATGGTAAGC AGAAATAGGC CCCTTTTAAT GNGNTGCTTC TATTTTACCT CANATTGGTG 420
 GNTNTAGGNT AATCANTAAA AATCNATCCA NNGCNTTCA CAACACTNNN AAA 473

SEQ ID NO:894

LENGTH:468

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01019

SEQUENCE DESCRIPTION:

GATCAGGGGG CCAGGCCAGC AGCTCGGGGG CCACAAGGAG ATGGATAATG TGCCTGTTTT 60
 TTAACACAAC AAAAAAGCCT ACCTCCAAAA TCCCCTTTT GTTCTTCCTG GACCTGGGCA 120
 TTCAGCCTCC TGCTCTTAAC TGAATTGGGA GCCTCTGCCA CCTGCCCGT GTATCCTGGC 180
 TCTCAGCTCA TGGGGAAGCC ACATAGACAT CCCTTTCTTC CTTGACAGC TCGCTAGCAG 240
 CTGGTAAGGT CTTACACCC TGATTCTCA AGTTTTCTGC TTAGTGGCAC TGACATTAAG 300
 TAGTGGGGGG ACAGTCCATG CCAGGACACC CTGGAGTAGC CTTCCCCTT GGCCGTGGGG 360
 CAGGNCCTAA CTCACGTGCG CTTTGGAGTT GAGGGTGTCT TTTCTNTTC TTTCTTAGT 420
 TCCTGTATTC TAAACATTAG TAAAAATAA TGTTTTTTAC ACAGGAAA 468

SEQ ID NO:895

LENGTH:462

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01020

SEQUENCE DESCRIPTION:

GATCCTGCAG GACTACAAAT CCCTCCAGGA TATCATTGCC ATCCTGGGTA TGGATGAACT 60
 TTCTGAGGAA GACAAGTTGA CCGTGTCCCG TGCACGGAAA ATACAGCGTT TCTGTCTCA 120
 GCCATTCCAG GTTGCTGAGG TCTTCACAGG TCATATGGGG AAGCTGGTAC CCCTGAAGGA 180
 GACCATCAAA GGATTCCAGC AGATTTTGGC AGGTGAATAT GACCATCTCC CAGAACAGGC 240
 CTTCTATATG GTGGGACCCA TTGAAGAAGC TGTGGCAAAA GCTGATAAGC TGGCTGAAGA 300

GCATTCATCG TGAGGGGTCT TTGTCTCTG TACTGTCTCT CTCCTTGCCC CTAACCCAAA 360
 AAGCTTCATT TTTCTGTGA GGCTGCACAA GAGCCTTGAT TTGAAGATAT ATTCTTTCTG 420
 ACCAGTATTT AAGGGTTTCC AATAAAATGT ACACCNCTCA AA 462

SEQ ID NO:896

LENGTH:462

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01021

SEQUENCE DESCRIPTION:

GATCTAAATC CTCATTTATC TCTNCTATGT CTAGTATTTT ACTGTCACTG GAGGCTCTGT 60
 GGGCTGTCAT AGTTAATTGA CCATAATTAG CAATATACTT TTAAAGTGGG AAAGCTGAAT 120
 GACACTNTTT AAGACAATGA ACATTATCAA AACAAAATGT ATAATTNCTT AATTTGAATA 180
 ATAAATTAGG CGTTTAAATG CTATTTGTAG TCTTGATATA CAGAAATAAA ATAATTAGGG 240
 TTGGTCTTTT TTATTTTAGG TTGTTTTATG TTGAATGTTT TATATCTTAT TAGTTAATTN 300
 GTATATTTNA TTAGTATTTN GGGAAATAGC ATATCTGAGA CTGAAGGGGA AATTGGCCAA 360
 TTCATTATT TGTGGTTTTT TTCCTCAGCT ATTCTGAGCT TATTTATTAA TTGNATGGCC 420
 TAATGGCTAA CCATTTACAT TAAAATGGTT TTTNCCCCA AA 462

SEQ ID NO:897

LENGTH:459

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01023

SEQUENCE DESCRIPTION:

GATCTNCTCT TTCCTCTCCT TTTCTCTATT TATTCCTAAA GGAATCTGAC CATTAAAACG 60
 NCTCTACGGC CCAAAAAAAG AAAAAATAA AAATTCCTTT TTATTCCTGT CAACTGGATG 120
 GAAACACAAA TTTTCATGGAG CTGTGTACCA TCGAAGAAAC CTGGTGTCTG GCATGAAATT 180
 ACTGTAAAGA ACTTCCTGTA AAACACGTTT TTTAACAAAC TGAATGAAA AGCATTGGAG 240
 CGTCTGANTG AAAGACGTGA CCTCTGCTG GGAATCTGAT GGTCTTCAGC ATTCACCTTC 300
 GTGTGTCTTC AGTGTCTCAT TGTATCCCT NGCTTCTGGN TTGGNCCTTA GGAGTNGTTT 360
 GGGATATAAC CTNAAATTGT NGGATGGGTA AANGGGAAAT TTNNATGNNG TTTTTTTGGT 420
 TTTTAAAAAT NATTTTNAAT NCGGGGTCAN TTTTTTAAA 459

SEQ ID NO:898

LENGTH:457

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01024

SEQUENCE DESCRIPTION:

GATCCACCTG AGCGACCTCC GGGAGTACAG GCGCTTTGAG AAGGAGAAGC TCAAGTCCCA 60
 GTGGAACAAT GATAATCCCC TTTTCAAGAG CGCCACCACG ACGGTCATGA ACCCCAAGTT 120
 TGCTGAGAGT TAGGAGCACT TGGTGAAGAC AAGGCCGTCA GGACCCACCA TGTCTGCCCC 180
 ATCAGCGGGC CGAGACATGG CTTGCCACAG CTCTTGAGGA TGTCACCAAT TAACCAGAAA 240
 TCCAGTTATT TTCCACCCTC AAAATGACAG CCATGGCCGG CCGGGTGCTT CTGGGGGCTC 300

GTCGGGGGA CAGCTNCACT CTGACTGGCA CAGTCTTTGC ATGGGAGACT TGAGGAGGGG 360
 AGGGGNTTNA GGTGGGTGAG GTTAAGGTGC GTGTTTCCTG GTGCAAGTCA AGACCATCAG 420
 TCTTATTAAG AGGTGGGTGC CAATTTTTTT TACNAAA 457

SEQ ID NO:899

LENGTH:457

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01025

SEQUENCE DESCRIPTION:

GATCCAGTAT CTCCTCGGC TTTTAGGGA GCAGGAAAAA TCGGTCTNAN AGCAACTTTT 60
 TTTAAAAACC TGCCCTGTTG TATATACTG TGTCTGTTT ACCGNGTGNC CTCCCAAGGG 120
 GGTGGGAAC TATATAAAC GTTTAAAGG GCCACGATT GCCCGAGGGT TACTCCTTTG 180
 CTCTCACCTT GTATGGATGA GGAGATGAAG CCATTTCTTA TCCTGTAGAT GTGAAGCACT 240
 TTCAGTTTTC AGCGATGTTG GAATGTAGCA TCAGAAGCTC GTTCCTTCAC ACTCAGTGGC 300
 GTCTGTGCTT GTCCACATGC GGTGGGCGTC TTGGGACCTT GAATGCCTGC CCTGGTTGTG 360
 TGGACTCCTT TAATGCCAAT NATTTCTTCA NTTTCTCTT GGACACCAG GGTGCCNGT 420
 TNGACAAAGT TTTGGNGAAC NTCCTAATTT AAAATGN 457

SEQ ID NO:900

LENGTH:454

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01026

SEQUENCE DESCRIPTION:

GATCCGANGA CCACATCAAT GGGCGCGTGC TCTACTATGC CACCTGCAAG TAATGCTACA 60
 GCTTCCAGCC CGTTGCCCA CTCATCTGCC GCCTTTGCTT TTGGTTGGGG GCAGATTGGG 120
 TTGGAATGCT TTCCATCTCC AGGAGACTTT CATGTAGCCT AAAGTACAGC CTGGACCACC 180
 CCTGGTGTGT AGCTAGTAAG ATTACCCTGA GCTGCAGCTG AGCCTGAGCC AATGGGACAG 240
 TTACACTTGA CAGACAAAGA TGGTGGAGAT TGGCATGCCA TTGAACTAA GAGCTCTCAA 300
 GTCAAGGAAG CTGGGCTGGG CAGTATCCCC CGCCTTAGT TCTCCACTGG GGAGGAATCC 360
 TGGACCAAGC ACAAAAACCT AACAAAAGTG ATGTAAAANT GAAAAGCCAN ATAAAAATCT 420
 TTGGAAAAGA GCCTTGGAGG TTCAACGGGG GAAA 454

SEQ ID NO:901

LENGTH:453

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01027

SEQUENCE DESCRIPTION:

GATCTTNCTT NTTAAGTGA TAAGACAGTC CCACAGTCCA GCCTAACTAT GGGACAGCTT 60
 TACGAGAAGG AAAAAGATGA AGATGGATTC TNATATGTGG CCTACAGCGG AGAGAACACT 120
 TTTNNAANCT GAGGGCCATT GCTGGGCTAG GTGCACCGTA ACTGCTTGTG TATCTTGTA 180
 ATAGCCAGCC ATTTNCAGTT ATTATACCAG AACCTCTTCA CATAGACCTA TTAGTGCATT 240
 TGTAAGTGGN TTTATTTCTT AATATATTGG AAGGTTTGT TCCTTAGNCT AGTAAATTAT 300

CATACAGNGT TTTATTTTGA GGTTTTCTT NNNTGTGCAT TNTCCTCATG GCCTGTAAAC 360
CNCCAGGAAA CCTTTTCCTT CTNGGAAATC ATATTTGAAA TGATAATTCN TATATCCGAN 420
GTGAGGNTAG GNNCCGGGTC CTCCAATAA ANN 453

SEQ ID NO:902

LENGTH:452

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01028

SEQUENCE DESCRIPTION:

GATCTTAAGT GAAGAAGGAA GACTTGGCCT TTTGTATTGC TTGAATATTA ACTGTCTTGG 60
AAGGAAGTTA TGCTACAAGA AGTCATACTT TCATAAAATT ATTTGCATCT GTGTCAAATG 120
CAGTTTAGTC AGAACGTAAG ACATAATAGG TGTGGACATG AACTCTGGAG TGTGAAATAA 180
AATCCACAGT TACTTAAGCA GTCTGTTTTG ATGGAAAGTA TCTTGGGATA ATACTTCCT 240
CTGTGGGATT TTGTTCAATT TAGATGGTGC ANGGNAGTAT CAGTCTTTAA TTTTTTTGTT 300
GTTGTTTTTA TCANTCAATT GCTCTGATGG TATGATGCAT GGGCTTCAGG ACTCCAGCTG 360
CACCCTGTA TAAACTCAG TTCAGGTTN CTAGCGGTCN TTGGNTAATT TTCGGGGCNT 420
ANCCCGATNC CAATTNTTTT TAATGTGNTA AA 452

SEQ ID NO:903

LENGTH:448

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01029

SEQUENCE DESCRIPTION:

GATCAGGGAC CCTCCNGCT TTCCTGGGCC TCTNAGTTGA ACAAAGCAGC AAAACAAAGG 60
CAGTTTTATA TGAAAGATTA GAAGCCTGGA ATAATCAGGC TTTTNAATG ATGTAATTCC 120
CACTGTAATA GCATAGGGAT TTTGGAAGCA GCTGCTGGTG GCTTGGGACA TCAGTGGGGC 180
CAAGGGTTCT CTGTCCNGG TTCAACTGTG ATTTGGCTTT CCCGTGTCTT TCCNGGTGAT 240
GCCTTGTTG GGGTTCGTG GGTTTGGGTG GGAAGGAGGG CCATCTGCCT GANTGTAACC 300
NGCTAGCTCT CCGANGCCCT ACGGGCCTGN CTNGTGTGAG CGTGTGGACA GTGGTGGCCG 360
GCGCTGTGCC TNCTCGTGTT GCCTACANTG TNCNTGGCTG TTGAGGCGCT GCTTCANGCC 420
TGCAACNCGT CCNTNGTCTC ANTACAAA 448

SEQ ID NO:904

LENGTH:461

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01030

SEQUENCE DESCRIPTION:

GATCGGTTTA CAGATGAGGA AGTGGATGAG CTGTACAGAG AAGCACCTAT TGATAAAAAG 60
GGGAATTTCA ATTACATCGA GTTCACACGC ATCCTGAAAC ATGGAGCCAA AGACAAAGAT 120
GACTGAAATA ACTTCAAATT CCAGCCAAAC GTTCCTTGTT GCCACTTTGG GTATTCTGAG 180
ATTTCTCTT GCATGCCCTT AGCTTTACAG CTTTGCATT TCCTGTTGTA TTTATTCTCA 240
GCCATTTTGG GCATATGTAT CTTTATAATC AGACTGGAAA CGGGACTTTC TATTAATATC 300

ATTTTTCAGA ATAAAAATA GGGTAATTA ACCTACCAGC CCTTCTCCCC CAATAACTGT 360
 GGGCCTATAC AGNGTCAATA TATTTTNC AGNGAAAGGT TTATTCGGCT CGATTTTTTT 420
 CTGGAANTCC ATAATTTAAC CTTTATGGG TTAAANTTAA A 461

SEQ ID NO:905

LENGTH:453

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01032

SEQUENCE DESCRIPTION:

GATCAGGGAC CATGAAAAGA AACTTGTGCT TCACCGAAGA AAAATATCTA AACATCGAAA 60
 AACTTAAATA TTATGGAAAA AAAACATTGC AAAATATAAA ATAAATAAAA AAAGGAAAGG 120
 AAATTTGAA CCTTATGTAC CGAGCAAATG CCAGGTCTAG CAAACATAAT GCTAGTCCTA 180
 GATTACTTAT TGATTTAAAA NCAAAAAAAC ACANAAAAAT AGTAAATAT AAANCCAAAT 240
 TAATGTTTTA TAGACCCTGG GAAAAAGAAT TTTCAGCANN GTACAAAAAT TTANCGCATT 300
 CCTTCTTTA ATTTGTANT TCTTACTGT GGGAAATAGCT CAGAATGTCA GTTCTGTTTT 360
 ANGTAACAGN NTTGGATAAC TGAGCAGGGN ANCGNAATTT TGGNTTTNTA AAATTCCTTG 420
 CTTTNANTAN ANNTCCCTT NNCCCGGTGG AAA 453

SEQ ID NO:906

LENGTH:445

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01033

SEQUENCE DESCRIPTION:

GATCCGATGG AGAAGGGGGG ACCCAGGCCA GCAGGAGACA GGACCCCGA AGCTGAGGCC 60
 TTGGGATGGA GCAGAAGCCG GAGTGGCGGG GCACGCTGCC GNCTTCCCCA TCACGGAGGG 120
 TCCAGACTGT CCACTCGGGG GTGGAGTGAG ACTGACTGCA AGCCCCACCC TCCTTGAGAC 180
 TGGAGCTGGC GTNTGCATAC GAGAGACTTG GTTNAACTTG GTTGGTCCTT GTNTGCACCC 240
 TCGACAAGAC CACACTTGG GACTTGGGAG CTGGGNCCTGA AGTTGNTCTG TACCNTGAA 300
 CTCCAGTTT GCGAATTATA GAGACAATCT ATTTTGTTAC TTGCACTTGT TATTCGACCA 360
 CTGAGAGCGA GATNGGGAAG CATAGATATC TATATTTTA ATTCNCTAT NGAGGGCCTN 420
 GTAAATAAAT TTCTAAAAGC CTAAG 445

SEQ ID NO:907

LENGTH:444

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01034

SEQUENCE DESCRIPTION:

GATCTCAATG AAATTAAT AATAACTATA TCTAGAAAAA CTCCCAATAT GTGAATATTA 60
 AGCAACATAC TTATAAAAAA TTCATAGTTC ATGGATGAAA TCAAAAGAGA ATTCAAAATA 120
 TTCAAAATA AATTATGATG ATTATATAAN ATGTAGAAAT GTGTGGGATG CCACTACACC 180
 AGTTCCTAGA GTGAAATGCA CAGCTTTCAA GGCTTCTGTT AAAAGAGTTG GGAATTACAA 240
 AACAAGGAGC AGCGACTGCC AATGGGTGTG GAGTCTTTT TGGGGTGATG ATGAAAATGT 300

TCAAAAATTG ATTTTATTGA TGGTTACACA CGTCTATAAA TATATTTNAN CGGNAGAATT 360
 ATATGGATAT ATATGTGATA TATGGAGGTA TATCCTCTGT AAAATTCCTA NGGGTTTAAN 420
 GGAGGATTGG GTATCCACAC CAAA 444

SEQ ID NO:908

LENGTH:440

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01035

SEQUENCE DESCRIPTION:

GATCCCAAGT TGCCTTAAC AGGGTGTCTG TCGTGCCGCA GTAGAGCACT GCTGCTTCCT 60
 CCAACCCCAA AATTATGTT CCTAAGTAAG TCAGGTCCCT AAGCCCCGTC CCAAGAAGTG 120
 ACACAAGTGG CCAACATCCA CACTGTAGGC TTGCAGGCTA CCCGCCCTGA GATTGGTAA 180
 AGAACACTGC CTTGTTCCCC ATCAGTAAAC AAGGTTACCT ACCTCAGGAG GCTGCTTG 240
 AGAGAGCAAA TGCAGTATCT TCAGANTGAT TTATTTTTT ANTTAATTGT AAAGACTTGT 300
 GCCATTGGCT GCTCTTTCTA GTCCCTAAN TTTCTGTTCT AGTTTAAANT TTCTCTAGAN 360
 CTTGCAATNG TTGGGGGGT TTTATANTGG TGTTTTNCA ATGNTTGT TCNTTANNNT 420
 AAANCCTTAA AAGTCCAAA 440

SEQ ID NO:909

LENGTH:439

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01036

SEQUENCE DESCRIPTION:

GATCGGCGTG GGGGTGCTGC TCATCTTCCT TGTCAAGTAC GACCTTAACA ACCNGGACAA 60
 GCACGCCAAG CTGGACTTCC TCAACAACCT GGCCACGGGN CTGGTGTTC TCATCGTGGT 120
 AGTCAACATC TTCATCACGG CCTTCGGGGT CCAGAAGCCC TTGATGGACA TGGCACCCCA 180
 GCAGTAGGAC ACCCAGGACC NTGGATGCTG CCTGCCNNTG CAACTCAGCT GCCCGACCCC 240
 AGGAGTCGCC ATACCTGTNA GGTGTCCACC TCCCTGCACA TGGCACTACC CAGANTGCCA 300
 GAGCCCAGGC TGGNCTCATC TGCACCATGT CCCC GGACCA GCCCTTGCTC TGANTGCGGG 360
 CCAAGNACCA NGTAGGAGGN CACTNTTGT TNTNAGCAGN TTTTCCAGG NGGGNAGTTN 420
 NNTTCTGGGA AATTGGGGN 439

SEQ ID NO:910

LENGTH:435

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01037

SEQUENCE DESCRIPTION:

GATCCAAGGA CCCACACTTT GTCACCTCAT ATCTCTCTCT CTCTCCCACT TTCGCTTTCT 60
 CTGTCTCTTC TTAGTTCTGC TTTCTCCAC TGTGCCTTCG CTCTCAGAGA GAGCTCTCCC 120
 CTGGCAGTGA CAAGATGGCT GCAGCAGCTC CAGCAACCTC AGAGGACTCC CCCATCCAGG 180
 GTCCTTGTA GCTCCTCATC TGTAGGATGT GCAGTAAACA CTCACGTGTC CTTTCTGAG 240
 GAGCCCAGTG GCTGGGGTGG GGGCTGAGGG GCAGCCCTA TGCCCTCACA GTGCAGCAAC 300

CTTGGTTAGC TCACCCATCA GGGCAGACTT GGGCAGAAAT CATGTCTTGG CATATTGTTT 360
 TGTAATCTGC TTTTAAATT GTCATATAT ATTATGAGCA TTTCCCTATA ATATAAATA 420
 TTCTTCCACA TTAATA 435

SEQ ID NO:911

LENGTH:433

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01038

SEQUENCE DESCRIPTION:

GATCATATGA AAAAGTAACA AGCTGTTCCN TGTTCCTGAT ACATAAAATN ATTTTAAGCA 60
 TTTTATCAAT CATTAAATTT TACTGCCAGT TGTGAGTGGC TTTTAAATTA ACTTGTCTTT 120
 CATTGCACTT CACTCTGCCT GTTTTCAAGG GGAGTAAGAT TGGTAACATT TGGGGAGACT 180
 GTATCTGTCT ACTTAGCGTG GCTGTTTTGA GGGACTGTCC CATCAGTGAA CAAACTGCAT 240
 GGCCTTGGAG AGAGACTCTG GGCTCTTGGC TCAGATGTGT TCATCAAATA CTCCTTTCAG 300
 AGCTGTTGTG GGTGTAAGTG ACATGATGTG GCCAAAAAAT CCAAACTGTG CAGTTGCGNT 360
 TGTGACAACC ATGCAATGTG NCTGTAAAAA TTNANTNCA GTTTAAATTN ANATNNTTA 420
 TATTNNGTGG AAA 433

SEQ ID NO:912

LENGTH:431

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01039

SEQUENCE DESCRIPTION:

GATCTTTCTA ATTCGAAAGC TGTGTTCTTT TTGAATACCG TGCATGGGGG TTAAGCTGAT 60
 GTTAAACAG TTTGCAATAA AAAAAATGA ATNAGCTTAA GTCATTAAAT CATTCAAGT 120
 GCATTCTGCA TCCTTTAAAA ATAAGTTTAA GAAATTTAAG AGAATTGTGT TTTCATTAAG 180
 TTTTGCAAT CTTTGTGTTAT GCCATGTAAA TNCCCTTTN CGTATGATTA AAGGAAGGT 240
 ATGATAAAT GATTAGTTCA TTTACATTCA CTTGTAGCAA TTACATGAGA ATTTGAATT 300
 NGTCGTGTT GGGTTGTNC ATTCCTGTGA ATGATGGTNC AGTTAGGTGA GATTNCTGT 360
 TATGGNACCC CAACTCACCA TTTGGNCCTC TTTAATCTTT GGGGGGTTCC AATAAAAT 420
 GGTCACNAA A 431

SEQ ID NO:913

LENGTH:431

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01040

SEQUENCE DESCRIPTION:

GATCCAAANT TTAAGGGATA TTGCCTATTT TGGAAGAATA AACTAAAAAT GTTAAACTG 60
 TTGAATTACA GAGAACAGAT GACTCTGAG ACATAATTTT AAACAAATAT TAAAAATANG 120
 GCAGGTTAAC ATTTGCGTTT AGGCACAATA AATCTGTATT AAAGGGAAGC ACATCAAGGA 180
 AATATATACA TGTTGANTAA TGTAACNAA AAATATTTT TAAANCCAC TAAAAATGA 240
 NAAATAATTT GATGGGTACT TTAAGCATTG TAGATAGAAA TTAATGTATA ATAGTGCCT 300

CCCNGTCTTT GTATGAAAAA TAAAAANCTC TCTAGTCCTT TAATGAGCAT GANTTTTATA 360
 CTTCTACATT TTGTTGCCTA GGNAAAATTN TCCTCNNGTA CCTTTGAGGT NATTCGGAT 420
 TTTATGGTTT N 431

SEQ ID NO:914

LENGTH:430

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01041

SEQUENCE DESCRIPTION:

GATCTATAGA GAGAGATATA TACACTTTTG ATTGTTTCT AGATGTCTAC CAATAAATGC 60
 AATTGTGAC CTGTATTAAT GATTAAAGT GGGGAAACTA GATTAAAATA TTTGTTTTTT 120
 AACTAGTTTA TTAGTTTCTN TGGAATCTGC CTGTGTCCCT GGGTTTGGGT TTTGCTCTTG 180
 GCAGCAGCAG GTGCCTCTTG GGTGCTCCTC CTGCTCCTGC CTGCAGCCCT AAGAGCAGGT 240
 GGGTGCCGAG TGTCTGGCAC AGCTTGGATG CCGCCCACTG AAGACAGCAG AGGGGGGTTG 300
 TTTGAAGCT CCCGNGACAC AGTCAAGCAT CTTCTGAGNC TTCGATGTCT TCGGNAAGTA 360
 AAAATGGGNN TTAGTAAAA CCCTGCCCCN GTTNTCACA GGGGGTTNTT TTGCAAGNNA 420
 AANTGATAAA 430

SEQ ID NO:915

LENGTH:428

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01042

SEQUENCE DESCRIPTION:

GATCAGATTC TAATTTGACA GGCAACCAGT CAATGAAACA GACACACCTG CACAGTTGGA 60
 AATGGAGGAT GAAGATACAA TTGATGTGTT TCAGCANCAG ACAAGAAAGT TCTACTGNAA 120
 AAGGANCCTG CTTCTTTACT CTAGAACTTT GTTCTTATAG ACCAAGATTA CATTCTCAAT 180
 TAGAAAACCTG CAATTTGGTT CCACCACATC ATGACTATTA CTATAGTATA GTTTTCTCTA 240
 TTCTTTTATT TTTCCCTTTA CCCATTCCCT TATTTGTACA TAAAATAATG GGTGTATGTT 300
 CACAAGCATT TTGCTGGTTT TNAATATTA ANTGGCCAAT GACATCCACT TGATGTCANT 360
 CAANACNATA TCTGTGGGGG NAAANTACCG NTTCTNGAA ATTTNCCTCC NNTTTTCCA 420
 TNAGTGGN 428

SEQ ID NO:916

LENGTH:428

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01043

SEQUENCE DESCRIPTION:

GATCGCCAGG TTCTACAAGC TGCACGAGCG GAGGTNTGAG CCCATTGCCA TGACAGTNCC 60
 TCGAAAGTCG GACCTGTTCC AGGAGGACCT GTACCCACCC ACCGCAGGGC CCGACCNTNC 120
 CCTCACGGCT GAGGAGTGGC TGGGGGGTCG GGATGCTGGG CCCCTCCTCA TCTCCCTCAA 180
 GGATGGCTAC GTACCCCCAA AGAGCCGGGA GCTGAGGGTC AACCAGGGGC TGGACACCGG 240
 GCGCAGGAGG GCAGCACCAG AGGCCANTNG CACTCCACAG TCGGATGCCG TGTNTCGGCT 300

NNGAGGAGGA GATGCGGGAA GTTCCAGGCC ACGGTGCAGG ANCTCCAGAA GNNGTNGGA 360
CAAGGNTTGG AGGAGACAAG TCCAAGNCA AGTAGNAGCC CCTGAAGGNN TTNCAATCAN 420
GGTTTCAN 428

SEQ ID NO:917

LENGTH:424

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01044

SEQUENCE DESCRIPTION:

GATCCAATAT TCAATTCATT TGTGTACTCC CACATGCAAA ATGCTAAATT ACAATGCAGA 60
CATTAAAGAAA AAGTATTGAC TGGAGGGGTT GAATTCCTTG AGAATTTATT TTATAGTCTA 120
AATCACAAT ACTTACTCA ATTTAGTTT TAAAATAGTA AACTGAATAT TTTTGTGTA 180
AGCCTATCAG AGTCAATCCT TCGTTTGGAA TTGTTTCCT GTTTTNCCTT ACTATAAATC 240
ATTTAAAAAC TGAATTCATT TTCTTAGATG GCATAAGTCT GTCTCTTGAG AAATAAGTAA 300
AATACTCCTA TTTTCAGTAT CTGTAGCACC TGAAATAGGT CTTTGTATAG CCAGAANCAA 360
GTTATGNTTG AAGTAGCTT TTCTTTGTCA CCAGTTTGG NCAATAAAAA TCTGAANGTT 420
TAAA 424

SEQ ID NO:918

LENGTH:422

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01045

SEQUENCE DESCRIPTION:

GATCAACATA ATGGACCACT CCTGAATGAG ACTTAATTTT GTCTTTCAAA TTTACTGTCT 60
TAAATCAGTT TATTAAATCT GAATTTTAAA ACATGCTGTT TATGACACAA TGACACATTT 120
GTNGACCAA TTAAGTGTG AAAAAATCTT TTGCATCATA GAACAGAAAT ATATAAAANT 180
ATATGTNGAA TGTTAACAGG TATTTTCACA GGTTTGTTC TTGATAGTTA CTCAGACACT 240
AGGGAAAGGT AAATACANGT GANCAAAATA NGCAACTAAA TGAGNCCTAA TAATTGGCCT 300
TCGATTTTAN ATATTNGTTC TTATAAACCT TGTCAATAAA AATAAATCTA AATCAAAAAA 360
AANTTGGTTC CACCTNTGCA GGTTTTATA ANTGGTGCCA ATTAAAGGT TTTGTTTTTA 420
AA 422

SEQ ID NO:919

LENGTH:422

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01046

SEQUENCE DESCRIPTION:

GATCCTTACT AAGTNTTCA TGGGAGACTT CCTTCATCAC ATCTTATGTT GAAATCACTT 60
TCTGTAGTCA AAGTATACCA AAACCAATTT ATCTGAACTA AATTCTAAAG TATGGTTATA 120
CAAACCATAT ACATCTGGTT ACCAAACATA AATGCTGAAC ATTCCATATT ATTATAGTTA 180
ATGTCTTAAT CCAGCTTGCA AGTGAATGGA AAAAACNNNC AAGCTTCAA CTAGGTATTC 240
TGGGAATGAT GTAATGCTCT GAATTTAGTA TGATATAANG AAAACTTTTT TGTGCTAAAA 300

ATACTTTTTA AAATCAATTT CNTTGATTGT AGGTAATTC TATTTGCACT GGGCCTTTCA 360
 ACTCCAGAAA CATTCTGANG GTGGTACTTG GGGTTTAANT TAAAAAGGTC CACTTTGGTA 420
 AA 422

SEQ ID NO:920

LENGTH:410

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01047

SEQUENCE DESCRIPTION:

GATCGCTGTT TCCAGAACGG GGAGGAGTAT CTCATTGTGA AACAGACTCT AGAGTGGTTC 60
 TATTTGGTCT TCAGTGTITT AGCCTCATTA GTTCATATTT GGCATGCAGC TTGTGGTGAG 120
 TACTGTTCTA GGACTGGCCA AAAATGGGCA AAATGTATCA CTCCAAACAC TACTGATTCA 180
 GCATTGTTTT CATGTCTTAA AATTGCCACC TGCACTTTGT TTCTGCACTA TTATGTAGTG 240
 CATTTTAACT TAAATTTTTT CCAGCAACAT GTTACTTATT TANGATACAT TACTGATATT 300
 TCATTATAAT TANGTTCATC TTCCCTGTGA AACAAGAGAA TTGTAAAATG TTGTGGGAAA 360
 ATGATACATA TGTGGGATGC TAATGNAAAT CATAGGTATT TTTGTGTAAA 410

SEQ ID NO:921

LENGTH:409

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01048

SEQUENCE DESCRIPTION:

GATCACANTT GANCTGGCAG CGGGATGGCG AGGACCAAAC TCAGGACACC GAGCTTGTGG 60
 AGACCAGACC AGCAGGAGAT AGAACCTTCC AGAAGTGGGC AGCTGTGGTG GTGCCTTCTG 120
 GAGAAGAGCA GNGATACACA TGNCATGTAC AGCANGAGGG GCTGCCAAAG CCCCTCACCC 180
 TGAGATGGGA GCCATCTTCC CAATCCNCCN CCCCCATCGT GGGCATTGTT GCTGGCCTGG 240
 NTGTCCTAGC AGTTGTGGTC ATCGGAGCTG TGGTCGCTGC TGTAATGTGT AGGAGGAAGA 300
 GCTCAGGTGG AAAAGGAGGG AGCTACTCTN AGGCTGCGTG CAGCGACAGT NCCCAGGGCT 360
 CTTAATGTGT CTTNACAGN TTGAAANGCC TGAGACAGCT TGTTTTGTN 409

SEQ ID NO:922

LENGTH:407

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01049

SEQUENCE DESCRIPTION:

GATCCAGGCT GTCATGTGAT TTATGGTGGC ATGTGTTGTG TATTTGTTGG CTACTTGTGT 60
 CTTGAAATCT AGAATTATTT CACGCAGAAT TGTCAGTGTG TGTCAGGAAG AGAAAATGGG 120
 CTAGTGGAAG CCCAGTCTTG AGTTCTTGTC TTGTTACCAT TAAAATTGA CATTTAATTT 180
 TCAAATCACT GTTGGTGCCT AATCACTNAA GTTATTAATT TATCTGTTG TATTCTTTTT 240
 TTTNAAATNG TAACATATTT ATCCGGTGGG TGGGACAGGA GTGTGTTCAA GTGGGTCATG 300
 TTTTNTCTGT GGTGACACAT GGTACAGGCT TGGAGCTTGC AGGTCCCTTT CTAAGTGTGGT 360
 TTTGGAGCAG GNCAATTTAA GTCCACTANG AAATNCACCN CTTTAAA 407

SEQ ID NO:923

LENGTH:411

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01051

SEQUENCE DESCRIPTION:

GATCCAGGTT CCTCCAGAAA TAAGATATAC AGATTACTTT GTNATTGTAA GTGGAAGTTC 60
TACCCGACAC TTACATGCCA TGGCCTTCTA CGTTGTGAAA ATGTACAAAC ACCTGAAATG 120
TAAACGTGAC CCTCATGTTA AGATAGAAGG GAAGGACACT GATGACTGGC TGTGCGTGGA 180
TTTTGGCAGC ATGGTGATTC ATTTGATGCT TCCAGAAAACC ANAGAAATCT ATGAATTAGA 240
GAAATTATGG ACCCTACGTT CTTATGATGA CCAGTTAGCT CAGATAGCAC CTGAGACAGT 300
ACCTGAAGAC TTTCATTCTT GGAATAGAAG GTGATACTTN ATCTGTNACT NCANTGGGNG 360
TAAAAATGTG GATTAAATTN TTTTANTGCA NTGNNGTTAG TCATTTTCAA A 411

SEQ ID NO:924

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01052

SEQUENCE DESCRIPTION:

GATCAGAGCN TATNTTATGA TTGTTGATAA CTAACCAAAG TAGNTGCCTG CAGAGACTTT 60
AAAATGTAAA ATAAAGATGT ATGCTGCCTG TCAGCTATTG TCATTTAAA 109

SEQ ID NO:925

LENGTH:405

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01053

SEQUENCE DESCRIPTION:

GATCCGAGGC TGGGAAGAAG GGGTTGCCCA GATGAGTGTG GGTGAGAGAG CCAAAGTAC 60
TATATCTCCA GATTATGCCT ATGGTGCCAC TGGGCACCCA GGCATCATCC CACCACATGC 120
CACTCTCGTN TTCGATGTGG AGCTTCTAAA ACTGGAATGA CAGGAATGGC CTCCTCCCTT 180
AGCTCCCTGT TCTTGGGTAA GGAAATGGAA TACTGAAGGG CCCTTCACTG CTTTGTCTCC 240
TCCCATGTTA TGCCAGCGT TTGATGGGTA GCAGAGAGGA CANANATCAC CACATGGCTA 300
TTTTTCCNC TGAATNCTGT CTNGNATTGN GTACCTNTCA AGTGTATTA GTGNATGCTT 360
TNGAAATGAA AAATTTGGGC NACCTTATGG GNAGGGNGTN GGAAA 405

SEQ ID NO:926

LENGTH:405

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01054

SEQUENCE DESCRIPTION:

GATCTTAAGC AGTAATCTGT CAGTGTTTGT ATTTGTATTC TCTGCAATT TACTGTGAAA 60

AAAAATTTGT TTTCAACAAT TGGTGTCAAT TTCTTGATGT CACTATTTGT NGGAGAGTTA 120
 AATGGTCTCT NCCCTTTGTG TATCTTACCT AGTGTTTACT CCTGGGCACC CTTAATCTTC 180
 AGAGGTGCTA AATTGTCTGC CATTACACCA GAAGGATGCC TCTGATAGGA GGACAACCAT 240
 GCAAATTTGT AAATAGTCCT GANGTCTTG GATTACTTTA CACCTCAGTA TTGATTTGTC 300
 CCAGAATTN CTGGCCTTNC ATGGCANTGA AANTNTNGG GGGAAAGATT TAANGTATTT 360
 NANTTTTAAN GAGTGTGTTA TAANNATANT TGTACTGNNT NCTNN 405

SEQ ID NO:927

LENGTH:404

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01055

SEQUENCE DESCRIPTION:

GATCTATGTT ACATTTACCA CACTGAAGTT TTTTTGTTG TTTTTGTTT GTTTTAAAG 60
 AATCACCTC ATTGTTGAAA GTAAATGTAC TCTTAGGGTG CGAATATTAG TGTCCAATA 120
 AGCATGTGAT TATATTAAGG TGGTGGTAGC GGAAGATAA TTCTGATTCC ATTGGGAATC 180
 TTAGGTTTTT GTAAATTTAT TGGGAAAATA GTTTTCTCTG TACTGCTGAA GTTCTTTTT 240
 GGTAAACAGT ATCTTTCTAA AAGAAAAAAG CATGAAGGGA GAAATTGAGG TGTGTATACA 300
 TTTCTCTCAA TGACCAGCAT TGTATTCGTG AATACTGTGT ATCTTGCAGT GAACAGTGTG 360
 GAAGCTGTTT ATTTTTCAT CTGAAGTAAA ATACTTCAA GAAA 404

SEQ ID NO:928

LENGTH:399

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01057

SEQUENCE DESCRIPTION:

GATCANGTGT AAATGTGACC TTGTACAGTT TACTAAAATT ACTGATATTT TTCACTACAT 60
 TGAGACAGTT ACTGTGAGAA TAGGACACAA ACACCAGCTA TTGCCTGCAT CTGGGAAATT 120
 GCTGAATCGC ACAGCAGTCA TGTCATAATC AGAAAATTAC TGCCAAATAA TTGTAAAATT 180
 TGAAAGTAT AAAGTATATA AAGTAGATAC TAAATACAGN CACTTCANTA TTTGTTGAA 240
 GCTATTGACT GTACANTTAG ACATTTTCAN ANGGGTGTAA TTTATTTANN GTTGTCTCAT 300
 TTTGGTAAAA TTTATGTGAA CTTTAAAGC TAANTATTAA NCCTTAATAT GCTATGTAAA 360
 TTTTTCCNT NTATACCATT TNCTGGTGGT NTTTTTTN 399

SEQ ID NO:929

LENGTH:397

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01061

SEQUENCE DESCRIPTION:

GATCTGCAGA AGGTATCTGG TGATGCAGAG ACTCTTTCCC CGCATCCNTC ACATGAAAGA 60
 CCCCATCGGT GACAGCTTCC AAAACGACAA GCTGGTGGTC TGGGAGGCGG GCAAAGCCGG 120
 CCTGGAGGAG TGTCTGGTGA CTGAAGTACA GGTCTGTCAG AAACTTGAG ACTGGGGTTC 180
 AGGGCTTGTG GGGGTCTGCC TCAATCTCCC TGGCCGGGCC AGGCGCCTGC ACAGACTGGC 240

TGCTGGACCT GCGCACGAGC CCAGGAATGG ACATTCCTAA TGGGTGGTGG GCATGGGAGA 300
 TGCCTGTTTA ATTTCGTCCG AAGCTGCCAA GGAAGAAGAC CAGAAGTTTG TGTGTTTATT 360
 TCATGATAAA GTGATTTTTT TTTTTTTTNA ACCTAAA 397

SEQ ID NO:930

LENGTH:402

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01062

SEQUENCE DESCRIPTION:

GATCCCAAC AATGTCAAGA CAGCCGTCTG TGACATCCCA CCTCGTGGCC TCAAGATGGC 60
 AGTCACCTTC ATTGGCAATA GCACAGCCAT CCAGGAGCTC TTCAAGCGCA TCTCGGAGCA 120
 GTTCACTGCC ATGTTCCGCC GGAAGGCTTC CTCCTCTGGT ACACAGGCGA GGGCATGGAC 180
 GAGATGGAGT TCACCGAGGC TGAGAGCAAC ATGAACGACC TCGTCTCTGA GTATCAGCAG 240
 TACCAGGATG CCACCGCAGA AGAGGAGGAG GATTTCGGTG AGGAGGCCGA AGAGGAGGCC 300
 TAAGGCAGAG CCCCCATCAC CTCAGGCTTC TCAGTTCCTT TAGCCGCTTT ACTTCAACTG 360
 CCCCTTTNCT NGTCCNTCAA GAATTTNGTG TTTTGCTTGC CN 402

SEQ ID NO:931

LENGTH:396

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01063

SEQUENCE DESCRIPTION:

GATCTGCCGA CCTTGCTATA GATGCCATGT TACCAATGAT TTCCTGTGGT GGGGGCTTGC 60
 CATTNNTTAC TCTCTTATTT ACCAACTTCT GGCCTAGGCA TGACAGTGGG CACCTTCCCC 120
 CAGCCCTGGN TGGGCCCAGC GCCTNNTTTC TGTGTTAGAA AGGTTTATA TATATATAAA 180
 ATTACATATA TATGTAGAAA TATATGTAAT NTTGGGGGCC CTGTTCTTGG CACATTTTAC 240
 AGTTACCTCA TTTTNNCCCA TGTATGTATT TGAGAAAATG CTAATATATA GNGAAAAAAA 300
 TGGGTTCTTA AAGCTNAAAT GTGNGGTTTT TNCCATTCCA GGGGNTCACA TTNGGTTTGN 360
 GGCATNGACN ATACCTNGTA TGTCGNNTA TAAANN 396

SEQ ID NO:932

LENGTH:394

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01064

SEQUENCE DESCRIPTION:

GATCCGTGGA TTTTGGTGC AATCCCTT TTATTTCTTG TCTGAAGAAA GCCTACTGCC 60
 TTCTGTTGGG ACCAAAGAGG CCATAGTGCC CATGGAGGTT TGGACTTAAG AGATATTCAT 120
 TGGCAGCTCA AAGACTTCCA CCCTGGAGAC CACACTGCAC ACAGTGACTT CCTGGGGATG 180
 TCATAGCCAA AGCCAGGCCT GACGCATTCT CGTATCCAAC CCAAGGACCT TTTGGAATGA 240
 CTGGGGAGGN CTGCAGTCAC ATTGATGTAA GGNCTGTAAA CATCAGCAAG NCTTTATAAT 300
 TCCTTNTGCC TAANTGTAA AANGGGGNC TGCATTCTTG TTGGAAGNAT GNACTNTNTT 360
 TNNGGAAAAC CACATTTTAA AAANTCCCG TAAA 394

SEQ ID NO:933

LENGTH:393

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01065

SEQUENCE DESCRIPTION:

```
GATCCACAGG CTTTGTACT CAACGCTGAC AACACCCTA AGAGGTAGGT ATCATTATAT 60
CAACCATTTT ATGAATAAGA AAACAACAGC ACAGAGAGAT GCAGTCACTT GCCCAAGGTC 120
ACACAGGGCC AGGGGTTGGG CCAGGATTCG AAGCAGGCAG GCTGTCTCCT GGGTCTGAAC 180
TCTCAACTAC TACACCCTAA TCAAACAATC CCTCTGGTCA AATGTGAGTG ATAATAATAG 240
TACCCACCTC GTGGGTGTTG AGGGTGAGCC CAAGTTAGCA TTCAGCGTGG GCATGTGAAC 300
AATTATAGTC AATATTGANT GGAGACCTAT GATGCTTTTA TGAAGGTTTC TATTTTGGGT 360
TAAAAAATGC ATAAAATTTC TCCTGACCAG AAA 393
```

SEQ ID NO:934

LENGTH:393

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01066

SEQUENCE DESCRIPTION:

```
GATCACCTTA AGTGAAATNA TTNCCCTTTA ATCTTTNATG TATTTATTCA CTTTGGGAAG 60
CTAGGAATGA GCAACACAAA TTTTACTCTG AAGTCAGAAG AGCTCATATA TAATANTTCT 120
AATGTCCAC CTAATTTTAC TTGTCCATTC CATGTACCAG CTTAGTTATG ATANNNGTC 180
ACATAATTAT CTTTGATAAA GGTAGAGGCA CAAAGAGGCA AACTAAGCAA GTCAAATTCT 240
AATGTGTGTA CTTCATAATA ATTTTATC CATTTCATC TTTATATTCT GTAACATGAA 300
NCTTACCTAA TCTTCAAATG TTAGCTTCCA TTTTACCT TTGAAATACT TAAATCTTC 360
TGGANTAAAT ATAATGGGGC CTNTAAANT AAA 393
```

SEQ ID NO:935

LENGTH:392

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01067

SEQUENCE DESCRIPTION:

```
GATCCTGTTT TTTAGCAGG TGAAAAATAA AACGCANTCA AATTCATGG TTTAATTTT 60
NAACTCAGAA GCACTCAAAA ATGCAAAATG TGATAATGGG CACTTGTTTA AAAGANTTAG 120
TGTATCCAGC CTTCACTCCA GCTGGTAAA AATGTTGCAC TTATCAGCAA CCNACCACT 180
TTCATCTGCT GAAAGGNCAA ATGTGCTTGG TTTTACTATT ATGTAATCAC AACTTCTTT 240
TNTGCTTGTA GTTGCTTAAA ATTATGTATT TGGTCTNGGG CTGCAATTTG GTTNATGCT 300
NTATNTGATT ATTACNGCAG TAGGTTGCCT NTCCNGTATG GAAAAATAA AGTGAATNG 360
CCCAATTAA ACCNCCTCTN TCTTAAGGTA AA 392
```

SEQ ID NO:936

LENGTH:391

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01068

SEQUENCE DESCRIPTION:

```
GATCAGGCAG CCTCTGATG CCAGANCACC TCAGGCAGAG CCTACTCAGC TGTACCTGTN 60
TGCCTGGACT GTCCCCTGTC CCCGCATCTC CCCTGGGACC AGCTGGAGGG CCACATGCAC 120
ACACAGCCTA GCTGCCCCCA GGGAGCTCTG CTGCCCTTGC TGGCCCTGCC CTTCCCACAG 180
GTGAGAAGGG TCCTGTCCAC CAGCACACTC AGTTCTNTTC CCTGCAGTGT TTCATTTNAT 240
TTTAGCAAAN ATTTTGCTG TTNNTGTTNA AACATGATAG TTGATATGAG CTGAACCCCT 300
GGGTNNGNG GGAATTGGTC AGAGTGGCAA CCTGGGACTG TGAGCCCTGT TCGGNACAGN 360
NTATGGATAT GAAAANTCTG NCCNNNGCNA N 391
```

SEQ ID NO:937

LENGTH:390

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01069

SEQUENCE DESCRIPTION:

```
GATCTTTCCC AAGATTGTAA CTGAAAAC TGCTCTCTTG TTTNTTCGT TTTGGGGGTG 60
GTGGTGTGG CTGGGCCATG CTTGTAAAGT GATGTGTGTC TCTGATTAA CGGATTCACT 120
GTTTTCTCTG CTAATTGAGA GAGCGTTATT TACATTATTT ATTTGTTTTG ACACAAGTNC 180
TTTCAGTGT TTATCTAGC TAATGGCTTC TTAAAGGTAA TAAACCCCT CCAACGTAAT 240
TGGTCAGATA AAACTTTTT CCTTGATGC TTAAATAAAG CAATTAGTGA AGCACTTCTA 300
TCCAAAATGA CTTTTTGTG CTTTTTAAA ACCAATTTAC TGTTACTGGA AACTTTGTAC 360
AATAAGCAA ATCACGCAGA TTAANGGAAA 390
```

SEQ ID NO:938

LENGTH:389

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01070

SEQUENCE DESCRIPTION:

```
GATCAGAGGG AAAGAATGAC CAACCNNGCA ATAAGTGAC TAAACTCTAC GCTCTGGTTA 60
ATGTAATGTA CTCTCCTGGA CTGAATGCAG TGTATAATN CTGTCTACAG CTAGAAGCTG 120
TGCCCCAGTT CCACATTGTA TTACACATGT NAGATTTGCT GCTGTTGCAG TATAAACT 180
AGGTATAATA GGATTTGAAA TTGCATTACA GTTCATAAAA NTNGAAAATG AGGAATTAAA 240
CCNGCAAGTG AACATTGAA CGNTTATNCT NTCTACATAA GACATGGTTG GGACATCAGT 300
ACTNACAAGA TGGTTTANGT ATGGTACTAG NGNANTTAAG NTTCTTTCT CTCTGGTTA 360
TNGATNGGGT TATTCCATT ATGTATTNN 389
```

SEQ ID NO:939

LENGTH:390

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01071

SEQUENCE DESCRIPTION:

GATCTCACGC TGCCTCTGTG GTTCCCTCCC TCATTTTTC TGGACGTGAT AGCTCTGCCT 60
 ATTNACAGGAC AATAATGGCT ATTCTAAACG CTAAGGAAAA AAAACAAACA CAGAACTGTT 120
 TCAAGTACTC AAGACTGACT TACAGACCAA CCAACCACCT TGCTGGAACC CTTGCTAGCA 180
 GGCATTCTTA TAAAAGAAAC TTTCGAGCCT CCTTATATTG CTGGAACTC AGCTGTGCTC 240
 CAGACTAGAG CCTCCTTACC TATGCTATGG ATTTTAAATT TATTTCTCT TATTTTCATGT 300
 ACACTGCTTT TTTTGTTTAC AGTGTATGAT GGATGTGTAT GAAAAAATG TATCTTTGGG 360
 GAACCAATTA CAGTTTGTGTT AATTGAAAA 390

SEQ ID NO:940

LENGTH:543

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01072

SEQUENCE DESCRIPTION:

GATCCACACA CGTTGGTCTT TTAACCGTGC TGAGCAGAAA ACAAACAGG TTAAGAAGAG 60
 CCGGGTGGCA GCTGACAGAG GAAGCCGCTC AAATACCTTC ACAATAAATA GTGGCAATAT 120
 ATATATAGTT TAAGAAGGCT CTCCATTGG CATCGTTTAA TTTATATGTN ATGTTCTAAG 180
 CACAGCTCTC TTCTCCTATT TTCATCCTGC AAGCAACTCA AAATATTTAA AATAAAGTTT 240
 ACATTGTAGT TATTTTCAAA TCTTTGCTTG ATAAGTATTA AGAAATATTG GACTTGCTGC 300
 CGTAATTTAA AGCTCTGTTG ATTTTGTTTC TGTTTGGATT TTTGGGGGAG GGGAGCACTG 360
 TNGTTTATGC TGGAAATATGA AGTCTGAGNC CTTCCGGTGC TGGGGACCAC ACANGNGTTN 420
 GTTGNAAGT TTGACCAAGN AGNCCTGCGC ATNNNCTCTG GATGCCTNTG GTATCCATTC 480
 TTNGANGCAA TCCGCTCGGG NCCCGTGGGC CCAATAAANC NGGTATTTNT CCCAANGGGG 540
 AAA 543

SEQ ID NO:941

LENGTH:132

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01073

SEQUENCE DESCRIPTION:

GATCTCAAGA TTTCTAAATT GTCAAGATTT ACATGGCATT GTGGTGGAAC TAGTTAACAC 60
 TTAGAGCTTT TGGTATGTAA TAACTATTTG CTATGGACTG ATTAAATGTT TCAAAAGATT 120
 GTGTTCTTCA AA 132

SEQ ID NO:942

LENGTH:387

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01074

SEQUENCE DESCRIPTION:

GATCAGCACT AAGTCCTGCA TTCCTGTAA AGCCACTTGG GTCATAAGAA GGGAGTAAAA 60
 AATGAAGTCT GACTAGNAAC CTATTGCAGA GGCCAAGTAC ATTTAGTATG GCATTGAGTT 120
 GTGATATAGT TTTACTTTGA TGTGCATTTT GAATTCAGC TACACCTAGA TAGACGTAAA 180

ATGATAATTA AAATGCTGTA ACCAACTTAT CTAATAAAAT TGGCAACCAG CCACTATTTT 240
 GTTGACTATG AGAAAGTTAA AAGTTTATGT TAATTTTNG GGTCTGATAG AATATTTTCAT 300
 GTGTATTACA GTGGTATTCA TATGCTATGT CTCTAAACTT TATTTTCAA AGCTTANGGC 360
 CCAATACAA NCTTCTCTGG GNNTAAA 387

SEQ ID NO:943

LENGTH:386

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01075

SEQUENCE DESCRIPTION:

GATCAGANAA AAAGTCCATA TGGACTGTGG ATACCTATCT AAAAGAAGAA AACTGATGGC 60
 TAAGTTTGCA TGAAACTGC ACTTTATTGC AAGTNAGTGT TTCTAGCATT ATCCCATCCC 120
 TTTGAGCCAT TCAGGGGTAC TTGTGCATTT AAAAACCAAC AAAAAAGAT GTAAATACTT 180
 AACACTCAA TATTAACATT TTAGGTTTCT CTTGCAGATA TGAGAGATAG CACAGATGGA 240
 CCAAAGGTTA TGCACAGGTG GGAGTCTTTT GTATATAGTT GTAAATATTG TCTTGTTTAT 300
 GTAAANTGG AATTTTTTAG ACACAGTAAT TGAAGTGTAT TCCTGTTTGT TATATTTAAT 360
 AAATTTCTTG GTTTTCATTC TTAAA 386

SEQ ID NO:944

LENGTH:383

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01076

SEQUENCE DESCRIPTION:

GATCTTCTAG CTACCATNCA TTTTCTTCAC TGTTCCACAA AGATGAGTGT GAAATTCAGT 60
 GAATGCTGTT ACTAATCCTG TTACGAGATG AATCTCATTT CACCAAAATT AAATTATGTT 120
 TTTCCGCTAA AATGATGATA CAAGTTGAAG ACACATCACT CTGAAATTGG AAGACCTCAC 180
 CACTTAAGGC TCCACAGTGG CTTACTCAGC TGAAGTCTAG GTTACTACTC TTTACTTTGT 240
 TCACCCATTG GGGGGTGCAG TTTTTTAAA ATGTTGGGAG ATGGCCATTG TAACTACTGT 300
 TGAATGTCTC TGTTTTGGGA AGGTATAACA NGAANTAAAA ANGNTATAT ATGANGGGAG 360
 AGNCTGGTTA TCTCCTCCCC AAA 383

SEQ ID NO:945

LENGTH:382

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01077

SEQUENCE DESCRIPTION:

GATCTCTCCA TGTACCCTGC AGGGGGCTTG GTACTGTGAA ATNAGTAACT TAATCCTGAC 60
 AACCAGTAGT CAAGGTATGG CCCATCTCCT GTACGCTTGG AGCGACCTTT GGCTACGTGG 120
 CTGGCCTTGT TATTTACCA CTCTGGATAT ACTGGAATAG AAAGCAACTT ACATACAAGA 180
 ACAATTAAGT GGAGCAAAGG GAGATATTTT TTTGTGCAGA TTCTGTAAGG GCTGGGCAGA 240
 AATGTGTATG GTCAAAGCCA AGCAGTTCCA TTTACAGCTC TGTTTTTTAC GTAGTTACAA 300
 CATGATGTGA TTGTAGCTTT TTAACTATG AAACCCTGA GAGATTGTAC CTTCTAGTT 360

GAAATAAAGT ATTTATAATA AA

382

SEQ ID NO:946

LENGTH:381

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01078

SEQUENCE DESCRIPTION:

GATCCGAACA CCTCCAGATT CCGGCTTCTA CATGGNNCAG ACGGGGACGC ACAGGCCACC 60
 TTCTTCTGG CAGGGACTCT TATTTATTCC CATTGCTCTA GGGCTTTCNN TTTCCNTTC 120
 TTCCGGTAGG CCGCGTAGAG GCATGCACCG GGTAGGTTTC CGCGGTGACC CCGCGGCGGC 180
 CTGAGGGACG CTCCTGCCC CATCCCGGCT GTTGGGCTGG GCCGCTTGC CTCTGCTTCG 240
 NCCTGTGCTG TGTCTCCAG CTTTGTAGCA GCAGCTTGAC AAACCCAGGC GCACTGTACC 300
 AAGGCAATGT AACTTTTAT TTTGGTCAA TTAAAGTTCT TTTGTACC AAATATTAAT 360
 AAACCAAGTT TGGACTTAA A 381

SEQ ID NO:947

LENGTH:380

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01079

SEQUENCE DESCRIPTION:

GATCTGAGTC CAGAGTTGGC CACTTTGTGT GGGTCCTCAC AAGCAAAGAG AGCACTAAAC 60
 TTGACATTGG GGGTCCACCA CTCCAATTT NCTTTCTGAA GGTTTTGGTG TACATTGAGC 120
 CCCAGAAGGA AAGGAGAGTA TCTGTGAGTG GGGGCTCCC TTGACCCAG TACGAAGTCT 180
 ATGCCCTGAA TCCCCAGAGT AGCCCTTCCT GGTGCCCAAC TGGCCTGGG ACAANCAGCG 240
 TCCACTACAT CTAGGCTGCC GGCTAAGTGG CACACTTCTT GACCTCCTAC CAGGACTTTG 300
 GTAAAAGCTA GCTTTGGGGA GGGGTGGGT AAATATGAGA GGTGGAGNG CCANTGGTAG 360
 AATAACATGG GTAGCTAAA 380

SEQ ID NO:948

LENGTH:380

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01080

SEQUENCE DESCRIPTION:

GATCTGCATC AGTTGTAAAG GGGAATTGGT ATATTCACAG ACTGTAGACT TTCAGCAGCA 60
 ATCTCAGAAG CTTACAAATA GATTTCATG AAGATATTN NNNNCAGAA TAAACTGCC 120
 CTTAATTTTA ATATACCTTT CAATCGGCA CTGGCCATTT TTTCTAAGT ATTCAATTAA 180
 GTGGGAATTT TCTGGAAGAT GGTGAGCTAT GAAGTAATAG AGTTTGCTTA ATCATTGTA 240
 ATTCAAACAT GCTATATTTT TTAATAATCA TGTGAAAACA TAGACTTATT TTAAATTGT 300
 ACCAATCACA AGAAAATAAT GGCAATAATT ATCAAACCTT TTAATAAGN TGCTCATATT 360
 TTTAAAAATA AGGTTTTAAA 380

SEQ ID NO:949

LENGTH:399

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01081

SEQUENCE DESCRIPTION:

```
GATCAAAGCA TGCAATAAGC AATACAAAAT ACCAAGCCTT ATACTTAAAA GAAGTTTAAC 60
ATATTGGTTA ATATACTGGT TAATATACTG GTTAAACATA TTGAATGTAT ATAAGTGGCA 120
AAACTAGATT TTTAAGGAAG TGTACATTAT AATATTGGAG CTCAGTACTG CATGANGAGA 180
CTTCATTAAA ACTAAGAAAN CATTTATTTG GGGAGAAATT TTAGGCATTT AAGANCTTGT 240
ATTTTCTAT TTTAAAAAGT TAAATTATTC CGTAATTGG ANGGAAAGTTT CGTTGAATGT 300
AGGCCATAAC CGTTTGANGG GTTTTCCTTT GGANAACCTG GTGTNTTNG GTGCCCTTAN 360
TATTTTGGTC CTTTAAATAA AAATGCNCCT GNATTTTCN 399
```

SEQ ID NO:950

LENGTH:379

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01082

SEQUENCE DESCRIPTION:

```
GATCAGGCCC TGGGCCCCC TGCATCTTTT ATAGCAGTGG GTGTCCAGTC CAGGACACTG 60
GTGCTTTTTT ATACAAGAGA ACGAGCCAGA GTTCACTCCT TCCTCCTGGC TCTCTATATA 120
CCTGTGAATA TGTGAAATAG TGTAATATG AAAGAAGCTG TACCTATCAC TTCAACCCCT 180
GCCTTGTA TAATACTATT CCATCCACAC AGTTTCCACC CTCACCTGCC CCNTCATACG 240
GAGTTGGATG GGGGCCGAGT NAGGTAACCA GGTGGCATCT ACCNNATGTT TTATAAGGAA 300
TTTTGTACAG TCTTNGTGAA ATAAAATAAC GTGCTTCATT TGNAAAAATN NNGTNNNTT 360
TNTNTTNT NTNGGGTTN 379
```

SEQ ID NO:951

LENGTH:376

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01083

SEQUENCE DESCRIPTION:

```
GATCTAGTAG AAATAAGGG ATGGGAAAAA CCTTTTCATT TTTCATCTNC TTTCCAACAA 60
TATGAATTC TTAGTTTCA AACTATACTC AGGAAAGCTG GGCTTTAGGA TTAAACATGT 120
AGTGATGAGT TCTGTGTGTA TTTTAATATT TNACTCAGGA TTCCTATTAA TTGAAAAAAA 180
TTTTTAAC TTATTATA AATCTTTTT TCAGGGAGGN GATATCACCA AACATGATGG 240
AACAGGCGGA CAGTCCATTT ATGGAGACAA ATTTGANGAT GAAAAATTTG ATGTGAACAT 300
ACTGGTCCTG GTTACTATC CATGGCCANT CAAGGCCAGG ATTACCAATA ATTCNTCATT 360
TTTGTATAC CACTGN 376
```

SEQ ID NO:952

LENGTH:375

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01084

SEQUENCE DESCRIPTION:

GATCAAGCCA CCACGTGCCC TACGATGGCC TAACAGGAGT GCCCATTGGC AGATTACACA 60
 TGTAATATG ACCTCAGACA AAAAGGAACC AGAGGCCCAA GGGCAATAAT AAGGTGGAAT 120
 TTNCAGGTCA GCCCAGGAAT TGGCAGAGGA AGTAGGTGTC TGATAACCCCT TTGTGGAGAA 180
 TGAGATTCCC CCCACCTGTG TGAGAAAAAT AAACAGCTCT GGAGTCTTGT NCCTGACTCC 240
 AGAGGAACGA GAGCATTCCA GGAAGAGAG ATTCCCTGGA AAATTGAAAA TGTGAATCCT 300
 AGGGGGAAAT TGGGGATTGT NTCTTCCCT GTTGAAAATG TTNNGTGGG AATAAATATC 360
 TTCAGGAACC ATAAA 375

SEQ ID NO:953

LENGTH:374

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01085

SEQUENCE DESCRIPTION:

GATCTTCTNC ACACACCCCA TCACCCAGAT AATTTACAGT TCTGTTAACA GTGAGGTTGA 60
 TAAAGTATTA CTGATAAAAA ATTATCTAAG GAAAAAACA GAAAATTATT TGGTGTGGCC 120
 ATCTTACCTG CTTATGTCTC CTACACAAAG CTAAATATTC TAGCAGTGAT GTAATGAAAA 180
 ATTACATCTT ACTGTTGATA TATGTATGCN CTGGTACACA GATGTCATTT TNGTTGGTCA 240
 CAGCACTACA GTGAAATACA CAAAAATGA AATTCATATA ATGACTTAAA TGTATTATAT 300
 GTTAGANTTG ACAACATAAA CTA CTGTNGC TTNGAAATGA TGTATGCTTC AGTAAATCA 360
 TATTCAAATN TAAA 374

SEQ ID NO:954

LENGTH:376

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01086

SEQUENCE DESCRIPTION:

GATCAAAGCA AAGAGCGCCT TTCCATGTAT CTCATGAAAG CTGACCTGAT GCCTTTCCTG 60
 TATTGGAATA TNATGCTAAG GGGTACTGG GGAGGACCAG CGTTCTNCG CAAGTTGTTT 120
 CATCTAGGNA TGAGTTAAGN ATGGCTCAGC ACTTGCTCAT CTTGGATGGC TTCTGGGCCA 180
 AAAGTGCAGT CACTGAATGA CCAAGAGCAG CACGAAGGAC TTGGAACCTA TCCTTGTAAT 240
 GAGTTCCTTG ATGGGTAATG GTGACCAAAT GCCTCCCTTT TCAGTACCTT TGAACAGCAA 300
 CCATGTGGGC TACTCATGAT GGGCTTGATT CTTTGGGAAT ANTAAATTGA AATANTACTT 360
 TTNTTTCTG AATAAA 376

SEQ ID NO:955

LENGTH:371

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01087

SEQUENCE DESCRIPTION:

GATCAGAACC TCCAAATACT GCCATGAGAA ACTAGAGGGC AGGTCTTCAT AAAAGCCCTT 60

TGAACCCCT TCCTGCCCTG TGTTAGGAGA TAGGGATATT GGGCCCTCAC TGCAGCTGCC 120
 AGCACTTGGT CAGTCACTCT CAGCCATAGC ACTTTGTCA CTGTCTGTG TCAGAGCACT 180
 GAGCTCCACC CTTTCTGAG AGTTATTACA GCCAGAAAGT GTGGGCTGAA GATGGTTGGT 240
 TTCATGTTTT TGTATTATGT ATCTTTTGT ATGGTAAAGA CTATATTNG TACTTAACCA 300
 GATATATTTT TACCCAGAT GGGGATATC TTTGTAAAA ATGAAATNA NAGGTTTTTT 360
 NAANTGGNAA A 371

SEQ ID NO:956

LENGTH:368

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01088

SEQUENCE DESCRIPTION:

GATCTGGGGA GGGCTAGCCC AAAACCTCCC GCATCGGGCA GGCACCCCT GAAGTACTTC 60
 CTTCAAGGTT TCCCTTTGT NAGGGTGTG AGTAGCCTCA CCGGCCTGTN TGGAGGAGCA 120
 GCTGGCTCTG CTCTGAGAAA CTCTGGCAAG TGGACGCCAT TCTNTGCCC TTAGGATTCA 180
 CTGCTCTCTC CTACAGCCGC CAGNCCTGGG GTCCTGAAAG ACCTTGGGTG GTAAAGCTGT 240
 ACTTGGTGGG AGTNAGGGCG TGGGGAGGAA CCATGCAAAT CGCCTTCCAT GGGTTTTAA 300
 NTGCAGTAAA TAACATTCT GGATGAGACT NGTTCCAAA NTAAACCNG CTATTATCTG 360
 TTTTGGAA 368

SEQ ID NO:957

LENGTH:369

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01089

SEQUENCE DESCRIPTION:

GATCCGAGCT CTGGAGCGTG GATACCGGAT GTCTCGCCA GAGAACTGCC CAGAGGAGCT 60
 CTACAACATC ATGATGCGCT GCTGGAAAA CCGTCCGGAG GAGCGGCCGA CCTTCGAATA 120
 CATCCAGAGT GTGCTGGATG ACTTCTACAC GGCCACAGAG AGCCAGTACC AACAGCAGCC 180
 ATGATAGGGA GGACCAGGGC AGGGCCAGGG GGTGCCAGG TGGTGGCTGC AAGGTGGCTC 240
 CAGCACCATN CGCCAGGGCC CACAACNCGN TTTNCTACTT TCCNAGACAA CNACCNTCGG 300
 TTTCAGGCCA CAGTTTTCTT CATCTGTCCA GTTGGGGTAG GTTGGGACT TGGNAAAATN 360
 TTTTTTTN 369

SEQ ID NO:958

LENGTH:366

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01090

SEQUENCE DESCRIPTION:

GATCGAGCCA CTGCACTCCT GGGGCAACAG AGCAAGACTT CGTCTCAAAA TAAATAAATA 60
 AATAAAGTGG CTCTGGGGA AAAGCAATTT AATGTACCAC GATGAATAGC TAACTGTTCC 120
 CAAGTGTTTG CTATGTGCAA CACACCGCGT GAGAGTGTTA CCTGCATTAT TACATTAGGC 180
 TGAGAGGTAA AATAATTGCG CCGAAGACAT ACAGCTAGTG ACGAATGGAC TGATGGTTTG 240

AACTTAACGT CTATTTGACT TAAGGTCCTG CACCCTGCCA CTTGTAATTT TCAGANTCAC 300
 TGATAATCTG AAATAATGCA GCTTAAACCA TGTTTTCTTA ATTAAGTA TAATTGGATG 360
 GTGAAA 366

SEQ ID NO:959

LENGTH:364

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01091

SEQUENCE DESCRIPTION:

GATCCTGAAG GTGAAATGAA ACCAGGAAGA AAAGGTATTT CTTTAAATCC AGAACAATGG 60
 AGCCAGCTGA AGGAACAGAT TTCTGACATT GATGATGCAG TAAGAAAACGT GTAAAATTCG 120
 AGCCATATAA ATAAACCTG TACTGNTCTA GTTGTTTTAA TCTGTCTTTT TACATTGGCT 180
 TTTGTTTTCT AAATGTTCTC CAAGCTATTG TATGTTTGA TTGCAGAAGA ATTTGTAAGA 240
 TGAATACTN CCTTAATGT GCATTATTAA AAATATTGAG TGAAGCTAAT TGTCAACTTT 300
 ATTAAGGATT ACTTTGCTG CCCACCACCT AGTGTAAGT AAANTCAAGT AATACANTCT 360
 TAAA 364

SEQ ID NO:960

LENGTH:364

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01092

SEQUENCE DESCRIPTION:

GATCTGGGGC CGNCCCTACG GGGCAGGGCT CAGTCCTGAC GCTTGCCACC TGCTCCTACC 60
 CGGCAGGAT GGTGAGGGC GGAGTCTATT TTACGCGTCG CCCAATGACA GGACCTGGAA 120
 TGTACTGGCT GGGGTAGGCC TCANTNAGTC GGCCGGTCAG GGCCCGCAGC CTCGCCCCAT 180
 CCACTCCGGT GCCTCCATTT AGCTGGCCAA TCAGCCCAGG AGGGGCAGGT TNCCCGGGGC 240
 CGGCGCTAGG NTTTGCACTA ATGTTCCNT CCCNGCGGGT GGGNGCGGGG AAATTCATAT 300
 CCCCTGTTTC GTNTNATGTT GTGTCNNCG NNCCCAAATT TAAAAAGGNA ATTTNAAAAN 360
 GGTN 364

SEQ ID NO:961

LENGTH:362

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01093

SEQUENCE DESCRIPTION:

GATCGAGGGG CGGGGTCAG CTATGCAGCC CATCACGTGT GTTTTTCATC TGGGATGAAA 60
 AAGCCTGGTT CTCTTTTGAA ATGCTTGATT GTACTTATTG AGCTAAACAA GNCTTGGTGA 120
 CTNTTGTTGA TTTGCCTCAA AAGTTTTAAG TCCTGGGTTT TCAGACTACT GTGTAGCAGC 180
 TGTGTGTTA ACATACTGTA GCTTTTCTC CTTGGGGG ACATACAAAT AGGATGTGTT 240
 GATGTGGACT CTAACTGTA ATTTTCCTGT AACTATTTG GAATGATGCA TATTTCTAAT 300
 GTTTGTATA CTGTACAGA GTATTGCTG TTGGTTGCTT TTTTTTTT TTCANNGGA 360
 AA 362

SEQ ID NO:962

LENGTH:360

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01094

SEQUENCE DESCRIPTION:

GATCCAGGCC AAGGCACTGG CTGTNAGTGG CAGAGTTTGG CTGTAACCTT TGCCCCTAAC 60
ACGAGGAACT CGTTTNAAGG GGGCAGCGTA GATTGTNTNA TTTGCCACCT GGATGAAGGC 120
AGACATCAAC ATGGGTCAGC ACGTTNAGTT ACGGGAGTGG GAAATTACAT GAGGCCTGGN 180
CCTCTNCTTT CCCAAGCTGT GCGTTCTGGA CCAGCTACTG ANTTATTAAT CTCACTTAGC 240
GAAAGTNACG GATGAGCAGT AAGTAAGTAA GTNTGGGGNT TTAAACTTGA GGGGTTCCCT 300
CCTGACTAGC CTNTNTTACA GGANTTGTGG NAATATTAAN TGCAAATTTA CAACTGCAAA 360

SEQ ID NO:963

LENGTH:358

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01095

SEQUENCE DESCRIPTION:

GATCCAATTT GTAGCTTCCT GCCTGGCTTC AGAGAGCCCA GCAACCTTCT AGGCCTGCTT 60
TCCAGACTTC TGAGATAGCC TGGGATGAGC AATCCTGTTA TAGTACATCT GGACCTTCCC 120
TACCTGGGCT CTGGGGAGGC TGTGGGCCTG GAGAGGGAAA AGGAGGGAGG GGGTGTCTGC 180
ACCACCTGGG AAGATAGCAC AAGGCCTAAT GAGGTCACCC TGA CTCCCA CCCCAGCATT 240
TCATTCATAC CAGATAATAG CTGCATTACT GCCANCTGAC CTTATAACCC TCTGCACCTT 300
CAAAAAGGTT CATGGTTTTT AATTGCTGCT TTTTAATAAC ATTTTGTNA AGNTTAAA 358

SEQ ID NO:964

LENGTH:195

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01096

SEQUENCE DESCRIPTION:

GATCGGCCCT ACTAAGATGC AGAGACCCCG NCAGAGCTNG CATTGACTAC CAGATTATT 60
TTTNAACCA GAAATNTTT TAAATTTATA ATTCCATATT TATAATGTTG GCCACAACAT 120
TATGATTATT CCTGTCTGT ACTTTAGTAT TTTNACCAT TTGTGAAGAA ACATTAAAAC 180
AAGTTAAATG GTAAA 195

SEQ ID NO:965

LENGTH:356

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01097

SEQUENCE DESCRIPTION:

GATCCAAGAC TGGCTGACTT CATTGAAAT GGTGAATCT GCTGTGTAAT AAAGTGGTTC 60

AACCATGATT AGGAACTGAA ATTTAGTAGA AGAGGGGAAA GGAGTTAATG TAACAAATTA 120
 TTTTAGCTAC AAACCCCGGT AATAGAGCAC TTGGGGGATG GGATGGGGTG GGTGTTGAG 180
 ACAATCAGAA TGGTAAATTG ATTAAATGCT CCTAACCTG TAATTTGTG CATAGAGCAC 240
 CCTATGCTGT GGAAATAACT GTTCTTAGAT TTCATTGTAA CTGGACTGTT CAGGTTGCCC 300
 AGAGGGAAAG ACCATTCCCTA ATTCTAATAA AATAACCTTT TATTTTGTTA TTCAA 356

SEQ ID NO:966

LENGTH:356

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01098

SEQUENCE DESCRIPTION:

GATCTCCACC ACCATCTCCC CTCTACTTCT CATTCCCTAA CTCTCTGCTG AATATGGGGT 60
 TGGTGTCTC ATCTAATCAA TACCTACAAG TCATCATAAT TCAGCTCTTG AGAGCATNCT 120
 GCTCTNCTTT AGATGGCTGT AAATCTATTG GCCATCTGGG CTTCACAGCT TGAGTTAACC 180
 TTGCTTTTCC GGAACAAAA TGATGTCATG TCAGCTCCGN CCCTTGAACA TGACCGTGGC 240
 CCCAAATTG CTATTCCTGT GCATTTTGTG TGTTCCTCA CTTATCCTGT TCTCTGAAGA 300
 TGTTCCTGA CAGGTTTGT GNTTCTTAA AATAAAATGC AGNGACATGT TTAAA 356

SEQ ID NO:967

LENGTH:356

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01099

SEQUENCE DESCRIPTION:

GATCTTCCAC AAAACATCTA GCCATCTAAA ATGGAGAGAT GAATCATTCT ACCTATACAA 60
 ACAAGCTAGC TATTAGAGGG TGGTTGGGGT ATGCTACTCA TAAGATTCA GGGTGTCTTC 120
 CAACCTGAAAT CTCAATGTTT TCAGTACGAA AAACCTGAAA TCACATGCCT ATGTAAGGAA 180
 AGTGTATTTC ACCCAGTAAA CCAAAAAAAG CAAATGGATA ATGCTGGCCA TTTGCTTNN 240
 CTGACATTTT CTTGGGAATC TGCAAGAACC TCCCTTTTCC CTTCCCCCAN TAGGNCCATT 300
 TAAGTGTGTG TTAACANCT ACAGNATACT ANNTAANAAG TTTGGCCAAN NCCAAA 356

SEQ ID NO:968

LENGTH:356

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01100

SEQUENCE DESCRIPTION:

GATCAGATTT TTGGGTCATG TCTGTTGTAT TTTCAGTAAT GTGATTTTCTG ATGGTCATCT 60
 GGATTCTCCC ACTTCTCTAC TCCATTATTT CTCTACTTTT CCTTCCAGCA NACCTGANN 120
 GTGAGGGAGA TGGATTAATG TGAGTAACAG GAATGTGTCT TAAAAAGCT AGAGTGGTTA 180
 CATTTAATCA GGCAGTAAGA TAATTTGGGT TCTTGAGTTG TTTGGNGTA ATATCCACA 240
 ACTGGGGTAG GAAGTCAGG ACTTTTTNT TAAAGCTAG TCATTTCAA AGCATATTGT 300
 ATTTTTTGA NTGACTACAG TATGCCCAAN TTCAANANCC AAANCCNCT TTGGGN 356

SEQ ID NO:969

LENGTH:356

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01101

SEQUENCE DESCRIPTION:

GATCCAACAA TTTTNAAGAG CTCTCTCTTA ATCTCTGACA TAATGAGTCT GAAACAAAGA 60
AAAGTTACCT TACCGTGTCT TTAATTCCTT TCTTCTGGGC TGTGAACTCA AGTGCCTTGA 120
GGGCCAGCTA AGAGCTTTTT GGGATATTTG TCTAACTTAA TTGAACTGTT ACTGAAAGAT 180
AAATTAACAA AATGGTTCAG AGTTTTGGAT TAAGACCTTT GTAACCTAAT GACCGTCAGC 240
ACAGGAGCTT CGGTTTCCTT CTCTGTAAAA CAGGGCTCCT CATTCCAATT CCACCTATCC 300
TGTAGCCTTG TGGGAATAAA AGGAGGCACC ACGTGGAGGT GCTTGGCAGG NTGAAA 356

SEQ ID NO:970

LENGTH:355

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01102

SEQUENCE DESCRIPTION:

GATCATANAA NGGCCATCTG GGCCCACTN GTGTACAGCG AGGGNGGGCA GCCCCCTCCA 60
CTCCACTCTG CTCCACAAA GTCGGCTCCC GAGAGCTCGA GGCTGCTTCT TTTTATATGT 120
GCAGGGCCCG GCGGGGTGAA GGGTCAGAGA GACGGACACA AGGAGCCGGC AGGAGNGCGG 180
ANCGAGGATG TCCTTTCCCG GGAGACAAGT CGGGAAAGCC TGGCTGGACT GCCTCAGCCC 240
CGNGTGANTC CTGGNCTNAA GGNTTCCCCG TCCTGAGCTC GGGAGATNTT CAGAGTCACA 300
CTGNCNCCT GTCTTGCCAC GGAGAGGTCA ACTTGCCACC GGNAGTNCNT GGTAN 355

SEQ ID NO:971

LENGTH:355

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01103

SEQUENCE DESCRIPTION:

GATCCAAACA ATATCTTCAA GGCATTCTTT GCGGCTCCTG GCGGCTTCAN CTTTGANGCA 60
TCTGGTCCAG GGAATTNNTT TTNCAATTT GGCTAATGAA GGGCAACCAC CCAGAACCCA 120
GAAAATNCAG ATTCACTCAG TTTAATCTTG AATGTGGAAA CAGTTCACCT CCTCCCTTCA 180
TCACGTCTCC GTGTGCTTAG AGCAGTTTCG TTTTCTCAGT TGGATGCCCT GTGTCTCTGT 240
GAGTGGGGTG GAGCAAAGGG AACCAATGCC GAAGACCGAG GGCAGGGGAG GGGAGGCGGG 300
GGTNGGACAG NGAGGCAGCT TGTGAATTTT TGTTTTACTG TTAACTTTA TTAAA 355

SEQ ID NO:972

LENGTH:352

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01104

SEQUENCE DESCRIPTION:

GATCNTAGGC TGGGGCCAAC TGGAAACCATT GGCAGCTGCA CGCTCATTAC TACCCTCCGC 60
 TCCTGCGCTC TGCCACTGTC CGGAAATTCA TGGTTGGCTA CGAAATGCTT GCTCAGGCTC 120
 AGAGGGACCT CACCCCTGAG CAGGCTGCAG AGAGACTAAG GGCATTCTT GAGGTTTATT 180
 ACCACCTGGG GCAGAAGGAC AGGGAGACAG CAACCATCGC CTGACCACGC CGACCACAGG 240
 GCCTTGAATC CTTTTTGT TTCAACAGTC TTGCTGAATT AAGCAGAAAG GGCCTTGAAT 300
 CCTGGCCTGG AATTTGGGCA GATATAGCAT TAATAAACT GTGCATCTCA AA 352

SEQ ID NO:973

LENGTH:358

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01105

SEQUENCE DESCRIPTION:

GATCAAGGGG GTTGGGAGGG GGGAAAGAGA CCAGCCTTGG TCCCTAAGCC TCCACNNAAC 60
 GTCTTCTTAA TCCNCACCTT TTCTTACTCC CAAAAAAGAA TGAACACCCC TGACTCTGGA 120
 GTGGTGATA CTGCCACATC AGTGTGTTGAG TCAGTCCCA GAGGAGAGGG GAACCCTCCT 180
 CCATCTTTTT TGCAACATCT CATTTCTNCC TTTTGCTGTT GCTTCCNCN TCACACACTT 240
 GGTGTTGTTT TATCTACAT TTGAGATTC TAATTTTATG TTGAACCTGC TGCTTTTNTT 300
 TCATATTNGA AAAGATGACA TCGGCCCAA GNGCCAAAA NTAAATGGG ANTTGAAA 358

SEQ ID NO:974

LENGTH:354

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01106

SEQUENCE DESCRIPTION:

GATCTTAGGC AAAATACCAG NTGATGAAGG CATCTGATGC CTTTCTGT TCAGTCATCT 60
 CCAAAAACAG TAAAAATAAC CACTTTTGT TGGGCAATAT GAAATTNTTA AAGGAGTAGA 120
 ATACCAATG ATAGAAACAG ACTGCCTGAA TTGAGAATTT TGATTCTTA AAGTGTGTTT 180
 CTTTCTAAAT TGCTGTTCT TAATTTGATT AATTTAATTC ATGTATTATG ATTAAATCTG 240
 AGGCAGATGA GCTTACAAGT ATTGAAATAA TTAATAATTA ATCACAATG TGAAGGTTAT 300
 GCATGATNGT AAAAAATACA AACATTCTAA ATTAAGGCT TTTGCAACCA CAAA 354

SEQ ID NO:975

LENGTH:351

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01107

SEQUENCE DESCRIPTION:

GATCAGAGCT TGAACACAGG CTTATTTTAA AAANNANAAA TATTTTAAAC ATGGGTTTCC 60
 TTATTGAAAA ATCAGTGAT TAGTCATAAA ACACCATCAT TAAGAATAAT TGAACAATAA 120
 AGTTTGCTT CAGATGCAGT TTTCAAATTA TAATCTCATT TCAATTTATA ACGTTCTCAG 180
 TCCTTTGTTA TAATTTTCT TTTTCATGTA AGTTTAATTA TCTGCATTTA TCTTTTCC 240
 TAGTTTTTCT AATACTAATG TTATTCTTA AAATTCAGTG AGATATAGGG NTAAATAAT 300
 GCTTTGAGGA GNATGTTTAA TAGGAAATTA AAATAACTTT TTCTGGCCAA A 351

SEQ ID NO:976

LENGTH:420

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01108

SEQUENCE DESCRIPTION:

GATCCAGAAC ACTTCAAGAA CTCGTCAAAC AGCTCGATAA GCCTTTTNA CTGTNTACAT 60
CTGTACCGGG AATAACATTC CTAGGCTGAA ATTTCCACAA AGAATAGAAC CTGTACCCAG 120
TTCTTCAGGC TGATTTCCCT GACCTCTTGG GCATTTGTAT TTGTAGTAAA GTATTGCAGA 180
GATTCCCTAAG TTTTTATAG CAGCCATCAA ATTTGGACTT TGTATTGTTT ATTCATAAAA 240
GACACTTGGT AATAGACTTC AGTGAACCT CTATGAATGC AGTAGTGTGC GTGCAAAATC 300
CGCTTCCTGA GCGTAGGGTG CTGAGCTGGC GCTAGGGCTC GGTGTGTGAA ATACAGCGTA 360
GGTCAGCCCT TGGCCTNAGT GTAGAAACCC ACGGTCTTTA AGGTTCCGGC CTTGGTCCAN 420

SEQ ID NO:977

LENGTH:349

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01109

SEQUENCE DESCRIPTION:

GATCCTCATG TACTCAGAGG CACTTCCTC CTAAGTCAAA GACCATCCTC ACTGACTATG 60
TGCCAAAGCC TCGTTTCAGG CTGTNACTC AACAAAGGGC TTTTCATTG ATAGAAGCAG 120
TTTGGGATTT GTAGTTGCGA CTTCTTCGAT AGTTACCTGC ACGTCCATTG CTGGCAACTG 180
ACTTGTCATT AAAACCTGGC TCTTTGGTTA AGGGAGCTAC GCTGTGGTTT ATTCTTAAGT 240
TACGTGGATA AACTAACCTC TAACAGAAAT ATACTTTGGT TAATTTTGAA ATGTGTCATT 300
TTTAAACAAT CTTAAAGTA ATACAGAATT GTGATTTATT AATTTTAAA 349

SEQ ID NO:978

LENGTH:349

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01110

SEQUENCE DESCRIPTION:

GATCAGAGTG GGTAAAGCTG ACCAGGAACA CCCATTTAAC CCCTTTTNC TTTTGCTTTC 60
ATTTTATAA AGGAAAAGAG GACCTGTCAG ATAGGCAGCC CCATGCTACG TGATTCTTTA 120
TGTTGTGTTG TTTGTTTTG TAAATTGTAT AATTTTAAA TATCTGAGTT TAAAAAAG 180
AAAAAGTAC AAAAAATCT TGTATGGCC TTAAGAAGGG NNTAGTGCAT CTTTCAGGGG 240
TCACTCTGCC ATGGGGATAA AATAGCTGTT TCACAAACAG TTTTATTAA AAAANCAANN 300
ACCANNAAN ANTCAAAATN TCATGNAANN TTTTNAACCT TCATTTTNN 349

SEQ ID NO:979

LENGTH:345

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01111

SEQUENCE DESCRIPTION:

GATCACGTGG GTGTCAGTAT CTTTAACGGC CTCATTCTT GGTGTNAGA TTTTATTTGA 60
 TATGCCCACT CACCCTCGAC GAATCTGCCC GCTTTGGGCT GTGGTGCCTG TGTATCTTTG 120
 CCCGCTCTGGT CTCAGTTGG TGAATNACC TTTTTGTAC TGCCACTTCT CAGCATCTTT 180
 NAAATTTGAC ATAATGTTGC TTCATTTAG TTTTTAAGT TCTGTAATTT GTTGATTGTA 240
 TTTAACTATG TNAGTTCTGT TGTNATGTTT ACTGTATTGT AAAGCACCTC ATTCATGTNA 300
 TGAGTGCTCT ATAAATCAAT AAATGATGAC TTAGAGGGCT GTAAA 345

SEQ ID NO:980

LENGTH:344

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01112

SEQUENCE DESCRIPTION:

GATCTGCTTG GNGTTTTCTN CCCCCACCC CAAACTTCTG TCGAGGAGCA AGGCTTGCCA 60
 GCAAGTCAGA AGGATTTGAA CCGAGCAGCC AATCTTTCCA GCCCTCCNT ACCGACCTCT 120
 GTCTGGAGAC GCAGCAGCCT GTGTCTCCA GGGCTCTGG TTTGTNGTAT TATAGTATAT 180
 TTNGCTGTGG AAAATGTCAC GTTTAGTCAC CTTGGAGCCA CTCACCTGGT CCTGTTGTTT 240
 TANCCCATCC CTCTNTNGN GGGCTATTGA TTTNTTCTNA GGAGAGTACA NCGTCACTAT 300
 TGTAGNGTAA CCCTGTACTC AATATTACCA TAGNCGNTG NCGN 344

SEQ ID NO:981

LENGTH:357

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01115

SEQUENCE DESCRIPTION:

GATCAGAAAC CAACCATGAA TGAACCCCTG GCTCCTTCAC CACCCCCACG ATTGGTATGA 60
 TGCTGCCGGC ACAGNTGGGA TACACACGGC TCCCCAGGC CTGAGCTGCT TCACTAGGGA 120
 ATCTGCCAC CACCCTGTCT TCCTCTGCAA GTGCTCAGG AAATGGCCTT NCCGCCGGAG 180
 NCATNCTATC TGNCTGACAG GCTGTGACTC TTCTCTCAAC CTGGGCCTTC TCCCCTCTTC 240
 TGAGCTAGTT GGTGGAATNN NNGTTAATGC TTAAGATTG TTTTCTCTT TTCACAGCAA 300
 CATTTTCTTG AATTTTTTTC TGCACAGCTT TTCCAAAATA AAAACCTTCC AAACAAA 357

SEQ ID NO:982

LENGTH:340

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01116

SEQUENCE DESCRIPTION:

GATCAGAAAT AAGATTGACT TGGGTGTTAT ATTTATCTC TCTCCAGACT CTAGGTATAT 60
 TTCCAACCTT ATATATCACA GTATTTAAAA AGACATGTTT GCATTGAGAA ATTAACCCTA 120
 AAGGGTTTT AATAGGGTGT AGACCTCCAG TACCTTTGTA ACTAAAGTCT GTCTAGTCAT 180
 NGTAAATATT TATCTGTCAG TTTTGACAGA TTGGGGCCAG CTTGATGTTT TAAATCTTCA 240

GCCCCGGTATG AAAACTTAAA GGTATATATT CANTTTTTTA CCATTTTATG GAAAATATTT 300
AAAAATCTGTT TTTACAGGGT TTTTTTTTTT TTTTTTTTTN 340

SEQ ID NO:983

LENGTH:340

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01117

SEQUENCE DESCRIPTION:

GATCTGGTTC GGCTGCTGTC GGATGAGGAC GTAGCGCTCA TGGTGCGGCA GGCTCGTGGC 60
CTCCCCCTCCC AGAAGCGCCT CTCCCCCTGG AAGCTGCACA TCACGCAGAA GGACAACTAC 120
AGGGTCTACA ACACGATGCC ATGAGCTGAC GGTGTCCCTG GAGCAGTGAG GGGACACCAG 180
CAAAAACCTT CAGCTCTCAG AGGAGATTGG GACCAGGAAA ACCTGGGAGG ATGGGCAGAC 240
TTCCTGTNTT TGAGGCTAAT GGACCCGTGG GGCTTGAAT CTGTCTCTTT CTACTATTTA 300
CATCTGATTT AAATAAACCA TTCCATCTGA AAGGGGCAAA 340

SEQ ID NO:984

LENGTH:339

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01118

SEQUENCE DESCRIPTION:

GATCTATGTA TTATTAGAAA AATGAAGTAT TTCTGACATG GAACAAAGAA AGTGGAAACT 60
GGTACTTAAT GGGGGAAGCA AAATTAGCTG GGACTAAAAC GGACATGTTT TGTTTTGTGA 120
ATTCTACCTA AATGTCTCTC TATCCACAGA GAAACTAGTA TTA CTGTAAG ATGTGAAAGT 180
TCCTGTGGTA GCCATACCTT GAAGCACAGT GTTGTACAT AAGTAAATAT CTGATTCTA 240
AATTAAATCC AGATTATCT AATATATATN ATTNATATC TTTGTTGTAT TAAANTGGTT 300
TAATANTCAC TANAANTANN ACATTTTGNA TGTGGAAA 339

SEQ ID NO:985

LENGTH:339

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01119

SEQUENCE DESCRIPTION:

GATCTCAGGA ATTTTGTAG GGGATTGAAG CCAGANCTAG TTGCGTCCCA GGGACCAAGA 60
GAAAGAAGCA GATATCCAAA GGGTGCAGCC CCTTTTGAAA GGGGTGTTTA CGAGCAGCTG 120
TGAGTNAGGG GACAAGGGGC AGGTCCCAGG AGCCACACAC TCCCTTCCTC ACTTTGGACT 180
GCTGCTCTN TTAGCTCCTC TGCCTCTGAA AAGCTGCTCG GGGTTTTTNA TTTATAAAAC 240
CTCTCCCCAC CCNCCACCN CCAACTTCCT GGGTTTTCTC ATTGTCTTTT TGCATCAGTA 300
CTTTGTATTG GGATATTAAG GAGATTAAAC TTGGGTAAA 339

SEQ ID NO:986

LENGTH:339

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01120

SEQUENCE DESCRIPTION:

GATCCTTTCC GACACACATG TCTGAAGACT TATTTTCAAA GNCAGCACAT TTTTGGAAAC 60
 TAATCTCTTT TCCGTAATAT TTCCTTTATT TCAATGATTC TCAGAAGGCC AATTCAAACA 120
 AACCCACATT TAAGGTTCTT TAGGATTATA GAATAAATTG GCTTCTGAGT GTTAGCTCAG 180
 TGAGCTAGGA AAGCACCAAT CGATATTTGT TTCCTTTAGG GATACTTTGT TCTCACCCT 240
 GTCCCTATGT CATCAAATTT GGGAGAGATT TTTTAAATA CCACAATCAT TTGAAGAAAT 300
 GTATAAATAA ANTCTACTTT GAGGACTTTA CCAAGTAAA 339

SEQ ID NO:987

LENGTH:337

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01122

SEQUENCE DESCRIPTION:

GATCCAAAGT GTTAAAAATG CTGAAGTCAT GTCAAGTACT GTCTGGAGGG TTTTTTAAAG 60
 AAAAGGCATT TGGCATTTAA CTGTCTCTTG TTTTATTTT AAGTTTTTGG AAACCTTTTG 120
 ACATAAAATG CTGCCAAGTA TCTAAGAAAT GTATATACTG ACAGAAGATA TTTGAAAGTG 180
 GAAAATTGGA AATGAAATAT GTTGCTGGGN GCGTTAATCA CCTCCGCCCA GGATTAGTC 240
 ACTTGCAGGA CCTCTTTATA GTCTAGGATG GCAGAGCAGA AGATTTTAAT ATGCTTTTAT 300
 TAAGTGATGT AAAATAAATG CTTTTTGGAT TATCAAA 337

SEQ ID NO:988

LENGTH:371

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01123

SEQUENCE DESCRIPTION:

GATCGGCCAG CCCCCACCTA CAGCAACATG GAGGAGGTGG ATTAGCAGGT CCCTGGCTGA 60
 TGGGGGGGAC TGGGTTTGGG ACACCCACAC AGNGGGCCAG CTCCTGCCG CTTCTCCTTC 120
 TCTAACCCAG AGGACACTGG CTCTGTCAGT GGGAAGCTGA GGGGTATGAT TTGGGTGTGG 180
 AGACCTCTCA GGTGGGACT TCTTGTCAGC TTGGACCCCT GACCAGTGGG CTTTGGCTTC 240
 TCCAGCCGCC TCCAGTGCTG CGTGATTGA TTCTGTTGTA CCTTCAATTC TTCTGACCCG 300
 CATTATAAAC ATTATAATTN NATTCTAAAA ATTGTAATTT TTTTGCAT TTTGGAAGTG 360
 ACTGCTGCTG N 371

SEQ ID NO:989

LENGTH:334

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01126

SEQUENCE DESCRIPTION:

GATCTTCTTT ATATTCTACT TGAGTGCTGT CTCCATGTTG ATGTATCTNA GCAGGTTGTC 60
 CACAGGTAGT CTAGGAGGGT GGCAACTTAG AGGTGGGGAG AGAGATTCTC TTATCCAACA 120

TCAACATCTT GGCAGATTG ACTCTCAATC TCTTACTAA AGTTGTTAAG NTCNNCCGGT 180
 GATAAGTACT TCAATTTCAA CTTGTAGNNT GGGGAAATTT AGAATTATGC AGNTTATGGA 240
 ATTGATATG ATGACATTG CAATAGGTCT ATTCTCTATC ATTGTAAGAA GNTGTGTGTA 300
 CTGGTATTG NCCCAAGTAA TAANCTAACT GAAA 334

SEQ ID NO:990

LENGTH:333

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01127

SEQUENCE DESCRIPTION:

GATCTGNCGT GCCCACCAC TGGTGATGGA AGGTTACAAG TGGCACTTCA ATGAGACGGT 60
 GCTCACTGTG TGGTCGGCAC CCAACNACTG CTACCGCTGT GGGCGTGTGG CAGCCATCTT 120
 GGAGCTGGAC GCGCATCTCC AGAAAGATTT CATCATCTTT NAGGCTGCTC CCCAAGAGAC 180
 ACGGGGCATC CCTCCAAGA AGCCCGTGGC CGACTACTTC CTGTGACCCC GCCCGGCCCC 240
 TGCCNNTTNC AACCTTCTG GCCCTCGCAC CACTGTGACT CTGNCATCTT CCTNAGACGN 300
 AGGNTGGGCG TGGGNGGGNN TGTNCTGGNT NTN 333

SEQ ID NO:991

LENGTH:329

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01128

SEQUENCE DESCRIPTION:

GATCGGACTG AACAGGAATC CTCGGGGGGT GAACAGCCAT TCCTTCGTGA CCTGTGCACG 60
 NCTTCTGCAA CCTGGAGCT CTGCTCGGCT AGTCTGACTC GAAAAGGGCG TGACTCAAGC 120
 TGACGGGACT CCAGTAGGGA CTTTGAGAGC ACATTTTGTA AAAATATTTA TCTAGACGCA 180
 AATGCTTATC CATGAATGTC CTCTTAGACC ATTTGGGGAT GAAGCCATCT TAATAATTAG 240
 TAATAATTAA TTAGTAATAA TTAGTAAGCA TTTTCTCAAT GCTCTGATTC CATCATGTTT 300
 TCTTAACATG ATAACTTAAA AAATTGAAA 329

SEQ ID NO:992

LENGTH:332

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01129

SEQUENCE DESCRIPTION:

GATCCTCCTC AGAAACTACC GGAATTGTTT TCTGTATTGG TGTGTTTTGT ATCTTGCTTG 60
 AACTTCCTGT TCTTCTGGT ATACTTTAAC ATTATNATNA TGTGGGATTC CAAAAGTGGA 120
 AGAAATCAGA AGAAATCAG CTAGCTGTAT TCCTAAACAA ATTGTTTCCT AAACAAATGT 180
 GAAAATGTGA ACAGTGCTGA AAGGTTTTGT GAACTTTTGT CTATGTATAA NTGAAATTAC 240
 CATTTTGAGA ACCATGGAAC CACAGGAAAG GAAATGGTGA AAAGTCATTG TTGTCTACAC 300
 AAAATAAATG TATATGGAGA CCAAAGACCA AA 332

SEQ ID NO:993

LENGTH:330

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01130

SEQUENCE DESCRIPTION:

GATCAAGAAA TCAGGATGGC CATTTATTTA ATATCCATTC ATTCATGTT AGTGGGACTA 60
TTAACTTGTC ACCAAGCAGG ACTCTATTTC AAACAAAATT TAAAACTGTT TGTGGCCTAT 120
ATGTGTTTAA TCCTGGTTAA AGATAAAGCT TCATAATGCT GTTTTTATTTC AACACATTAA 180
CCAGCTGTAA AACACAGACC TTTATCANGA GTNGGCAAAG TTTTCCAGGN TTCATATACA 240
GNTAGGCTAT NNGNCATGTA TTTTGAAACG CAGTGTTNCA TNATGAAAGN GCTCTCAAGT 300
NGCTTNAAG NTANTTTATT AAANGGGTNN 330

SEQ ID NO:994

LENGTH:330

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01131

SEQUENCE DESCRIPTION:

GATCCGGGCC TTGCGTGCAG CCTCCCAACC ATGGGCTGGG TTTNGTGCTT ACTGTATGTT 60
GGCGACTTGG NNAGGGCAGG AGACGCAGCG TGGAGCCTAC CTCCCGACAT TCACGCTTCG 120
CCCACGNTGC TCCGACTGGC TGCAGCGGAC ACTGCCCAAA GCAGAGGGGA GTCTCAGTGT 180
CCTGCNAGCC AGCCGAACAC TTCTCTCCGG AAGNAGGCTG GTTCGACTGT NAGGTGTTGA 240
CTAACTGTT TCTCTGACTC GCCCANAGGT CGTGGCTAAA GGCCTTAGG CGNCTTAAAT 300
TTGTAAATAA AATGTTACTA CGGTTTTTAA 330

SEQ ID NO:995

LENGTH:338

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01132

SEQUENCE DESCRIPTION:

GATCTGAATG ATGATGGAAG CATGCAGACA GCCTCTCAGT CTTACTATTT AATGTTGTAG 60
CTGGGAAAAA ACCCAGAGAG GTTAACTGAT ATACTGGGTT GGGACTAGGA TGTGGGTTTT 120
GTNACTCTNA ATCCCATGTC CTCAAACACT GCTGCCTTCC GAAGTCTGGC ATTTGTNAGC 180
TCATGCTTCC TTGTAGTCCA GCTTCTTATG TGCCTGTAAT ATTCTCCAGT ANGATTGTAA 240
GCCCCTTAAG GGCAGGGACG TCTTTNCATC TCTAGCACTG CTATAGTGTT CTATCCTTAG 300
TTATGGACCT AGATAAATAA NTNGGTGGTG GCAACAAA 338

SEQ ID NO:996

LENGTH:328

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01133

SEQUENCE DESCRIPTION:

GATCTTTATA TTNATACTC TAAANTCGTA CAAGCCAATC TNCATTTTNA CTAGTGGAAG 60

CTGTATAGCT GGTCACTTT CCAGGACCCT TTTATCAAGA AACAAATGCAG CTTCTACATT 120
 TGTNCTGCTT CTACACCAA ACAGCTGGAA TGTATATNGT ATGGTCTCGG ATGCTCTTGT 180
 ATACCTNACT CTTCAATTTCT NACCTAACCC ATGTGCTATG ATTTGAATGT TTCTCCCCTG 240
 CAAAACATCAT GTTGAAATGT AATTGCCATG NTAACAGTAT TANTAGGTGG NNTATTTNAG 300
 NGGTGNTTAG GGTGGGATTG GTGNTGTN 328

SEQ ID NO:997

LENGTH:326

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01134

SEQUENCE DESCRIPTION:

GATCTTGTGT CTTAGAGAAG CCCCCATACC TGGTAGAGCA TGTACCATCT TACATGCTTA 60
 AATAACTCCA CATTTATTTG TGTATTNAC TCTGTGTTAT AAATATACAT TTGTNGGTCT 120
 CTCTCTTGGA TTATTTTGT TCTTTGTCCT GTAACCTACCA CTGAAAGGGT GCAATACAGC 180
 TTTCTTGAAA TGTGTATTGA ACGGATGAAT GTATAAATAA AANTTAAATT TTGTAAATTT 240
 CTGCTTATNC TTAGAAAAAG AATCTAAATN GTGACAAATC AGAATTGAAA AANGTATTCT 300
 AATAAAGANA AACANGCTTT TATAAA 326

SEQ ID NO:998

LENGTH:325

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01135

SEQUENCE DESCRIPTION:

GATCCCCAGT GTTGGAGGTG GGACCTAAGT GGCAGGTGTT TGGGNCATGG GGATGGATTG 60
 CTCACAAACG GCTCGGTGGC CTCCCTGCAG TAACGAGTGA GTTCACACAC TATTAGCTCA 120
 CATGAAACCT GGTATTATTA GAGTCTGGGA CCTCCCTCCA TGCTCTCTCT CTTGCTCCTT 180
 TCTCTACCA CATCACACGT GGCTCCCTT GCCTTCTGCC ATGAGTGAAA GCTTCTGAG 240
 GGCCTCACCA GACACAGATG CTGGTGTCTAT GCTTTTGTGA CAGTCTGCAG AACCCCGAGT 300
 CAAATAAACG TCTTTTCTTT ATAAA 325

SEQ ID NO:999

LENGTH:322

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01136

SEQUENCE DESCRIPTION:

GATCACTTTC AATTGAAGTC AGGGTATTGT GCATAATAGA AAGTATTGGA CTGAGATATT 60
 TGGTTACCAT GGAGGCCAAT GCTTTTTTCA TCTTATTAAG TGTGATGTGA CTTTTTNCTT 120
 TGTACAGAAG AGTACTGTAT TTTTGAATAG CCTACTCCCA AGTAAGAGCA AATCTGTATG 180
 ATAACATTTT TNCNCTGGA CATAAGACAT AACAGTAACA CGATGTACAT TTACAAGCGG 240
 CCTTATGTAC ATTTCCCAAC ANTCTTTTGA AGGCAAAATT GTGACCATAT GTGTATAATT 300
 AAAATCGTTT TTAATCCNTA AA 322

SEQ ID NO:1000

LENGTH:322

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01137

SEQUENCE DESCRIPTION:

GATCTTAGAA ACCTCTGCAC AGAAGCTGCT TTGCTGGCTC TGCAAGAAAA TGGACTAGAC 60
GCAACTACAG TNAACAAGA GCACTTTCTA AAATCACTTA AGACTGTAAA ACCGTCGTTA 120
AGTTGCAAGG ACTTGGCTTT ATATGAAANC TTATTTAAGA AAGANGGATT TTCTAACGTG 180
GAAGGTATTT AAAANTCACC TTAAACTCTT GTNCAGTTCA CATTAAATTGA AATGTGAACT 240
TGCCTGTCGT TTGCAACTTC AACTTTTATG AATTTGTGTT TATATTCCT GTANGTGAAT 300
AAATANANCA NNNCAGNNCA AA 322

SEQ ID NO:1001

LENGTH:353

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01138

SEQUENCE DESCRIPTION:

GATCTCAGAA CAACCTTTCT TGTTAGTAAC ATATTTTGG CAATACATAN CAACCTGGGC 60
CTGGTGATA ACCAACAAGA TGGGGAAGAA AAGNATTGAG AACTTTAAGA GTGGTGTGGA 120
TGCAGACTCT TCTTATTNA AAATCTTTAA GACAAAACAT GACTGAAAAG AGCACCTGTA 180
CTTTCAAGC CACTGGAGGG AGAAATGGAA AACATGAAA CAGCAATCTT CTTATGCTTC 240
TGAATAATCA AAGACTAATT TGTGATTTTA CTTTTAATA GATATGACTT TGCTTCCAAC 300
ATGGAATGAA ATAAAAATA AATAATAAAA GATTGCCATG GANTCTTGC AAA 353

SEQ ID NO:1002

LENGTH:320

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01139

SEQUENCE DESCRIPTION:

GATCTGACCT GGTGAGATTA TTTCTGATGA CCTCATCAAA AAATAAACAA TTCCAATGT 60
TCCAGGTGAG GGCTTTGAAA GGCCTTCCAA ACAGCTCCGT CGCCCCTAGC AACTCCACCA 120
TTGGGCACTG CCATGCAGAG ACGTGGCTGG CCCAGAATGG CCTGTTGCCA TAGCAACTGG 180
AGGCGATGGG GCAGTNAACA GANTAACAAC AGCAACAATG CCTTGCAGG CAGCCTGCTC 240
CCCTGAGCGC TGGGCTGGTN ATGGCCGTTG GACTCTGTNA GATGGAGAGC CAATCTNACA 300
TTCANGTNTT CACCAACCNN 320

SEQ ID NO:1003

LENGTH:318

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01140

SEQUENCE DESCRIPTION:

GATCCTNCNA GTTAGCCTAG TACTGCTGTA CTGGCCTGTA TGTACATGGG GTCCTTCAAC 60
 TGAGGCCTTG CAAGTNAAGC TGGCTGTGCC ATGTTTGTAG ATGGGGCAGA GNCATCTAGA 120
 ACAATGGGAA ACTTAGCTAT TTATATTAGG TACAGCTATT AAAACAAGGT AGGAATGAGG 180
 CTAGACCTTT AACTTCCCTA AGGCATACTT TTCTAGCTAC CTTCTGCCCT GTGTCTGGCA 240
 CCTACATCCT TGATGATTGT CCTCTTACCC ATTCTGGAAT TTTTTTTTN GNNGATANNT 300
 ACAGAAAGCA TTTTGAAG 318

SEQ ID NO:1004

LENGTH:320

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01141

SEQUENCE DESCRIPTION:

GATCTTTCTG TCTTCTGGGT TCCATTTTN AAATGTTTAA AAATATGTTG ACATGGTAGT 60
 TCAGTTCTTA ACCAATGACT TGGGGATGAT GCAAACAATT ACTGTCGTTG GGATTAGAG 120
 TGTATTAGTC ACGCATGTAT GGGGAAGTAG TCTCGGGTAT GCTGTTGTGA AATTGAAACT 180
 GTAAAAGTAG ATGGTTGAAA GTACTGGTAT TGTGCTCTG TATGGTAAGA NCTAATTCTG 240
 TNNCGCCATG GTNCATAATT NCCTATNCAC CTTNCCTNCC CCTTNCAGC CCAATTAAAG 300
 GTTGGGGTCN TAACCTCAAA 320

SEQ ID NO:1005

LENGTH:315

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01142

SEQUENCE DESCRIPTION:

GATCTGGGGG CTCGAGACTC TGAAGGCAGG GACCCTCTGA CCATCGCCAT GGAAACAGCC 60
 AACGCTGACA TCGTACCCT GCTACGACTG GCAAAGATGA GGGAGGCTGA AGCGGCCAG 120
 GGGCAGGCAG GAGATGAGAC GTATCTTGAC ATCTTCCGCG ACTTCTCCCT CATGGCGTCA 180
 GACGACCCGG AGAAGCTGAG CCGTCGNAGT CATGACCTCC ACACGCTGTN ACCCGAGGCC 240
 CACGGGGCCG CGCCTGCNTC CCTTCCCCGN NACCGNGCNN TCTGCCATTA AAGCCTCCGT 300
 GCTTCGNTCT TCAAA 315

SEQ ID NO:1006

LENGTH:315

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01143

SEQUENCE DESCRIPTION:

GATCCCTTGC NTGCCCCCTCC CTGTGGCAGG GCTAACTGCC TGGCCCTCCT GGCTCGCAGC 60
 CAGCCAGNCC CCTGGCAGCA GGTTCCTCTC AGGGCTTGGN TCTTCAACCT GTGGCGACAG 120
 GAGGCAGGGC AGACTGTGGA GGACAGGATG CAGGTCAGGG AGAGGGAAGG CAGGGGTGGA 180
 CCGCCATGAG CATGAAAAGC CCGAAGCAAG TTGACTCTTN AATTGCAAC TGTATGNTC 240
 TGAAAATGAG AACGATGTAT CAANTTGATG CANTTTNGAT GTTGTACTTA CAATAANGTT 300
 TTAATGTGTN TTAAG 315

SEQ ID NO:1007.

LENGTH:315

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01144

SEQUENCE DESCRIPTION:

GATCTGAGGN CAGGANTTAA ACCACAGAAT GTATNTGCCT GTAAAGCACA GGGGAAGAAA 60
 CGACTCATTA GAACTACACC TGTTACATAC CATTGGGTAA ATGNTTTAAG NGGGGAATGG 120
 TGTGACAAAC CTTCAAAAAA NATGAACACC TTAATGTTCA GGAAGTGAAGC TAACTCCCTA 180
 TGNTTAGGCA CAGCTTGATA CGAGCGGAGA CTTGGCAGTC AATTCCANGT CTTTATACT 240
 NATTACCTCA TCGTNACTGT NAGTGCAACT ATAGTCTGTT GTNGGAATTT GGNCATCCCT 300
 TAGTNTCNGA TGGTN 315

SEQ ID NO:1008

LENGTH:314

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01145

SEQUENCE DESCRIPTION:

GATCAGAAAA AACAGAAGCC AAATCGGGG TCATCTTGT TTTAAAGCT GAAGTGGGAC 60
 TGTCTGGCAC TCTGTGTATT TATGCGTTCC AGCATCTGGA ACCTCCCATC CCTGCCCTCC 120
 TCCTGTGTAG CTGCCACCTC CCCGCTGGGC CCAGCATGGC TCACCTGTCC CGTGGGCTGT 180
 GTTCTTGTT GTTTTCTCT TTGCAAAGAC ATAGCTAGGA AAGCGAATGA TAAGGGAAAA 240
 GTTCTCAGGG AATTGAAGTG TTGTTGCTAT GGTGACGTCC TTTGCTGTG AATAAAGGTG 300
 CTCTTTGCAG CAAA 314

SEQ ID NO:1009

LENGTH:313

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01147

SEQUENCE DESCRIPTION:

GATCCACAAT AGTGGCATGA GGCAGGCGAC TGTNTGTNAC CTCTATGTCC GCAGAGTCCA 60
 GCACGCTAAC AGCTGGGAGA TAAAAGCAGT GGAGAGGGCT GTGGGGGAC ATGCCATGGA 120
 AACTACCTAG GACCTGTTCC CTGAGTTAAC ATTCTAGCCT CATCTACTTG TTTGCCCCCT 180
 GCAGCTCATA TACANACTGG CCCACCATT ACGNACCATC CCCTCAAGTA ATCTTAAAGG 240
 TTCTCAGCCC ANACANATTA ACTGTTCTGA CCCACCTNC TTAATAAACA ATCCTGGGNT 300
 CAGCCATNTG AAA 313

SEQ ID NO:1010

LENGTH:311

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01148

SEQUENCE DESCRIPTION:

GATCTGGCAG TTGAAAATTG TGGGAAAGAG AATTTGTATG GGCACGTGTAT CTATGAAATA 60
 CCTCATAACT TACGTTTACA TGTTTTCCTA ACTTTTNGTA TTTTCNTNGT ATAGCCACCT 120
 AGAGAATTCT TCATAGATTA AGAACTACAG TTTTNACCAC TTAACATAAG TAAAACAAAG 180
 TCCTTCATAA TTNAACCATT AGCATCTTTG GCCAAACCAA AATAAAGANA AGCATCTNCT 240
 CCTAGTTGTG TGTGGGCAAC AGANACANGT TAAGGNAACA NAAATACTTA TATATACACN 300
 GANCANANGT N 311

SEQ ID NO:1011

LENGTH:308

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01149

SEQUENCE DESCRIPTION:

GATCTCCCTT GGTCTTCCAT GGGATGGTTA GTGTGGAGGG GAGATATAGA TTGTCCGGCC 60
 GNTTGTGAT TCCATGGGAT TGATTCAGTC TTCTGGATTT TTTTNTCTGT ATATTNNGG 120
 TACTGGAGCT TTTAAAAATG CTGCGNTTCA GGTATTTTNA TTCATGTGAA GTGTATATGA 180
 TTCTNTTGAG ATAAGGTTTT AAGCTAAAT GTNACTCCCT GNTTNAGCNT CTGAACCTG 240
 ACAGATTNAC AGGGACTTTG CTGGTGTAGG CTTTTTAAAG GGNTTANTAN TCCACTTTGA 300
 GCCTNAAA 308

SEQ ID NO:1012

LENGTH:308

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01150

SEQUENCE DESCRIPTION:

GATCTGGAGT TACCTGAGGC CATAGCTGCC CTATTCACCT CTAAGGGCCC TGTTTTGAGA 60
 TTGTTTGTTC TAATTTATTT TAAGCTAGGT AAGGCTGGGG GGAGGGTGGG GCCGTGGTCC 120
 CCTCAGCCTC CATGGGGAGG GAAGAAGGGG GAGCTCTTTT TTNACGTTGA TTTTNTTTT 180
 TCTACTCTGT TTTCCCTTTN TCCTTCCGNT CCATTTGGGG CCCNGGGGGT TTCAGTCATC 240
 TCCCCATNTG GNCCCCGGGA CTGTCTTNGT TGATTCTAAC TNGGNNNGGA AAGAAANTAT 300
 TATTCAAA 308

SEQ ID NO:1013

LENGTH:307

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01151

SEQUENCE DESCRIPTION:

GATCCATGGG GCCGCAATGA AGCTTGGAGA TACATGGGTG GCTTTGCAA GAGTGTTC 60
 TTTTCTGATG TATTCTTTAA AGGATTCAAA TGGGGATTG CTGCATTTGT GGTAGCTGTA 120
 GGAGCTGAAT ATTACCTGGA GTCCCTGAAT AAAGATAAGA AGCATCACTG AAGATAATAC 180
 CTGGAAGCAT CATAGTGGTT TCTTAACTCT CCAAAAATAAG ATTTCTTCTC TGTAGCCTAC 240
 TTGTCTGGTT TATCCCTTAC AGAATATTAG TAAGATTAA TCAATTAATA TATATATATA 300

TGCCAAA

307

SEQ ID NO:1014

LENGTH:306

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01152

SEQUENCE DESCRIPTION:

GATCGGTCCA CGAAAGTTAG CCCATATGTA TATCTTGAAT AGTATAGGGG AGGGTATTCA 60
TAAAGTCCTT ATGTGGTTTT AACTAAGTGA AATTATGGAC AAGAGAANN NTTGTAAAAT 120
CGTCTTAAAG GCAAATTTAA TTTNACTCC TGTTCATGGG ACATTGCTC TATTAAGTGT 180
CAGACACAAT TTCTGTTTTT ATCTGAGAGC CAGTTTTCTT TTATTTCTAC ATCTAAAATA 240
AGANCATATT GTACACTATT ATATAATACA GAATTGTCTT AAACCTTAAT AAATTCGCAT 300
TTTAAA 306

SEQ ID NO:1015

LENGTH:306

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01153

SEQUENCE DESCRIPTION:

GATCTCAGCA GTGGGGCAGG AGGGTGCCTG ATTTGGGGGA GTCCTGACCC GAGCCTGTTG 60
TCAGAGTTGG GAGGGGCTCT GAGCAGTGTT GGGCAGGCCG GGTCTCCCAT CCCGAGGCCA 120
GCGTTCCTGT GCAGAGCCCC ATCCACTGGT TCTTGCCCTG AGCCACATAT GTCTGTNCCA 180
TGGGCTGAGT GCCACGACAG GCCCGTGTGA CAGCTGCTGC CCACGCATNT NGAAGCTAGG 240
TGGGACTCAT TCCTAATTCT GCCGTTGTAA TGAGACTTGA TTAACACACC GCCACTTTTT 300
TGCAAA 306

SEQ ID NO:1016

LENGTH:304

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01154

SEQUENCE DESCRIPTION:

GATCAACAAG AAATGTTATG AAATGGCCTC CCACCTTCGG CGTTCCCAGT ACTGACCTCG 60
TCTGTCCCTT CCCCTTCACC GCTCCCCACA GCTTTGCACC CCTTTCCTCC CCATACACAC 120
ACAAACCATT TTATTTTTTG GGCCATTACC CCATACCCCT TATTGCTGCC AAAACCACAT 180
GGGCTGGGGG CCAGGGCTGG ATGGACAGAC ACCTCCCNNT ACCNATATCC CTCCCGTGTG 240
TGTTTGAAA ACTTTTGTGTT TTTGGGGTTT TTTTTTCTG AATAAAAAAG ATTCTACTAA 300
CAAA 304

SEQ ID NO:1017

LENGTH:304

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01155

SEQUENCE DESCRIPTION:

GATCTAAAGC AGGTNGTGTT GTTTACATGT TTCTACACAT TTCATCCTTT AAAAAGTTGT 60
 TGAGAGAGGT TGTATTTACC TTCCAAGGT TGGAAAGCAG GGGAATTTCC CAGTGTCTTA 120
 GTTTCCACC AGAGGAATAT GTGTAAGTAG CAAAGTATTT GCTGCTTACA TATAGTGTGT 180
 ATGTATGTAT ATATGTAAAT NGTGTGTAA AGAGCTGATA CTGATTTTCA TATGNCAATG 240
 TTAAGGCAAA GGCCTCCCTG CATTTGANGA GCAGGTNTTC ATTTATATGT ATTTNGGGA 300
 TAAA 304

SEQ ID NO:1018

LENGTH:304

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01156

SEQUENCE DESCRIPTION:

GATCAGAAAT NAAGTGCAGC AATATCATGA ATTCTNAGAA GNCTTTAAGG GAGCCAGTNA 60
 GTCATACAGT ATCCACAGTT GANTCACTTA AAGATGTCAG TATACGAACA TTATTCACAA 120
 TCCTTGGGCA ATCTCATTTT TTTCCCTTC TCCCCTCCTC CCCTGCCCCC ATACATTTNT 180
 ATCCTTAANG TAGTTTTGGA GGGGCAGGAT GTACTTAACA TCTCANAAGC TAGATTGGGA 240
 ACATNTCANT ATAAGACTGA GTTTAAATTT ANGGTTAAAA TGNCATCAGA ANANTTGGGN 300
 GGGN 304

SEQ ID NO:1019

LENGTH:169

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01157

SEQUENCE DESCRIPTION:

GATCTAATAC TACTGTCAGT TTAAATGTGC ACTGTGTTTT ATACAGTATC TTTTTTTGTT 60
 CACTTNGGAA ATTTTACTA AAAATTGCAA AAAATAAAGT ATTGTGCAAA GATGTAAGGN 120
 TTTTGANAC TTGNNGTGCA TTAATAANTA GACGATTAAN TCAAGGAAA 169

SEQ ID NO:1020

LENGTH:303

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01158

SEQUENCE DESCRIPTION:

GATCCTCTAC CACAGACATT AATAGCTGAG CAGGAGCCAC ATGGATTGAT TGTATCCACT 60
 CACCATTGAC GATGGCATTG AGCGTANTAG CTTATTTCCTA TCACTACGTG TTTTGAGCT 120
 TGCTCTTACG TTTTAAGAGG TGCCAGGGGT ACATTTTTCG ACTGAAATCT AAAGATGTTT 180
 TAAAAACAC TTTTCACAAA AATAGTCCTT TGTCATTACA TTATTACTC ATGTGTTTGT 240
 ACATTTTGT ATGTAAATTT ATGAATGATT TTTTCAGTAA AAAATACATA TTCAAGAACC 300
 AAA 303

SEQ ID NO:1021

LENGTH:303

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01159

SEQUENCE DESCRIPTION:

GATCCTTNGG CTCAGAATCT CGAGAACCGC CTGCTCCTAA CAATTCAGCA AGTCAGGGGC 60
TTCCTCTCTG TTAGTCCCCA AATCCTTACT TATTTTAAAA AGACTAGACC CTCTCTAAAG 120
ACTGTTCCAT TTTAACATGT CCTGATTCTG CATCCGTGGG TTTTGTGAAA GAGAGCTAGC 180
TGGCGGTTAG AGCCTGGAAG AAGGAGGGAA GTGGCACCTC ACTAGCATTT ATCACTTTTT 240
TCCTTCTCTT TTTAAAAATA AAACCAGACT CTGTTCTGAA AATAAAAAAC TTGAGACTTG 300
AAA 303

SEQ ID NO:1022

LENGTH:303

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01160

SEQUENCE DESCRIPTION:

GATCTGNCTT ATCCGAGCTT GTTATTGGGG AGCCATAAGA GTCAGTTATC CAGAACACAG 60
TTTTGCATAA GCTTGTAT GATTTCAGTAA TGCAGGTGAG AGTGTCTAGC AGTTCTTGGT 120
AAGTACTCTT GGACATCTTT AAATTATTTA TCCTAATGGA TTCCATTCTG GTTTATGTAT 180
AATCGTTTCA AGACTTTGGG AGTCTTTTAT GAACAAATGC TCATTGCACT ATATTATATG 240
CAAATTGTNN NGCTGCTAGG TTTTCAAAAT TTGAATAATA AAGCCTTTTC ATGTTCTTTT 300
AAA 303

SEQ ID NO:1023

LENGTH:303

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01161

SEQUENCE DESCRIPTION:

GATCAAAATC CTGTACAATA CTATAAATAT ATATTNATNT TTTCACAGTC ACCAAGTGTA 60
TTGTAATGTA TACTTGAAAA ATGTTATAAC TTATGAAGTA AAGTTTCTNA TAGTAGTCTT 120
TAAAAGATAT AAGACTTAAT ATGTTTTATT CAGCTTCTAT AAGTGTGACC AGTTTNNATA 180
TTTATTTATG CTAATATTTT TAACAAGTCA TTTCAAAATA TGTGTATCTC AAATCCTCCC 240
NAAAGTGTG TGGCCTTAAC TGTTCAAGTAT TGCAATAAAA NATATATNTN NNTATGTGGT 300
AAA 303

SEQ ID NO:1024

LENGTH:302

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01162

SEQUENCE DESCRIPTION:

GATCTATGGA AAAGCTGGGAA TGTAATGTAG GATTCTGTCA GAGCTCCTAC AGAGCACAGT 60
 TGCCTTTAGT TTCCTTTAAA GATGTAAAAA TATTGTATAA TACAGTTTTG TCCCTACACA 120
 ATTGTATTG CCAAGCTTAG TGCATTATGA TACCTTTATT TATTTGTTTT GGGCAGTATT 180
 ACTATATATA TATAANCATA CAGTTACTGT TTTATATATT CTTAGGTCAT TCAAAGCCAT 240
 GTATGCTGTA AATGTGCTAG TCTTTAGAAT GACACATAAT AAATAACTGA CAAGATATTA 300
 AA 302

SEQ ID NO:1025

LENGTH:435

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01163

SEQUENCE DESCRIPTION:

GATCGAGCCA TTGAAAGCTC ATTACCAGTA GGACATAATT TTTGGCTCTC CCTATTCACA 60
 ACCAGTGCAC AGTTTGACAC AGTGGCCTCA GGTTCACAGT GCACCATGTC ACTGTGCTAT 120
 CCTACGAAAT CATTGTGTTT TAAGTTGTGT TTATTCCTGG AGTGACATGC CACCCCGAAT 180
 GGCTCACTTT CACTGAGGAT GCTGTCTCTT GATTTAGCTG CTGCCTCCAG CCTCTGGCTT 240
 GAGAACTTAC TAAAGGCACT TCCTTCCTGT TAAACCCCTG TTAACCTCTC ATAAATTTGG 300
 TGATTCTCTG CTAGGCCTAA GATTTTGAGT TAACATCTCT TGAAGCCAAA CTCCACCTTC 360
 TGTGCTTTT TGCTTGGGGA TAATGGAGTT TTTCTTTTA GGAAACCAGT GCCAAGGAAT 420
 GNCAAAGGTN TTAAA 435

SEQ ID NO:1026

LENGTH:298

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01164

SEQUENCE DESCRIPTION:

GATCCACATC CTCTACAGGT CGGGGACCAA AGGCTGATTC TTGGAGATTT AACACCCAC 60
 AGGCAATGGG TTTATAGACA TTATGTGAGT TTCCTGCTAT ATTAACATCA TCTTAGACTT 120
 TGCAAGCAGA GAGTCGTGGA ATCAAATCTG TGCTCTTTCA TTTGCTAAGT GTATGATGTC 180
 ACACAAGCTC CTTAACCTTC CATGTCTCCA TTTNCTTCTC TGTGAAGTAG GTATAAGAAG 240
 TCCTATCTCA TAGGGATGCT GTGAGCATT AATAAAGGTA CACATGGAAA ACACCAAA 298

SEQ ID NO:1027

LENGTH:328

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01165

SEQUENCE DESCRIPTION:

GATCCACTTT GTTGGTTGTT GTTGCAAGAG ACTGAACTGT TTTGGAATAN TTAACAATTA 60
 CAGAAACAGT CAAGTGTTTT CCAATGTGGT TGTCCGTTTT CTATGGCCTT GCTGTGTAAT 120
 TTCCCTCTTT TTGACAGTAA ACTTCTGCCT ATGGCTTACA GTTTGACATT TAATTTATTA 180
 GCGCTGCTCT GCACCCCTNC CTTGGGAGGG AGACTTCATG TGGTTTATTG CGAGTTTTTT 240
 TGTTTACTTT TCAGGGTTNG TACCTACAAA GGTTTAAATA ATAAAAANCA AAGNTTTTTT 300

NGGCNATTNG TCTTGTCTTN GTGGGAAA

328

SEQ ID NO:1028

LENGTH:297

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01167

SEQUENCE DESCRIPTION:

GATCTACAGT GCTGATGAGA AGAGAGCCCT TGCATCCTTT AACCAAGAAG AGAGACGAAA 60
GAGAGAGAAC AAGATTCTGG CCAGTTTTCG AGAAATGGTT TACAGAAAGA CCAAAGGGAA 120
GGATGACAAA TAAAGATTTT NTGATTGTCC AGAAGACATT TTAAACAACA AAAAAGAAAAG 180
TCTGGGTTC ACACATACAT AGAAAAAGAT TATTATGTTC TGAGAAAGCT TTACAGTGCT 240
ACTGTGCCTT CTATTTAATT CTTTCAGTCC TTCAATAAAA AGCTGCTTAT TGATAAA 297

SEQ ID NO:1029

LENGTH:297

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01168

SEQUENCE DESCRIPTION:

GATCCTGCTG AAATACATCT GCAGCTGACA ATGAGAGAAG AAACAGAAAA TGTCATGTGA 60
TGTCTCTCCC CAAAGTCATC ATGGGTTTTG GATTTGTTTT GAATATTTTT TNCTTTTTTC 120
CTTTCCCTC CTTTATGACC TTTGGGACAT TGGGAATACC CAGCCAACTC TCCACCATCA 180
ATGTAActCC ATGGACATTG CTGCTCTTGG TGGTGTTATC TAATTTTTGT GATAGGGAAA 240
CAAATTCTTT TGAATAAAAA TAAATAACAA AACAATAAAA GTTTATTGAG CCACAAA 297

SEQ ID NO:1030

LENGTH:296

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01169

SEQUENCE DESCRIPTION:

GATCCAGAAC ATGGGAAGTT AGGGAAAATG TGTGATTTTG TGTTTTGAAT TACTGTCAGA 60
ATTACATACA CAATTACAAC AACTTTTTT TAAAAGACAT TTCATTGTAC TGCAAAAATC 120
TGAATATTTA TATTTCTNGT TTTTTCCTTT ATATGTTTTG CATTTTANTA TGTTGAGCCA 180
CTGGAAAATT TGTAACAGNT TANTTTGTTA TNGGCGTTTA ANTGTGTTGT CATTGNCTCC 240
ATTGTCTTTG TCCAGAGCCT ATTATTATGG AACCAATAAA NTTAATGGG GTCAAA 296

SEQ ID NO:1031

LENGTH:294

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01170

SEQUENCE DESCRIPTION:

GATCCTAGTC CCCTGCCCTC TGGCACAGCT GCTTCCTGCA AGANAGCAAG TNTTTGGTCT 60

CCCTGAGAAG CCATGTCCCT CGTNCCTGNT CTTGCCTGTC CCACCTGTGC CCTGCCCTCC 120
 AGCTTGTATT TAAGTCCCTG GGCTGCCCCC TTGGGGTGCC CCCNGCTCCC AGGTTCCCCCT 180
 CTGGTGTNAT GTCAGGCATT TNGCAAGGAA AAGCCACTTG GGGAAAGATG GAAAAGGACA 240
 AAAAAAATTA ATAAATTTCC ATTGGCCCTC GGGTGAGCTG AGGGTTTTTG CAAA 294

SEQ ID NO:1032

LENGTH:293

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01171

SEQUENCE DESCRIPTION:

GATCTTCAAG AAGTGAAAGA GACCGAAAAT CAGACAGGAA AGACAAAAGG CGTTAATGGA 60
 AGAAGCCAGG CTTTCTTAGC CATTCTTTGC AGCAGAAGAT TTCTTGATAA AAAAGGATTA 120
 CCTTTCCTTG TAAAGAGGAT GCTGCCTTAA GANTTGCATG TNGTAAAANN NCTTTTGGGA 180
 AAATACAGAC TGTTTGTTTA CCAGACATTC TNGTACTGNT NGCATAATNN GGTAAGAGTT 240
 ATTNATCAAA ATNATGTGAG GTTCCAAAAT ATGTAAAANT GATATNATAA AAN 293

SEQ ID NO:1033

LENGTH:293

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01172

SEQUENCE DESCRIPTION:

GATCAGCGGT TCTTTTGGCA GCAAAGCCTG CATCTGTGTT GACTTGCAAG ATTTTGCATT 60
 TATTCAGGCA AAAACTGGTC AAAATGGTTA CTACATGATT TGTTCCCAGA GGTTTGAAAC 120
 ATTCAGTGAA ACTTTTAAAA ACTTTGATTG CATGATGTAT TTTTTTTTNA GAAAGTTATT 180
 GTTTGAGAAT AATGTCTTTT TATACCAGGA AAATAGTTAT CCNGAATGAC GTTGAAAACT 240
 CCCCTCCCC TTNATTTTNN TTTAATCANT ACATGTGAAA GTNNCCANGC AAA 293

SEQ ID NO:1034

LENGTH:308

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01173

SEQUENCE DESCRIPTION:

GATCCCAATT CCACATAAGC ACTTTTGGAA GAAAACAGCC AAAGTTGGCC TAAAATTGGC 60
 GCTGGAATTT GGNCTGGGAA AAATCTGTG GTTATTTCTT TAAAAAGGA ACAAACCTTT 120
 AGTATTTAAT TAGTTGATTT ATTTAATGTA ATTNCAAACA ATTAAATTAT GAATAATGCA 180
 ATGTACAGTA GAATCACGTT TTGATTTTAT TAACACTGAC CAAGTTTAAC TCCATATGAN 240
 GTGTAAGCTT GATATCGTTT ATGATGTCTA TCAACTGTAC CAAAAGTAAA ACATTTAAAA 300
 NCANNAAA 308

SEQ ID NO:1035

LENGTH:292

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01174

SEQUENCE DESCRIPTION:

```
GATCTCAAGT GACCCGCCTG TCTCGACCTC CCAAAGTGCT ATGATTACAG GCATGAGCCA 60
CTGCACCCAG CCAAACATGA CTTTCCATC CAGAGTAAAT CCAACTAACA AGAATCCACC 120
CTTGGAGTTC ATGTAAAAAT ACATGACACA GGGTGATGAA AGTGCTTTGA AACTAGATAC 180
AGGCAGTGGT TCTATAGCAT GGTGAATGTA CTCAAGGCAA CTTCTTTACT TTAAAATCGT 240
TAATTTTATG CCATGTGAAT TGCATCTCAA TAAAAATTGT TTTCAATTTA AA 292
```

SEQ ID NO:1036

LENGTH:363

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01175

SEQUENCE DESCRIPTION:

```
GATCGGGAAC TCCTGCTTCT CTTGCCTCG AAATGGACCC CAACTGCTCC TGCTCGCCTG 60
TTGGCTCCTG TGCCTGTGCC GGCTCCTGCA AATGCAAAGA GTGCAAATGC ACCTCCTGCA 120
AGAAGAGCTG CTGCTCCTGC TGCCCTGTGG GTGTGCAAGT GTGCCCAGGG CTGCATCTGC 180
AAAGGGACGT CAGACAAGTG CAGCTGCTGT GCCTGATGCA GGACAGCTGT GCTCTCAGAT 240
GTAAATAGAG CAACCTATAT AAACCTGGAT TTTTTTTTTT TTTTTTTTNN AAAANCCCTG 300
NCCNNTTGT AAAATTTTTT TTTNNNTGAA ATANGNAANG GNAATAATTN ATCNGGNNTN 360
TTN 363
```

SEQ ID NO:1037

LENGTH:288

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01176

SEQUENCE DESCRIPTION:

```
GATCTTGGA AGCACTAGAA ACTAAACATC TTCACCAGGT GCTGAAGAAA AGTGTCTTCG 60
TTTTAATTGC CAAGCAGGGA TGTGGACATT TGGATGGTGA CTTTCCTGGG TGGTTCCCCA 120
TAGATTACCA ATTGCCTCTA ATGGTGTCTA CACCCGTCAT ACTACCAGCT GAGATGGTGG 180
TGGGCATAAG GAGAATTGT GCCTATAACC CTTAGTGTGT TCTGGTTTTT TTTCTTTTAA 240
TTTTTAAATT GTCGTAAAAT ACTCATAAAA CATACTGTCT TCACCAAA 288
```

SEQ ID NO:1038

LENGTH:288

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01177

SEQUENCE DESCRIPTION:

```
GATCACCTTG TAGTCTTTAA ATTCTTGGTC CCTGAGGCCA AGTCCACAAC TTGCCTTCTA 60
GTCACCTTGC TGCCCGCAGT GGTGGTGGAT GTGTTAGCTG GTAGATTGG AATCAGTCAC 120
CAGTCTTTCT GTACTGTCTT GGTTAGCTCT ATATAAGTAG GGGCAGCTTA GCCCTGAGGC 180
CCAGAGACCT GCTGTCTTTT TTCTCCTTGA GGGAGGAAAT AAAACTGCGG AATACAATGT 240
```

CCTTCCATAG CATGGGAAGA AGAAAATAAA CATCTCCTTT CCAACAAA

288

SEQ ID NO:1039

LENGTH:288

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01178

SEQUENCE DESCRIPTION:

GATCCACCCT CCTGTAAATA TGGAACAAAT ATCTGAATGA AATCCACCCT AGGAGACGGA 60
GCAAACTAAA CTTGTGGTTT TNCATTTAAC TTTTGACTAC AGCATGGCCC CATGGCATCC 120
ACACCAAGAG GGTGTTGTGA TGAGGTGCCG GTGTGCAAAG GGAACTTAG TTTTCCACT 180
GGTTCTTATC TGCTAGCCTT TTACATACAT GTGTACTATA TTTGTTTATA GACTGTAGGT 240
GGATATATAA TTTAAAAGCT TGATTTAATA AACATTTAAC CCCNTAAA 288

SEQ ID NO:1040

LENGTH:287

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01179

SEQUENCE DESCRIPTION:

GATCTTCAAG TATTTGCNAC TTTCGAGTAC AGCTAATTGG ATAATCTCAA ACCCTTTAGT 60
GAAAATATCT TAAATGCATT GAGAATATTT CCTAATTACC TGTGTATGCT ACAGTACAGA 120
CATTAATTCT ATAAACATGT TCATAGGTCT TCCCCCTCGC CCCGNCCTGC TTCTAAGGGC 180
ATTTCTGTT TCTNTNAGT GAGTTCATGN ATGTTTACCG GTTCTGGCGN AANGTTTCTT 240
GCATNCTGAG CATAAAAATA NTAAACCNA CTGATANTTG CTTGAAA 287

SEQ ID NO:1041

LENGTH:289

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01180

SEQUENCE DESCRIPTION:

GATCTGCACA CGCATAATAA TCAGCATTGA GGGCAACAAA ATGCCATTGT GACCTTGCCT 60
GGAATGTGTC CCCATCTCTA CTCTAAGAAA TGCGCAATGG ACTCTTTGGA GAAAGAAGAT 120
ATTTTAAAAC ATTTTATAGT TGTCTGTAAG TGGTTCAGCG TGTATCAGAT GTTGTCATAG 180
GACTCACATT TCTCTCAGTT ATATTTAAAA CCGTTGTGTA CTTGTACAA NGGAATACTA 240
GTCATACTTC TATAAACTTT NCACAATAAA ATTNTCATTG TGGGTAAAA 289

SEQ ID NO:1042

LENGTH:287

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01181

SEQUENCE DESCRIPTION:

GATCGCACCA CTGCACTCCA GCCTGGGNAA CACAGTGAGA CCCTCTCTCA AAATAAATAC 60

AGNCAGGCAT AGTGGCTCAT GCCTGTAATC CCNGCATTTC GGGNGGTAGA GGTGGGTGAA 120
 TCACCTGAGG TCAGGAGTTC ANGCCCAGCC TGGCCAACAT GGGGAAACCC CATCTCTACT 180
 AANTATACAN AANTTAGCCA GGTGTGGTGG CCTGCACCTG TAATCCCAGC TACTCAGGAG 240
 GCTGAGGTAG CTTGANCCCN GGAGGCANAN NTTGCAGTTA NGCCAAN 287

SEQ ID NO:1043

LENGTH:286

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01182

SEQUENCE DESCRIPTION:

GATCTCTCCT GGAGTATGAA GACCTCCAAG GACTCACTTT CCTCCCTTC TGATGCCAGA 60
 GCAGACCAAG CTGTCACT CCAGTCTCAT GCTGAAGTCT CCAGCTTCTC AAGCTTAGAA 120
 GAGTTTTTNG AAGAGTCACT TTCAGCTCAT GCAGCTCTCA CAAGTGTGAA GGGAGTGGAT 180
 TGGGGGTGTT TTCCTTGCCA TTTTCGAAAA GAAAAAAATT ACCTGGTGAT TGGTGGAAAG 240
 ATACAACTGT CAAAAATGCA TGATTGAAGC AATTTAGGTT GGGAAA 286

SEQ ID NO:1044

LENGTH:286

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01183

SEQUENCE DESCRIPTION:

GATCAATAAA TNATACCAAA TATATGTTA CAGTATGATT TAAAGTCTGA TTCAGACCAG 60
 GGACTCTATT TTAAGTTCAA CTGAAATAAC ACTGGGTTTT AATTATATCA CAGGAAAAAA 120
 AAAGTGCATT TAAGTATTGT NATCGTGGAC TTTATAAAAG CAAAGGAAAT TGAAAGTAAC 180
 TTTNGATTCT GTATCANGAA TCATATTNC ATACAGTCAT AACTGTCTTN CTGTGACCCT 240
 TTCACAGGGC ACTGTAGGAT GGATTAAAGG TGGCAATTA CTGAAA 286

SEQ ID NO:1045

LENGTH:439

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01184

SEQUENCE DESCRIPTION:

GATCATACCG GTAAAGCAGG AATNACAAAG CTTGCTTTTC TGGTATGTNC TAGGTGTATT 60
 GTGACTTTAA CTGTTATATT AATTGCCAAT ATAAGTAAAT ATAGATTATA TATGTATAGT 120
 GTTTCACAAA GCTTAGACCT TTACCTTCCA GCCACCCAC AGTGCTTGAT ATTCAGAGT 180
 CAGTCATTGG TTATACATGT GTAGTTCCAA AGCACATAAG CTAGAAGAAG AAATATTTCT 240
 NGGNGCACTA CCATCTGTTT TCAACATGAA ATGCCACACA CATAGANCTC CACAGCATC 300
 ANTTNCATTG CACAGACTGA CTGTNGTTAA TTTNGTCACA GNGTCTATGG ACTGANTCTA 360
 ATGCTTCCNA AANTGTTGGT TTGTTGTCAN GTTTTCGANC CGTTGTTATG GCANGANGTT 420
 NGTTTAGTTT CNGNTTGTN 439

SEQ ID NO:1046

LENGTH:285

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01186

SEQUENCE DESCRIPTION:

GATCTGGAAG CAGTTGAAAA CGAGACAATA TAGCCGGAGA CGCCTTATAT GATGATGCAG 60
TATCGACTAC ATTAATGAAA GTAATGCCAA ATNCAACAAG AAAGCTGAAG ATTCTATGGG 120
AATACACAGC TGAATTAACA GATTGGAAG AGAACANCTG NTAATCCTTC AGGACTGTTA 180
TAGAGTTNAG ATGGGTAAAT TCTCCTANAA ATCAAGTCTT TTGAATTTC AGAATCAGAN 240
TTAGAGCCNG CTCTACTAGA TTGNATAANT GNGGTCTAAC GGAAA 285

SEQ ID NO:1047

LENGTH:285

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01187

SEQUENCE DESCRIPTION:

GATCCGGGNG GACCCCTTTG CCCTTCCCTC GGCTCCCAGC CCTACAGACT TGCTGTGTGA 60
CCTCAGGCCA GTGTGCCGAC CTCTCTGGGC CTCAGTTTTC CCAGCTATGA AAACAGCTAT 120
CTCACAAGT TGTGTGAAGC AGAAGAGAAA AGCTGGAGGA AGGCCGTGGG CCAATGGGAG 180
AGCTCTTGT ATTATTAATA TTGTGCCGC TGTGTGTG TTGTTATTAA TTAATATTCA 240
TATTATTAT NTAATACTTA CATAAAGATT TTGTACCAGT GGAAA 285

SEQ ID NO:1048

LENGTH:283

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01188

SEQUENCE DESCRIPTION:

GATCGAAGTG ACAAAGTGTG TTTTCANTCA CAGTGGAGGC TACATCAAGC AAGGGGAGGT 60
CCAGCCCTCT TGCAAGTGTG GTGAGAGGCT CTACTAGCAA AGACATGGGC ACCGGAGTAG 120
GTCCCGTGTA GCATGCCGGT GCTGTAGAGA AAATTCAGTG ACGTACATGG CTCTGGTTCT 180
GGACACAAAA TCTGTACTGG AGAGGAAATG ACTGCTGAAA TAAGGCGATT GTATGAATAT 240
TTAAAATGCC TGGAACACTA AAGTAAAGTA ATGATATTTC AAA 283

SEQ ID NO:1049

LENGTH:283

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01189

SEQUENCE DESCRIPTION:

GATCCTCGCA GCTTCCTNCG AGCGGGGTGT CGCAGTCTTG TGCACAGAGT AAACCTTNC 60
AGCTGCCCCCT TTCTGTAATA GTGAAAGTTG GTATTTAACA TTTATNCATT TTTAAATAT 120
TTGGAAGGTC TGANCTTGTG AAAAGAAAGT GGTGGNCTG AGGTTGGAGG NAGCTGAATG 180
GAATCTNACG GTTGGNAGTG GTGGAAATTG GAAGGATACC AGGAGGTATT TGGGAAGGCC 240

AATGGCGTGG CTCCTTTGAG GAAATAAAAC ACTAAGCATG AAA

283

SEQ ID NO:1050

LENGTH:281

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01191

SEQUENCE DESCRIPTION:

GATCCTTTTC ATACCTNATT TGAATTGCT GGATTGTAAC TTTGGNAGA AGAACAGATT 60
 AAACCTGTTA ATCCTGTCTT TTGCATGCCT GAAGAAGTGC TTCAAAGAGT GAATGTTTCAG 120
 CCTGAGCTAG TGAGCTAGAT TCATTGAATT GAAAGTTGCA TAGTATAGTT TTGCCATTTT 180
 AACATTCTG TATTTNAAGT GCTTATCGAA TCTAAAAGTG ACTACTGTNA ATATTNNGTA 240
 TATNGTGTNA AATTAATTNN ANTAAATNAT ATAATTNTAA A 281

SEQ ID NO:1051

LENGTH:226

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01192

SEQUENCE DESCRIPTION:

GATCAATGAC AGAGCCTTCT GGAGGACATT CCAAGACAGT ATACAGTCCT GTGGTCTCCT 60
 TGGAAATCCG TCTAGTTAAC ATTTCAAGGG CAATACCGTG TTGGTTTGA CTGGATATTC 120
 ATATAAACTT TTAAAGAGT TGAGTGATAG AGCTAACCCCT TATCTGTAAG TTTTGAATTT 180
 ATATTGTTTC ATCCCATGTA CAAAACCATT TTNCTTACA AATAAA 226

SEQ ID NO:1052

LENGTH:277

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01193

SEQUENCE DESCRIPTION:

GATCACAGCA TAAAAGAATC ATAAGATAAA ACATCAAACCT ACCCAGCAAC CTGAGAAGCA 60
 CAGAGTGTTA AAGCCTCCAC CGTGTGAGAA ACTAAATTAG GGTAAGTAGC TATTGAGTAT 120
 ATTGAGTACC TTCAAAGCAC TCAACTGACA GGTTTTACAG ACTGGAAATT ATAATACTTA 180
 TGACATTTCT ACCTTTTATA TAACCAATAA TCTACCATAG AATGTAGTAT TTTTANAGCT 240
 ATTAGCANGC AATATATTAN NNTANTANTG NATTAAG 277

SEQ ID NO:1053

LENGTH:277

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01194

SEQUENCE DESCRIPTION:

GATCCAACCC GAATAAGATT AGAAGCTTTC CATCAGTAAA AGGATGTTTT CTTTTTTCAC 60
 ACAGTAAAAA TTCTTATCAT TCAAGGATAT TGAACCACA GGACTATTTG GATAAAAAAC 120

ATTATTGCA AATTAATGCG CATAGGCCAT CTTACTTTTA TTGCAAAATG GCATGTGCTG 180
 CCATCTATTA TTCATTTTAA AATGGTCATT TCTTATTCAG TGAGTGCTTT AGTGTTTAA 240
 ACTATATGGA TAAGAATGCA GGTAGGATAA TATTCTN 277

SEQ ID NO:1054

LENGTH:283

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01195

SEQUENCE DESCRIPTION:

GATCCTGAGG ATTACAGCTG TGGAATTTT GTCCATGCTT CAAATAATTT TGAAAGAAAT 60
 TTTCCCATAT NAAAAAAGGA GAGAACACTN GCATCTGTG AAATTTGGAA NTTCTGAAAT 120
 NATAGTATTT TTAATAATTG CACTGAAGTG TATACACATA AAGCAGGTCT TTTATCCAGT 180
 GAACAGGATG TTTTGCTTTA GCAGCAGTGA CATAAANTTC CATGTTAGAT AAGCATNTGT 240
 TNACTTACCT NGTTATTAA TATTNTTGG AAAAGCAGTG AAA 283

SEQ ID NO:1055

LENGTH:277

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01196

SEQUENCE DESCRIPTION:

GATCTGTGTA TGCTGTTGGG TCGGAGTGCC AGTNACTGCT TTGGAAGTCT GNGTTCTGGG 60
 GCTGCAGAAT GACAAACGTG TCATGGGATT AAAACCAATC AACTGTGAAT TGTGAAATTG 120
 AAGCTACTCT TTCGGTTTTA TTTCTTTAG CATATTGAGT ATAGAAATCT GAAACTTATT 180
 TAAATTTAT ACTGCTTTTG TTGATGGCTC ATTTGGGCTG TGTATCCTCA CTTATGTACT 240
 GATTTCTGAT AAAGGCTTGA CATTATTATA ACANAAA 277

SEQ ID NO:1056

LENGTH:103

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01197

SEQUENCE DESCRIPTION:

GATCGACCTT NTCTGTTTTN TTTGTTTTN NTTCTNTTT CCTGGCCATG AGGACAAAAA 60
 TTAGTGAGTG GCCCTTAAAG AGGGAAGTTT GTTTTCAGCT GTN 103

SEQ ID NO:1057

LENGTH:291

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01198

SEQUENCE DESCRIPTION:

GATCGACCAC ATCCTGGATG CCCTGTAGCC CCTGCCCGCA TCCTCCAGGG GGCCAGGGT 60
 GCCTGCACTT TNCTGTGGCA GGCAGATTGG GTGGTAGTGG GAGGTTGTGC ATGGAGGCCA 120

GTNAAAGCTG ACATCTGTAA AAGGCCTTCA AGGAAGAGAA ACCAGGCCCT GCGTCAGGCA 180
GTGTGAGTTT GCCGTTTGTG CTTAACTTTC TTTTTTTTTT TTTAAAAAAN GGAAANNTTT 240
AAAAAANCTC CCTTTAAAC CAAANCAATNT TTGNNTTNN NCCAAGGGAA A 291

SEQ ID NO:1058

LENGTH:276

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01199

SEQUENCE DESCRIPTION:

GATCCCGCTC TGTNTTTTCC AGGTTTGTGC TATTCTNATT ACATTATCGA CTAGTCTGAA 60
GCAGAGCTGA TATCTCTTTA CCTGGGGAGT CAGCTTCACC AGCCACAGCT GCTGAAAGAA 120
TAGCTTGGAG ATTCACCCA CTGCATTCT GTNGCTCAAA CTTTTTGACC TTTGTGCTAT 180
TTGAGAAATC TTTGAAATGC TGAAGGTATG ATTCTCCTTC AGGGGGAACA TGCTTTGGGA 240
AAAACGCCCA CTTAATAAAA TGTATTCNT TTCAAA 276

SEQ ID NO:1059

LENGTH:276

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01200

SEQUENCE DESCRIPTION:

GATCTGTATA TGGTAAACAG GGGTTTAACC ACATGTGGTT AACATGGATT AATGTGGGAN 60
TTTGGCTTCA AGAACACAAC CTTAGGACCT TGGNCCCCAA AAGCTGGTGG TGAAATGAGA 120
GGNGCCAATT TAAGAAGACC CTTATGGAGA CCTGAGGCTG CAGAACTGG TAGGTTTCAT 180
CAGGTGGTTA AAGTCGTCAA AGTTGTAAGT GACTAACCAA GATTATTTC TTTAAAACC 240
ACAGAATAAA AATGACACCT GAGCTTCTCT NTNAAA 276

SEQ ID NO:1060

LENGTH:276

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01201

SEQUENCE DESCRIPTION:

GATCTAGTTC CCCTGGAAAA GCTGCTGTAT TTTAATTTT TAATGGAATG TAGCTTTTNN 60
AATCCTGTCA CTGGCATCAA CAAAAGGAAT TATACCATGA GACCTTATAG CTGTACTTAA 120
AAGCCATTCA GTTCAGCTAT TGGGAGTTCA TGATGAATTA GCATATGCCA GAAAGGTTGC 180
TAACCTTAAC ATCTGAGAGC AGTAACACTG ATTTTATCTG CTGTATGAGA CTTTGTGCAT 240
TTTACTTTGA AATAAAGATT TTTTCCACA CTGAAA 276

SEQ ID NO:1061

LENGTH:276

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01202

SEQUENCE DESCRIPTION:

GATCCTGTTT CTNGCTCTGA GTNCTAGCTA GCCAGCTGTN TTCACACTGT AAACATTCAT 60
 CAAGCTGTAC ATTTGGTGCA CTTTCTGTG TCATACCACA ATAAAAAAAA NCCTATCATC 120
 TTACAAAAAC AAGACACCCA AGTCCAGGCC CAAGGAGTAA GTACAAATAT TCCTGTTTCT 180
 GANCCATTAC TGTAATTGGC TCTNAAGNCT TGAGGTANCC TTATAGGTTA CTCATAGGGC 240
 ATATACAAAT AAACNGTTT GTTTCTTTT TNCAAA 276

SEQ ID NO:1062

LENGTH:275

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01203

SEQUENCE DESCRIPTION:

GATCTTCAAC GGATACTAGA AAATGAAAAA GACTTGGAAG AAGCTGAGGA ATATAAGAA 60
 GCACGTTTAG TACTGGATTC AGTGAAGTTA GAAGCCTGAA ACTTTTCTCG TATGGGGTGG 120
 TTTTGCATT AAATCCTGGG GTCCATTTA CAATCCATTA TTTTGACCA CTGCTATGTG 180
 TTCAAGTAGT ATGAGAATGT GATTGTTTTT ATCTGGTTAC ATATATATTT CTTTGTCTAA 240
 TTTAATATGT CAAATAAATG AGTTCATCTA ATAAA 275

SEQ ID NO:1063

LENGTH:274

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01204

SEQUENCE DESCRIPTION:

GATCTCACCT CTCCTCAGG ATGGGGAGCT CACTCCGAGA ACAGGAGAAA TCAACATTGC 60
 AGTAACAAGG TAGAATGGTT TTGAAGAAGA AAAAACCTGC TTTCTGACTG ATTTTGCCCT 120
 GAAGGAAAAA AGAACCTATT TTTGTGCATC ATTTACCAAT CATGCCACAC ANGCAATTTAT 180
 TTTTAGTACA TTTTATTTTT TCATAAAATT GCTAATGCCA AAGCTTTGTA TTAAGAGAAA 240
 TANATANTAN AATAAAAAGT CTGTGCTGTT GAAA 274

SEQ ID NO:1064

LENGTH:274

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01205

SEQUENCE DESCRIPTION:

GATCCAAGTT CCTAGACCTC ATGGCTGTCC CCTCCCACCA GTCACCTCCA CTGCACAACT 60
 CGGGCGGGGG TGTGACACCT CTCCCCACC NCCGACTCCG TGTTTCCGT ATCGTCAACC 120
 CTTAGCCGC CGACCCGGGA GGGGTCTGGC CTACACTGGT CTTCCCTTC CCATCAACTC 180
 TTTCTGCTTG ACAATGTAGC AACCAGGCC CCCACCCAC GGTCTCTCCC TTTTCTCTCT 240
 CCCTGACAAT AAAGTCTGAA TTTGTTCTGC NAAA 274

SEQ ID NO:1065

LENGTH:269

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01207

SEQUENCE DESCRIPTION:

GATCTATCCA TCCAATGTTG TCATTATATT TGACTGTGGT TCAACAGTAT TCGGTTGTCA 60
GACTAGGAAA GTTAAACGAA CAAAATGGTT TTAGTTTTCG TGAAGACTGG CCTTATTAAT 120
GGACAGCTTT CCTAACAAGA GATTATTAAC TTTTATCAGG TGTTAACATC TGTTTCAGGA 180
ACATGGCAGT ATGTTTACAT GTCAGAAGTT TTGTTTAATT CTATGGTATT TCTAAATTGA 240
CTTGTTTAAA TAAATTCAGC AAATGGAAA 269

SEQ ID NO:1066

LENGTH:269

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01208

SEQUENCE DESCRIPTION:

GATCTGGTTG GCATTTTCTC CCTGATGATG GGAGCGTCAT TCTTTTGTCT TCATGGTTAC 60
TTGTGTGATA TAACATACAT CTGTNAAAGA AAATCACTTC TTTCTAGGGG AGGGAGGTAG 120
AAAAGTATCT TTCAAACCTG GTTTTNNAGT TTGTNTCTTG TCTTAACTTT GTGTNGGCTC 180
TAACTNAAAC ATGCTGATAT GTGTTTNCAN GANTTTTGGT TTAAGGANGT ATTGTATGGA 240
NGTCCACANA TTGGNAGGTN GTTCATCTN 269

SEQ ID NO:1067

LENGTH:269

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01209

SEQUENCE DESCRIPTION:

GATCGATTAA GGAAGGTGGT TATGGCTGGG TGGTTCAGGG GTTTTTTTGG GTTTNTTTTT 60
TTTTTCTTT GTCTTTTNA CCTAAAGCTG TTAAAGTTGA AGCATTCTNA GATGTTTGGG 120
GGGAAACATC CTCTNAAAT GGGNCCTGT GCTTGCNTTC TGGGGAGGCG GTCCTGAGCA 180
GGTGANTCAT ANGGCATTTA TGCATATGTN ATATGNGGAC TGNACCCACC TTTCCCCCN 240
AGCCTTTGCC TCTTGGGTTG TTGTNCTGN 269

SEQ ID NO:1068

LENGTH:268

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01210

SEQUENCE DESCRIPTION:

GATCCTCTTT GTTTGTNCAA AGGACCAGTT TTCCTAGGCC AAAGAAGTCT CTNCCCCATG 60
TAAGNCCTAT GCCTTNAAT ATCATGCACC ATGACCACA GCCATCTGGT TATGTCTTAT 120
TTTTTCTTA AAAGATAATG TTTATNNTTA AAAAGGAAGG ANGGAGCAAG TGAAGTTTCA 180
TTCTGCTCCA GCGGTGGGGG ANGCCGCTGA ATCCACCTGN TTCTCCTTTT GCAACCGNCA 240
GCANGCAGCT TTTCTCCGGG CNNCAGGN 268

SEQ ID NO:1069

LENGTH:267

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01211

SEQUENCE DESCRIPTION:

GATCTAGAAG GTGAAGAATT TTTTATGTA TATATAGACA TATCTATATA AATNGTCTGG 60
CTGAGGCAGG GCCTTCANCT ATCATTGGT TAATAAATAC ATTNAGTAT TTNCATTTC 120
TACTGCCTGC AGAGTTTCAG GTGCTGTNG TGTGAAAGTC CTGTAGATGT GTGCAAATTT 180
AACGAAATGA AATTGTATGT GTAAAANTGT ACGATTTTCC ACTGTGCAAC TGTAATNAT 240
AAATAANANA TATTTTNTCT ATCAAAA 267

SEQ ID NO:1070

LENGTH:266

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01212

SEQUENCE DESCRIPTION:

GATCCTAGTG ATTCAGCCC ATGCATTAAG CAGGAAACAA TAATAAATTT GTAGAATTCA 60
TATTTTCTA AAGGGAACCT AAAAAGTCT GCTACATGTT ATGTACAAAA CTGGTTTATG 120
CCACATGGAC AGAGAATCAC ANGTTTGGTT TTGGTACTTT NNGTTCCTCT TTGTATTGAG 180
TTGTATAGAC CTNCCAAATT CAGAATGAGA NGAAAGCTGT CTGTATCAAA CCATTANGC 240
ANTAATTGTT ATATNTNANA GCTAAA 266

SEQ ID NO:1071

LENGTH:266

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01213

SEQUENCE DESCRIPTION:

GATCCAAGTT ATACATGAAT AGAAAAAGAT GGTGTTAAAT TTGTGTGTAG GCTGGGAATT 60
CTTGCTGAAG GAATTGGAGA AAACCTGTTG CTGCAAAATT TTACATGTTT CAGATGGAAA 120
GGGAAGTCTA AGCNCTTTTT AAAACAATTT TTTTGTGAT TTAATTAAGC AATTNCAGTT 180
ATCTGGGATT TTTGGGTCAG AATTTTAAAT TCTGTTTGAT TCTCCATATT CCAGTNAATA 240
AAATACAAAA GCATTGTNTT TTTAAA 266

SEQ ID NO:1072

LENGTH:265

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01214

SEQUENCE DESCRIPTION:

GATCTTCAAT TCCTTGAGTC TGAGCTTGTG GGTGGAATTC TAAATTTGTA TCATAATCTG 60
TCTTTTGTGA AACATTTTGA AAATATGTAT ATATAATATT GTATATGCAA ATTGTGTTGT 120

TTCACCTGTA AAGGGAAAAG GCTTATTTN CTTTATATTT CTGATAACTT GTTTTGCATA 180
 TGACCAGCAC TGACTGAAAG GCATGTGTAG CTGCAAACAC TGTGCTTTT TTTGTGAAAT 240
 GNAATAAAAA GTATTAAAT ACAA 265

SEQ ID NO:1073

LENGTH:265

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01215

SEQUENCE DESCRIPTION:

GATCGTGCCA TTGCACTCCA GCCTGGGTGA CAAGAGCAAA ACTCCATCCC CCTGCCCCAA 60
 AAAAAAATN AATTTTACA GAAAATTAAT AGCATAGGTA TTATNATCCT CATTTTACAG 120
 AGAAAGAAAC AGCCATAGAG AAAAATGACT TGCTCACAAC ACAGGCAACT TTGACTCTAG 180
 AGATANCACT TATTACAGTA AAATCCCTCT TCAGNCACAA AATACATGAT TATCTTAAAC 240
 ACATTCTTAA TAAAANTTTA NCAAA 265

SEQ ID NO:1074

LENGTH:268

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01216

SEQUENCE DESCRIPTION:

GATCAAAGAT TGTAATAATA ATTTTGTAAG TTGTAAGCAA AAAGTTATTT TTATATTATA 60
 TACAGTCTAA TTGTTTCATCC TAATTGTTCC TGTTTTCATC TAGTCAGAGA TTCAGTAAGT 120
 NCCTTGGAAC AATATTGAAT TCTCTTAGCT TGTGTGTGTT TCTTTAATAT TTGAACTCAA 180
 GTGGGATTAG AAGACTATNA NNNTACATGT ATGTTTCAGG ATATTTGACC TGTCATTAAT 240
 AAAACAAAC AGTTTACAG TGCCTAAA 268

SEQ ID NO:1075

LENGTH:305

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01217

SEQUENCE DESCRIPTION:

GATCTCCATG TAGTCCATAT GAAACCTGCA GAGTGATTTT CCAGAGTGCT CGATACTGTT 60
 AATTACATCT CCATTAGGGC TGAAAAGAAT GACCTACGTT TCTGTATACA GCTGTGTTGC 120
 TTTTGATGTT GTGTTACTGT ACACAGAAGT GTGTGCACTG AGGCTCTGCG TGTGGTCCGT 180
 ATGGAAGGCC TGGTAGCCCT GCGAGTTAAG TACTGCTTCC ATCATTGTT TACGCTGGAA 240
 TTTTCTCCC CATGGAATGT AAGTAAACT TAAGTGTTG TCATCAATAA ATGGTAATTC 300
 CTAAT 305

SEQ ID NO:1076

LENGTH:263

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01218

SEQUENCE DESCRIPTION:

GATCCTGTAA GTTGTCACTA AAATATGATT TAGAAATATT GGCCAAGGTG TTGCTTTAAC 60
 TGAGGAGAAA AGAAAGCACA CTGCCTAAAT GTGTAAAAGA AAAATGCAGA GGTTATTAAA 120
 ATGTAAAGAA GTAACAATCT TTGGATTTGT CTATACATAT ATATATATAT ATATNGNTTT 180
 GCCTTAATAT ACCCCCTTTT TTGTTTGTGA CTTTCAACTG TAATCAGTTA ATAAAGTATT 240
 TATTCTCTGC ATTCAGGTTC AAA 263

SEQ ID NO:1077

LENGTH:354

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01219

SEQUENCE DESCRIPTION:

GATCGACAGC AAGCAATCCT TAAGGGACTT TCAGAACTGA GACAGGGCCT TCTCCAGAAG 60
 CAAAAGGAGT TGGAAAGTAG TCTCCTGCCT TTAGCTGAAA ATCAAGAAGA GAGTTTGGT 120
 TCTTCATTTT AAATGTAGAA AATCAAATCC TTCACATTG ATTTGTGTCT TCCAAATTAT 180
 AAAATGTGCT CACTGGCTCA ACTGTATTTT TCAAAATAGCC TAGATTACT TATTTTTTTA 240
 ANNGNNCATT AAAAATTGT ATACTATGTA GTAAAATGCT GTAATTGTNC TATACAATAA 300
 ANCAGATACT TCTTTTGTA AAGCTTAGTA GTAAAACNCC ACCNNNNNN NNTN 354

SEQ ID NO:1078

LENGTH:260

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01220

SEQUENCE DESCRIPTION:

GATCGTGCCT GTGAATAACC ACTGCACTCC AGCCTGGGCA ACATAGTAAG TAAGACCTTG 60
 TCTCTTAAAA AAAATACATT CTGAAGAAA GTTACTTAT GANTACATT TATTTATAAC 120
 AAATGGTGA AAATTTTAGA CCAAAACATG TCTTCTGGG TTGTAGTGAT TAAAAAATGG 180
 TTAAGAGAAT GTTCCCTATA CAAGGCATAT GTTATTAANC ATGAAATTGA GGNTTAGTTT 240
 TCTCTTTGAA NNTCCTTTN 260

SEQ ID NO:1079

LENGTH:260

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01221

SEQUENCE DESCRIPTION:

GATCCCGAGA CTTGTGTTCT CTTGGCTGAA NACACTNAGG TGCTCCCATC TGTNCGTGGC 60
 CCATGANCTG GGATGGTCCT CCAGCTGCCC ACAAGGTCCG CCCCTCTNC TCTGCACCAC 120
 CTGTTTGCAT AAACACACTT TGCTACAATC TTGCTAGTNC GTTTTCTTAA AAGATAATCT 180
 ATTTACTGTA AAAATAAATT GGACTTTGCA AAAGCTTTTA GAAGGAAAAG AAAGAGGATT 240
 AAAGAGAATT GCTGGTGA 260

SEQ ID NO:1080

LENGTH:259

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01222

SEQUENCE DESCRIPTION:

```
GATCCAAATT TCCTTTTGAT ATTATTTTAC TTCTGCCTGA AACATTTTCT TTAACATTTT 60
TTATAGTGTG GTTTTACTGG TGATGATTTC TTTCAGGTTC TAAGTGCCTG AACAAAATCT 120
TTATTTCAAC TACATCTTGA AAGATAGTTT CTCTGAGTCT ACAATCCCA GCTGACAATG 180
TTTATCTTCC AGTACTTTAA AGATGTTGCT TCATTATCTG CTAATTNNT TTGTTTCAA 240
TAAATGTTT GCTGGCAAA 259
```

SEQ ID NO:1081

LENGTH:316

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01223

SEQUENCE DESCRIPTION:

```
GATCTGCGGT GAAGCCAAGC CGCAAGGTTA CAAGGCATCC TCACCAGGGA TACCCGCTG 60
CTGCTCCCAG GTGGCCTGCG GCATNGCTAT GCTCAAGGAC CTGGAACCC ATGCTTCGAG 120
ACAACGTGAC TTTAATGGGA GGGTGGGTGG GCCGCAGACA GGCTGGCAGG GCAGGTGCTG 180
CGTGGGGCCC TCTCCAGCCC GTCCTACCCT GGGCTCACAT GGGGCCTGTG CCCACCCCTC 240
TTGAGTGTCT TGGGGACAGC TCTTCCACC CCTGGAAGAT GGAAATAAAC CTGCGTGTGG 300
GTGGAGTGT AGGAAA 316
```

SEQ ID NO:1082

LENGTH:259

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01224

SEQUENCE DESCRIPTION:

```
GATCCAAATG GATTACCAGT GTGCTACAGA CTTCTTATTA TAGAACAGCA TTCTATTCTA 60
CATCAAAAAT AGTTTGTGTA AGTTAGTTT GGTACCATC TAAAATATTT TAAATGTTC 120
TTTACATAAA AATTTATGTT GTGTTTTAAA ATCCTTAGGG GCTTTATCTA TTTTCTAAG 180
TCAGTAACT GTACTTCTAA AAAAAGTATT TTGTATCTAC TTTTGTAAC TCGTCAGAAT 240
AAAATATATT GAANGCAAA 259
```

SEQ ID NO:1083

LENGTH:258

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01225

SEQUENCE DESCRIPTION:

```
GATCGCTTCA CATNTATAAA AAAAATAANA ATACCCGGGC AAGCTTTCTT TGAAGNTGCT 60
ACAGCATTA ATATCGAGAA TTTTGGGTGG GAGAGAGCAG TTCAATTTT TTTACCAGCT 120
```


GAAGTTCATT TATGATACAA AAGAGATGAA ATGGAAGTGG CAATATAAGG GGATGAGGAG 180
GCATGCTGGC AACCTTCTT TTAAGATGTG CTCAATTTGT ATAANTGGTG TTTCATGNAA 240
TAATCATCTT GGAGGAAA 258

SEQ ID NO:1084

LENGTH:342

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01226

SEQUENCE DESCRIPTION:

GATCGCCGCC CAGGGTTTCA CGGTCGCAGC CATCTTGCTG ACGTCTGNCT GNCACTGCTA 60
TGAAGTCTCG ACCCTAAGCC CAGGGTCTGG CCTTGAAAGC TCCGCAGAAA TGATTCCANA 120
ACCCAGGGAG CAACCACTGG CCCTACCGTG GGACTTACTC CCTCCTCTCC TTGAGAGGC 180
CCATGTGTCG CTGGGGAGGA AGTGACCNTT TGTGTAAGTG TAACCGAAAG TTTTTCAAA 240
AATCCTAGAT GCTGTTGTTT GAATGTTACA TACTTCTATT NNNGCCACAT CTCCCNTECA 300
CTCCCNTEGCT TAATAAACTC TAAAAATCCA CTTGTATTTA AA 342

SEQ ID NO:1085

LENGTH:260

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01227

SEQUENCE DESCRIPTION:

GATCTAAGAA GANACTAGCC TTGTGGAGTA TATAGATGCT TTTCATTATA CACACAAAAA 60
TCCCTGAGGG ACATTTTGAG GCATGAATAT AAAACATTTT TATTCAGTA ACTTTTCCCC 120
CTGTGTAAGT TACTATGGTT TGTGGTACAA CTTCATTCTA TAGAATATTA AGTGGAAGTG 180
GGTGAATTCT ACTTTTATG TTGGAGTGGG CCAATGTCTA TCAAGAGTGA CAAATAAAGT 240
TAATGATGAT TCCAAATAAA 260

SEQ ID NO:1086

LENGTH:256

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01228

SEQUENCE DESCRIPTION:

GATCCTTAAT GTTTTGATTN TTGTTTCTG AAATTGGATT TTATTTTATT TTATCTTATA 60
ATNNCAGTTC ATCTAAATTG TGTGTTCTGT ACATGTGATG TTGACTGTA CCATTGACTG 120
TTATGGAAGT TCAGCGTTGT ATGTCTCTCT CTACACTGTG GTGCACTTAA CTTGTGGNNT 180
TTTTATACTA AAAATGTAGA NTAAAGACTA TTTTGAAGAT TTGANTAAAG TGNNGNNGTT 240
TGCATTACAC CTCAAA 256

SEQ ID NO:1087

LENGTH:254

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01229

SEQUENCE DESCRIPTION:

GATCTTTAAA CTCTGGCTTC TTCCTCCTCA ATCTTGACAG AAAAAGGGTG CAGACGTCTG 60
GTTCAAAGAG TTGGATATCA AACTGATGG TGCAGTTAAC TTCCAGGAGT TCCTCATTCT 120
GGTGATAAAG ATGGGCGTGG CAGCCCACAA AAAAAGCCAT GAAGAANGCC ACAAAGAGTA 180
GCTGAGTTAC TGGGCCCAGA GGCTGGGCCC CTGGACATGT ACCTGCAGAN TAATAAAGTC 240
ATCAATACCT CAAA 254

SEQ ID NO:1088

LENGTH:297

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01230

SEQUENCE DESCRIPTION:

GATCCATCCC ATTCACCCAG TGA CTCTTTT TTGCCCAGGC CGGGACTTTT TGCATCAGTN 60
ACGTTAACCA GATGACTTTG CCTGTAACCA AACCTCATGC ATCCACGTTT GCGTCTGGGG 120
AGGAATAAAA AGACATCGTT CCCGCTTCTN CGTTTTGTNA TTCCTACTGC CGCCATAGGA 180
ATTATTTTCGT TGGCTGANC G TTACCAGCAC CCCGAGANCA CATTTTGATN GANTCAGAGT 240
AGAGGNCATG GCTGTNTTCT NAAAANGCCN CGCCATGNAA NTGCCAATCC CCTTTTN 297

SEQ ID NO:1089

LENGTH:253

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01231

SEQUENCE DESCRIPTION:

GATCGCATTT TTGTAAAAGA ACCATGTGTG TTTATATGTG TTTATATATA TACTTGTGTA 60
TGCAAAGGTA AAAGTCTGAA AGGATATATG CTAAGTGTTC ACAATGATAA CCCCCCAGGA 120
ATGGGATTGG AGGGGAGGGG GCTTCTGTGT TTGTNATGTA TGCTGGGTGG GANNITGTGC 180
TTTTATTCT ATATTGTTG AATTTTTTTA CAGTATGTAT TATTTTGTGA ATAAAAATT 240
TAAAAAATTC AAA 253

SEQ ID NO:1090

LENGTH:252

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01232

SEQUENCE DESCRIPTION:

GATCTGCCTT GAAATTTAAA AATCTAAATA GCTCTTAGTT GAACAGGGGA GATATAAACA 60
AAGTTTGCAA AATTCCTAAA ACACGATGAT AATAAACATC ATACATCAGA NTTTTGAGAT 120
ATAATTAAAG CAGTACTTAG AAGAAAATGT ATAGCCTTAA ATATTTAACA TCAGTAAAAAN 180
TGANAGGNTG AAAATTGGGA TTAAATTCC CAACTCAAAG AGCTAGAAAN NGANTTACAA 240
AGCAAGNNGA AA 252

SEQ ID NO:1091

LENGTH:251

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01233

SEQUENCE DESCRIPTION:

GATCTCATGG GCTTTCCTGG AGGAAAGTTT TTTTGTTCG TTTTITTTTA AGACTTGAAA 60
CTTGTAAC TG AGATGCTGTA GTTTTTTGCC ATCTGTAGTG ATGTAAAGAT TTAAACCTGA 120
GAGACTTTTN CTTGTGTTAGA TTATGAGAAG NACTAGATGC TTTAGGTTTC ATTTCCCTT 180
AATTGCNATT CTTGTGCCGT NGTTGGGNGG GAACTGTTAT TTTCCNCAAT AAAAAGTAAG 240
TCTTATCGAA A 251

SEQ ID NO:1092

LENGTH:250

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01235

SEQUENCE DESCRIPTION:

GATCATTAAA ATCAACGTTA TCTAAGACAG CTGTATCACA TTTTGGGAT ACATCATGGT 60
ACAGTCAGAA GCATATAAAA TTATGGTTCT GCTTGCAGN CNCATACAGA ATCCAATACA 120
TTTTGACAAA CTGCCCATTG CTGCAAGTTA ATGCCCTTTT TGAAGCTTCA TTTCTCTTG 180
TAAAGTACAG ATAGGAATCA TTATTTGTG GAGTTGCTGT AAAGATTAAN TAAAGGTGAA 240
TGAAAATAAA 250

SEQ ID NO:1093

LENGTH:248

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01236

SEQUENCE DESCRIPTION:

GATCCCAACA AAGATACAAG TGAAAACGCA GAAGGTCAAA GNGATGAGAA CAAGGACGAC 60
TATACAATCC CAGATGAGTA TAGAATTGGA CCATATCAGC CCAATGTTCC TGTGGGTATA 120
GACTATGTGA TACCTAAAAC AGGGTTTAC TGTAAGCTGT GTTCACTCTT TTATACANN 180
CNAAGAAGTT GCAAAGANTA CTCATTGCAG CAGCCTTCCT CATTATCAGA AATTAAAGAA 240
ATTTCTGN 248

SEQ ID NO:1094

LENGTH:248

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01237

SEQUENCE DESCRIPTION:

GATCACTGNC AAAGTGGGAG CACTAAGGGG TGGGTGGGGA AGTGAAATGT TAGGCGATGA 60
ATTCCTGAGC ACCTTGTTTT TNTNCCAAGG TTCGTAGCTC CTCNTGCCC TTCCAAGCCT 120
GTAACCTCGG AGGACTATCT TTTGTCCTTN ATCCTTTGTN TTGTTTGAGT GGGNCAGCCC 180
CAGAGGAACT GATAAGCAAA TGGCAAGTTT TTAAAGGAAG AGTGGAAAGN NCTGCAANTA 240

AAANNCCN

248

SEQ ID NO:1095

LENGTH:246

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01238

SEQUENCE DESCRIPTION:

GATCTCCATG CGGTCCCTGG AAGTACCCAT TGAAACATGC GTATTGTGT ATAGCAGAAC 60
TCTGAAATAA TATTCTGACA GCAGTTATCT CTGAGGAATT GGGTTATAGG TGATTTCCC 120
TTTCCGCATG ATAAATTTAT GTAATATTTG ACTGACTTGA CCGTAAGTAT GTTACTTGTA 180
TAATAAAAGG AAAAAAGGTA CTTCTATTTT GAAAAATAA AAATAAAAGC CTTGGGGTTC 240
TTGAAA 246

SEQ ID NO:1096

LENGTH:315

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01239

SEQUENCE DESCRIPTION:

GATCCTGTCA GGGNGTCCCC CATGCCTGGA AGAGGAGCTG GTGGCTGCCA GCCCTNGGGC 60
CCGGCACAGG CCTGGNCCTT CCCCTTCCCT CAAGCCAGGG CTCCTCCTCC TGTCGTGGGC 120
TCATTGTGAC CACTGGCCTC TCTACAGCAC GGCCTGTGGC CTGTTCAAGG CAGAACCACG 180
ACCCTTGACT CCCGGGTNNN NNGTGGCCA AGGATGCTGG AGCTGAATCA GACGCTGACA 240
GTTCTTCAGG CATTTCATT TCACAATCGA ATTGAACACA TTGGNCAAT AAAGTTGAAA 300
TTTTACCACN TGAAA 315

SEQ ID NO:1097

LENGTH:245

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01240

SEQUENCE DESCRIPTION:

GATCCCGGGA GCCTTGCCGC ACTGCCTTGT GGGTGGCTTG GCGCTCGTAA TTGCTTCCTG 60
TGAACGCCTC CCAAGGACGA GCCCAGTGTA GTTGTGTGGC GTGAACCTCTG CCCGTGTGTT 120
CTCAAAATCC CCAGCTTGGG AAATAGCCCT TGGTGTGGGT TTTATCTCTG GTTGTGTTC 180
TCCGTGGTGG AATTGACCGA AAGCTCTATG TTTTCGTAA TAAAGGGCAA CTTAGCCAAG 240
TTAAA 245

SEQ ID NO:1098

LENGTH:245

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01241

SEQUENCE DESCRIPTION:

GATCTGCAGC AGCCGAAAAT GCGTTNTGGT AAACCTGGCC TCAAATTCAT ACTACCATAA 60
 CTGTTTTTAT ATATTGCCAC TAATTTTGAC TGGATTAAAT AGCACTTTAT TGTACANCTA 120
 CAAAAAATAA TATATNCCTA GAATNGTNNC CAGTGTAATT CCTCTAATGT CCTGGTGCCT 180
 TTTCATATAT TTCCAGNATT TTNATACTAT ATNGGTATTT CCTTTGTATA AATNGATNGA 240
 TNAAN 245

SEQ ID NO:1099

LENGTH:251

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01242

SEQUENCE DESCRIPTION:

GATCTTAGGC TTTTCACTTT TTTTGTTTTG TTTTGTTTT GAAAGAAAGA AAAAAATACA 60
 ATTAACAAGC CTCTTTTGTA AATGGGTTTC CTTTCTATGT ATAAATCGT GGTGGTCCCT 120
 TGTTTTACA TGTTCATGCT GTGTAATTTT GAGATGTTAC TGAGATATGT TCTGAACATA 180
 ATGTGCATTT TTTNCTGTAC AGATGAAATG GGAGANTTTA ATAAAGAGTT TGCAGGTTT 240
 TNCTTGTTAA A 251

SEQ ID NO:1100

LENGTH:247

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01243

SEQUENCE DESCRIPTION:

GATCCAGCCC TGAGCATCAC CCAAGTGCCT GATGCCTCAG GTGACAGAAG GCAGGACGTT 60
 CCATGCCGAG GCTGCCCCCT CACCCAGAAG TCTGAGCCCA GCCTCAGGAG GGGCCAAGAA 120
 CCAGGGGGCC ATCAAAAGCA TCGGGATTG GCATTGGTTC CAGATGAGCT TTAAAGCAA 180
 ACATAGCAGT TGTTTGCCAT TTCTTGCACT CAGACCTGTG TAATATATGC TCCTGGAAAC 240
 CATCAAA 247

SEQ ID NO:1101

LENGTH:266

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01244

SEQUENCE DESCRIPTION:

GATCTTCCCT AAAGAGCAGN GGACCANATA NGAAGAGGAA AATTTCTACC TTGAACCGTA 60
 TCTGAAAGAG GTTATTCGGG AAAGAAAAGA AAGAGAAGAA TGGGCAAAGA AGTAATCATG 120
 TAGTTGAAGT CTGTGGATGC AGCTGTTATG AAGATGGTTA AACTTGAANC AAACAATTTT 180
 AAGANTTATT TNGTCTGAAN GATGTTTTAC TTAAATAAAA TGTCTCNTTG NAATGGCTGG 240
 AGGTTTTTGG GNGCCAAACC NTTAAA 266

SEQ ID NO:1102

LENGTH:256

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01245

SEQUENCE DESCRIPTION:

GATCCCAGGT CCCAAGGAGT GACAGGGGCT TCCTCCCACC TTCTGTCCTT GTCCAGTNAT 60
GTAAATAATG TGCTTTTCCT CTCCCCGAGT CTTTTTTTTT AAAACCTACC GTGGTTCCTN 120
AGCTAACTGC ATTCCTACC CAGGCAGAGA CTGTCCTATG CCTCGNGCTT CCAAACGAGA 180
CTCAGACCGC GACANAGCCA CCGTATTTAT GGATTGCCAA ANTAANTAAN GCCCAAANCC 240
ATCGGTCTCT GTGAAA 256

SEQ ID NO:1103

LENGTH:240

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01246

SEQUENCE DESCRIPTION:

GATCCTGGTG CTGGACAACG CTGCCATTGT CTGCAACTTT GGCAGTGAGC TCAGCCTGGT 60
GTATGTGCCC TCTGTGCTGG AGAAGCTGGA CTGAGCGCAG GGCCTCCTTG CCCAGGCAGG 120
AGGCTGGGGT GCTGTGTGGG GGCCAATGCA CTGAACCTGG ACTTGGGGGA AAGAGCCGAG 180
TATCTCCAG CCGCTGCCTC CTGACTGTAA TAATATTAAA CTTTTTAAA AAACCATAAA 240

SEQ ID NO:1104

LENGTH:245

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01247

SEQUENCE DESCRIPTION:

GATCTGGGCA GTNAGATAGT GCTCTATGCC TAAGGTGAAG CCACACTAGG NTGAAGCCTC 60
ACTTCCCTGT TTAAGCAATG CAGTGCCTGC TGCCCGTGTG CANGAAGTA CAGCCATTCA 120
GATAAGTGGA ACTATTGAGT TACATAAAGA AAGTAGATTT GCANTNNTCN GGCAGACGTT 180
TATACANCAC CACGGTGCTT TTATACATTG TNCTNATTTT AATAAACTG ANGTTCTATG 240
TGAAA 245

SEQ ID NO:1105

LENGTH:240

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01248

SEQUENCE DESCRIPTION:

GATCTGGCTT CCATTGGCC CCCTCATTTT CCAAATGTTT AAATGTATTG GATTGGATT 60
CTCAATGTAT AAGTTGCCTT ATCTGTTAAT GTCTATCTTC TGTCTCTTTA ATTTTGATA 120
TCTGCTGTTT TGCTTTTGA TACATTTTCT AATTAGAAGT CACATGATAA ATATAATCAG 180
TATAGTAATA ATACCATAAT GTGCACATAC TCAATAAATA AATGACTGCA TTGTTGTAAA 240

SEQ ID NO:1106

LENGTH:240

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01249

SEQUENCE DESCRIPTION:

GATCCATTN TCCNTGTAAC TNGGAGAAAG GCCAGTCCCT GTAACGGGGC AGCCCTCTCT 60
TTCCCTCGGT CAGCTCGTGT NAATCCTGGN ACCTCTCCG GTCGGCTCTG CCCGCTGTT 120
TGGGGTCGAC TGCCACGACT TTNNATTCAA GAAGCTTCCT CCAGGCGGNA GCGGCTATTT 180
TCCCTAAATN AGAATTGTTA CATTGCAAAT NGTTGAATAA AATATTTNGC GGTCTTAAA 240

SEQ ID NO:1107

LENGTH:239

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01250

SEQUENCE DESCRIPTION:

GATCTGAAGA AATGATGGAA TGGGGAGTGT AGAGAAATGA GAGTCTGTAT GATTCTGGAA 60
CAGAGACATC AGAAGGAAAG ACTGGTGAAA AGATGTATCT TTGTATATTA ATAGCTGTAA 120
TGTAGCTTCC TGATGCTTGA CTAATTGAGG TGTTAATTCT GACTTGAGAA TCTTTTTCAT 180
GAATGATTTT AAAGAAAAAT TTGGATTTTA AAGGTATTAA AATATTTTNG TTTTGTA 239

SEQ ID NO:1108

LENGTH:239

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01251

SEQUENCE DESCRIPTION:

GATCCGCAGT CGAAAAAGAA CAAGCCACAG AAACGGGCTC GTCGTGCCAG GACACAGCAG 60
TGTCTTTCAA AAAATCAAAA CCAGAAGNTT TATCANCAGC AGGAAGNATG TGGGCTCTGT 120
CAAGTTACC GTCACCATCA AGCCACTGCT GTGGAAGAGT TTGNCAACAG GNCAGTGTC 180
CAGCACANCT TCAGANGCAG CATCCGNGTG TCGTCCAACA GANGNCCTNG TCCGGTCAN 239

SEQ ID NO:1109

LENGTH:238

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01252

SEQUENCE DESCRIPTION:

GATCTATGTC CGGTGTGGGT TTTTGTCTC TCGAGTTTTG TCTCTAATAA AGGCCTTTTT 60
TGTTTCAAT TACATACGCT TTTTACTGCA CAATTTTGT ATTGACCTTA TTCAACTGA 120
AGCGATTATT TCCAGCAGGT TTAATTCGA CAATAAGATA TATTNAATA GTTTTACCT 180
TCGCTAGAAT TTTGTATTGT TTA AACAGT AAATGAATAA NTTTGCTGAT GATTCAA 238

SEQ ID NO:1110

LENGTH:238

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01253

SEQUENCE DESCRIPTION:

GATCAATGAA ATGCACATAA ATNAACTGGT TCCATCAAGA CTGTGCACCC AGGCCTTACA 60
GTCCAACCTT TTTCTGTGTC TGGCTAATAT TTAAACTAG AAAAATATT CCTAATCAAC 120
ATGGAGTGA GAGTTTATTC ACTGTCTTAT CTGCAGAAAT TTGCTGTCAA TATATAACCC 180
GCCTGCAGTG GAAAGTGTAT AGTGTTTTGT AATAAATGGC CTGATGCTAA TGTGTAAA 238

SEQ ID NO:1111

LENGTH:237

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01254

SEQUENCE DESCRIPTION:

GATCTACCGG GGGCTATTAG TTTCAATGTA GTGATGAACA CAACTATAT TTTGAGTTCT 60
CTGCAGCAAG TGAATGTGG TATGAAAATA TCTGATATTT ACAAAGATGA TACTGCTAAG 120
TCAGAGTCAC GTTTATTGCT AATATGATGG TGGAGTGTG TCTTCATTCA TAATGAAGGG 180
AAATGTTATT TTTAATAGNG GTTAGTGAAA TAAAANTAAN CCTATTTTCT AANCAAA 237

SEQ ID NO:1112

LENGTH:268

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01256

SEQUENCE DESCRIPTION:

GATCTGGAGC ATTTGAGCAA GTTTATAGAA GAACATGCCA CAAAATGAG CAGGACCAAG 60
GAAGAGCTTT GAAGGCCTGA GGTCTGCGNA AGGTGGGAGG AGGCAGACGC CCTGCGTGGC 120
CCATGGTCGG GGCCTCCACG CCGAGGCCGG CAACAAACGA CAGTATCTCG GATTCCTNTT 180
TTTTTTTTT AAATTTTNA AACTNNGGGG TTNCACTNCA NGNTCTGAAT ACTGANTANC 240
CATGAATNCC TGAATAGTTT AGNCCAGN 268

SEQ ID NO:1113

LENGTH:236

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01257

SEQUENCE DESCRIPTION:

GATCAGCGCT GAGGACGGNC TCAAGCATGA GTATTCCGC NAGACCCGNN NCCCCATCGA 60
CCCCTCCATG TTCCCACGT GGGCCGCCAA GAGCGAGCAG CAGCGTGTGA AGCGGGGCAC 120
CANCCCAGG CCCCTGAGGG AGGCCTGGGC TACAGCCAGC TGGGTGACGA CGACCTGAAG 180
NAGACGGCT TCCACCTTAC CACCACGAAC CAGGGGCCCTC TNCNGCGGN CCNGGN 236

SEQ ID NO:1114

LENGTH:235

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01258

SEQUENCE DESCRIPTION:

GATCTGTTGA CTTCCCTGGG TAGGACACTG CCACCTCTGG GCTCAGGTCC TNATGCCTCC 60
AAATGGCATC TAGAGTTTGA GCAGCCTTCT TGGCTGCAAG GCAGGCCTAG CCTGTGGCAG 120
CGGGCTAGGG CCCGCAGAGC ATTTGGTGCC CCTCCATGTT GCAATGCAAA CACCTTCACC 180
ACTGGGGCAG TGGGGAGAGA TGGCTATATT AATAAAATAA CGTGTGTCTT TCAAA 235

SEQ ID NO:1115

LENGTH:235

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01259

SEQUENCE DESCRIPTION:

GATCATNATT TTTNCTGCGT AGTTGACAGA CTTAGCATAT TAGTTTTTNN TACTCCTACA 60
AGTGTAATT GAAAAATCTT TATATTAATA AAGTAACTG TTATGAAGCT GCTATGTACT 120
AATAATACTT TGCTTGCCAA AGTGTGTTGN NTTTTNTGTN GTTTGTTGT TTGTTTGTTT 180
TTGGTTCATG AACACAGTN TCTAGAAACC CATTTTGAAA GNGGAAANTT ATTAN 235

SEQ ID NO:1116

LENGTH:234

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01260

SEQUENCE DESCRIPTION:

GATCACAATT NGCTTCATGA ATCAAGGTGT GGAAATGGTT ATATATGGAT TGATTTAGAN 60
AATGGTTACC AGTACAGTCA AAAAAGAGAA AATGAAAAAA ATACAACTAA AAGGAAGAAA 120
CACAACTTCA AAGATTTTTC AGTGATGAGA ATCCACATTT GTATTTCAG ATAATGTAGT 180
TTAAAAAAA AAAANGGNAA AAACNTTGTT GNAANTNCCN CCTTNCCTC NGGN 234

SEQ ID NO:1117

LENGTH:234

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01261

SEQUENCE DESCRIPTION:

GATCCCCCGN TCAGCNCNA AAGTGCTGGG ATACAGGCAT GAGCACCACG TCCGNCTAGA 60
CTTTACCTTT CTAAGAAAT TGTTTACTGG ATTTATAAGA AGTTAATTTT TGAAAAATNAC 120
ATATTTTGT NTGATAGAAA GAATGGAGCA AGTNGTGCCT ATTTCTCCA AGTCAGATAA 180
GGTTTCTAAA ATAAATAAAT TTCTAGCATA TAAAGGGTAG AGATAAACTC NNNN 234

SEQ ID NO:1118

LENGTH:233

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01262

SEQUENCE DESCRIPTION:

GATCACAGGT CTTCCCTGTG AACTTTGGTT TCTTCTATA AATGTGTGTG GTTTTCAGCG 60
 CTCAACTCCT GTCTTCAAAT GGTAGTAAGT NCTACTTCTA CTCTGTGCAT TCAGAACATT 120
 TTATGTCAAA TGATGTAATG CAGAAATNCT TGTGCATATT TGTAAGTGAA GGAAGCTTTT 180
 TAGATTATT TNNGTTTTTA ATAAAATTCA GATTCCTATT CTAACTGGT AAA 233

SEQ ID NO:1119

LENGTH:230

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01263

SEQUENCE DESCRIPTION:

GATCTNCTAT GCAGTCTGCG CATGCNTCCT GTTGGTCTCT CTGTGTTCTT TGTTACTTGG 60
 GTGCAATAGC AACTTCCCTA CCCCCTGCAT TCCATCTTTN ATGTTGTGTA AAGTTCTTCA 120
 CTTTTTNNTC TGAGGGCTGG GGGTTGGGGG AGTCAGCATG ATTATATTN AATGTAGAAA 180
 ATGTGACATC TGGATATAAA ATGAAAATAA ATGTTAAATT AAATGGAAAA 230

SEQ ID NO:1120

LENGTH:237

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01264

SEQUENCE DESCRIPTION:

GATCTAAGTT AGTCCAAAAG CTAAATGATT TAAAGTCAAG TTGTAATGCT AGGCATAAGC 60
 ACTCTATAAT ACATTAAATT ATAGGCCGAG CAATTAGGGA ATGTTTCTGA AACATTAAAC 120
 TTGTATNTAT GTCATAAAN TTCTAACACA AACTTAAAAA ATGTGTCTCA TACATATGCT 180
 GTACTAGGCT TCATCATGCA TTNGTAAATT TGTGTATGAT TTGCNNNTNT GNNNGNN 237

SEQ ID NO:1121

LENGTH:234

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01265

SEQUENCE DESCRIPTION:

GATCTGGCCA GTTGTACTTT TAGCTCCCAG AGGGAGAGTT GGTGGTATTA TGAGTTGAGT 60
 AAAAACCATC CAGGGGAACT TGAGGGAGCA GTCTGTTGCC AGTAATGTTT CTTGTGTGCC 120
 ATTAACCAC CTCCAGATGA GTGGAGGAAC ATCACTTTTT AATTTTTTAA TTGTATTTGG 180
 AATTGTTGCC GTGTACTAAG AACTTGACCT AAATAAAATC CCACAAAGTA TAAA 234

SEQ ID NO:1122

LENGTH:232

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01266

SEQUENCE DESCRIPTION:

GATCCTCAGG ACGCAGGTCA CATTACCTG TGGGCAGAGG GACAGGTCAG ACACCCAGGC 60
 CCACCCAGAG GACCTCCAT GAACTGTGCT CCCAGCCTTC CCGGCAGGTC TGGGAGTAGG 120
 GAAGGGCTGA AGCCTTGTTT CCCTTGCAAG GGGGCCAGCC ATTGTCTCCC ACTTGGGGAG 180
 TTTCTTCCTG GCATCATGCC TTCTGAATAA ATGCCGATTT TATCCATGGA AA 232

SEQ ID NO:1123

LENGTH:235

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01267

SEQUENCE DESCRIPTION:

GATCAGGAGG CATCATTGAG GCCAGGAGCT CTGCCCGTAA CCTGTATCCC ACGTACTCTA 60
 TCTTCCATTC CTCGCCCTGC CCCAGAGGC CAGGAGCTCT GCCCTTGACC TGTATTCCAC 120
 TTACTCCACC TTCCATTCTT CGCCCTGTCC CCACAGCCGA GTCCTGCATC AGCCCTTTAT 180
 CCTCACACGC TTTTCTACAA TGGCATTCAA TAAAGTGTAT ATGTTTCTGG TGAAA 235

SEQ ID NO:1124

LENGTH:238

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01268

SEQUENCE DESCRIPTION:

GATCGATGCC ACGTTCGTAA GGTTCCTAAGT CCTTCTTGGC TCCTNATGTG GTCCCTCTCC 60
 TCGGAAGAAC TGCCAGCCA CGGGTTTNA ACCACCTGT TGCTCCTNAG GTCGTCATA 120
 TATCAACAGT CACAAACCCA ATGGCAATAA AGGCACTGAC GATAGCTGGC GCGCGCNACG 180
 CCACACACCA TTTNAGATG CCGTTGCAAT TAAATCTTGC CACACTGTCC TCCTGAAA 238

SEQ ID NO:1125

LENGTH:231

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01269

SEQUENCE DESCRIPTION:

GATCCCTGGC TGGAAATGCA TACCATTGAC CCATTGAAG AGTTAAAGCT GGATTGACT 60
 GCTCTATTCT ACCAGGAATA TTGTTAGGGT AGCCTTTTAC CAGTTTCTAA ACANTNGTAA 120
 TCATTTATTG ACTCAGCAAT TCCTCAGATA ACAGGTCAAA AGATGTACAG ATACATTNN 180
 NAGTTTTCTT GCTATTAAAG GCACAAGAGT TTCCTGTAT TTTGACTGAA A 231

SEQ ID NO:1126

LENGTH:230

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01270

SEQUENCE DESCRIPTION:

GATCTACAGT CATGCTTTAG CATGGCTATG GAGCTAATTA TCAAGCTTAA AGGGTAACTT 60
 TGGGAGGACT CCTCCCTTCA CTCCTAGTCT CCCTTGGAAG AGCAGTCCAG GCTCAGGGAA 120
 GGGAAATGGAT AGGATGACAC AGTAAGTACA GAAACTGAAG CTGTCAATAG TGAAGGAAAA 180
 AGGGGAATTC TTCGTTGCTT TGGCATTNAC ACATAAGTAC TTTGATTAAA 230

SEQ ID NO:1127

LENGTH:229

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01272

SEQUENCE DESCRIPTION:

GATCCAAAAT TTATAGCATT CTTCTACCAC CACAGGGGCT CATATGACAT TAACAGACAA 60
 GACACTTTTC AGAAAGACAG GTTGTCTTTT TGGGCCACAT CTAAGAAATC TTTGTCTAGC 120
 CAAAAGCCAC AAATAATTC TCATTTTTTG GCTTCTGGAA GATGTACAGT TAAATGTTAT 180
 ATTTGGGACT GTTATCTAAT TTGATTAAAT TGCACCTCTAC AATATGAAA 229

SEQ ID NO:1128

LENGTH:229

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01273

SEQUENCE DESCRIPTION:

GATCAGGGCT GAGGGTAAGG AAAAGAAGAG ACTAGGAAAG CTGGGCCCAA AACTGGAGAC 60
 TGTTGTNTT TCCTGGAGAT GCAGAACTGG GCCCGTGGAG CAGCAGTTTC AGCATCAGGG 120
 CGGAAGCTTA AAGCAGCAGC GGGTGTGCC CAGGACCCAG ATGATTCCTA TGGCACCAGC 180
 CAGGAAAAAT GGCAGCTCTT AAAGGAGAAA ATGTTTNAGC CCAGTCAAA 229

SEQ ID NO:1129

LENGTH:227

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01274

SEQUENCE DESCRIPTION:

GATCCTTACT ACTGGAATTA CCGGGTTAAA AGGAAATGCT TACCACTAAG ATGTCAGTAT 60
 TCTCCTCATG GATATTTTCA ATCTCAATGT TGCCAGTCTA ATAGTATAGT ATGTGGTTGC 120
 TTTACTGCTG TTCTCCCCAC CCCCCTGGAG TTGTGTCATT ATTTTAATGA ATGTGAGCTC 180
 TTGACTTACT CTAGAATTCT AATACAGATA CTTTCTGCAC TAGTAAA 227

SEQ ID NO:1130

LENGTH:227

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01276

SEQUENCE DESCRIPTION:

GATCCGCTTG GTGACGGGCG TCTTCCAGA TGCTGGCGTC ACCGCTAGAC CAAGGAGCCC 60

TCTGGTGGCC CTGTCCAGGC ATAACAGAAG GTCGCACTC CTGTCTTCTG GTCACCTTCTC 120
ACTATGTCCC CTCAGCTCCT ATCTCTGTAT GGCCTGGTTT TTCCTAGGCT ATGATTATTG 180
AGTGAGGATT ATCATAATAT TGGAATAAAA AGTAATTGCT ACCCAAA 227

SEQ ID NO:1131

LENGTH:227

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01277

SEQUENCE DESCRIPTION:

GATCAGGATT GTCCTACAGT TGTAATAAG ANTAGGTCCT GTTTATTTTG ACATCTNTTT 60
ACAAATGCAT TGTATTAGGG TGTGAATATT CTGAACCATC CTCTTGTTTA AAGTTTGAA 120
ATTTTATTG TAAATGTAA CATTTTAATG GTTGAATAA TTATTGTAT AGATATGAAT 180
ATAGTATTTN ATTTAAGANA ATAACTTTG CATTTTGTCA TNGTAAA 227

SEQ ID NO:1132

LENGTH:227

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01278

SEQUENCE DESCRIPTION:

GATCTGAAAT TTGTGTATNC TAAAGTAATT TNGTTTTATG TATTGGAAGT TCACTTAAAA 60
ACTGGAAATA TTTCTAGAA GGGTACCACA CAAAAGGAAT CATCTTTAAG CTGTTTAATT 120
AACCTAATAA AATAATNTGA TGGGGAAGGC ATTCTAATTG TTTCTGATTT TNNGAGTGGT 180
TCCTGCTAAN TCATCANTAT CANTACAGCT TGATTGATT TAAGAAA 227

SEQ ID NO:1133

LENGTH:226

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01279

SEQUENCE DESCRIPTION:

GATCTTAAAT GTTATATTGA TAACCATGCT CAGCAATGAG CTATTAGATT CATTTTGGA 60
AATCTCCATA ATTTCAATTT GTAACTTTG TTAAGACCTG TCTACATTGT TATATGTGTG 120
TGACTTGAGT AATGTTATCA ACGTTTTTGT AAATATTTAC TATGTTTTTC TATTAGCTAA 180
ATTCCAACAA TTTTGTACTT TAATAAATG TTCTAAACAT TGCAA 226

SEQ ID NO:1134

LENGTH:225

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01280

SEQUENCE DESCRIPTION:

GATCTTTACC AAATTCCTGA CTCAGAGTTC CTCCCATTTN CTTCTGACTC TCATTTTATT 60
CTTACCTCTC ATTTTATTCT TATGATGTTT ACCATTTCTN TTCTCCTCAG TGTCCTCTC 120

TGAGTGGTAA GAGTATGTTA ATAAGCCAGT NCTGAGACCG GAGCACGAGG CAACTGCTCA 180
 ATGTTGGTCA TTGTCACGTG TATTAAATGT AACTTAAGGG NNAAG 225

SEQ ID NO:1135

LENGTH:224

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01281

SEQUENCE DESCRIPTION:

GATCTGACTT AAAAACCAC CAGCATGCTC AATCCCTTGT NATCCTTATG GAATCTGTAT 60
 GTTAACTCTC TGGGTGTTCA GGCTTCTATT TGACTGCTGT TGTNACCCTG TTGCAAAAT 120
 GAATATGACA CTCTGTGGAT TATTNCTCT GTAAGGCACA AGTNCTTCTN ATGATTANTT 180
 TGACGTTCA NGAGCAAAAG CAAATTNANA CTCTCTTCAG CAAA 224

SEQ ID NO:1136

LENGTH:223

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01282

SEQUENCE DESCRIPTION:

GATCCAATAG GAGACACCAG TTCCTTGACT GANCCATGCC CCCACCTAAG TNACAAAATG 60
 AGGGAAGTGG GGAGTTAGAT TTCAGAGTCC AGGCCCTAG GTTGGGACCC ACTCCAAATA 120
 ATCTCCTCGG TGTGGGTNGT GGTTCTATAG AGGNATANAT GAATAATAAA CATTGTTAAA 180
 NTATACGATA ATGNATAAAG TAATCCTTTC ATCANNTGTG AAA 223

SEQ ID NO:1137

LENGTH:222

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01283

SEQUENCE DESCRIPTION:

GATCCATCCG ATGGCCTACC AGCTGCAGCT CCAAGCCGCC AGCAACTTCA AGAGCCCAGT 60
 CAAGACGATT CGCTGATTCC CTCCCCACC TGTCTGCAG TCTTTGACTT TTCCTTTCTT 120
 TTTTGCACCC CTTTCAGGAA CCCTGTATGG TTTTNGTTT AAATTAAAGG AGTCGTTATC 180
 GTGGTGGGAA TATGAAATAA AGTAGAAGAA AAGGCCATGA AA 222

SEQ ID NO:1138

LENGTH:432

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01284

SEQUENCE DESCRIPTION:

GATCGCACAT CCCTGCGCCC CCATGCCCCC ATGCCCTCT GAGTCACACA GGACAGAGGA 60
 GGCAGAGCTT CTGCCACTG TTATCTTCAC TTTCTTTGTC CAGTCTTTG TTTTAATAA 120
 GCAGTGACCC TCCCTACTCT TCTTTTAAT GATTTNGTA GTTGATTTGT CTGAAGTGT 180

GCNACTGTGC ATTCCTTGAA TAATCACTTG TAAAAATTGT CAGTGCTTGA NGCTGTTTCC 240
 TTTACTCACA TTGAAGGGAC TTCGTTGGTT TTTNGGAGTC TTGGTTGTGA CNNCAAGAGC 300
 AGAGTGAGGA AGACCCCAA GCATAGACTC GGGTACTGTG ATGATGGCTG CAGTCCAGTT 360
 TTTATGATTG TGCTTTTAT GTGTCCCTTG ATACCAGTGG NCTTANCAAT TATACATTNC 420
 CTCATANTTA AA 432

SEQ ID NO:1139

LENGTH:220

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01285

SEQUENCE DESCRIPTION:

GATCAGACCC AGAGAAAAGT AGTTGTCAGT CATAGCACAC ATCGGACATT TGGAAAACAG 60
 CAGTGGCAAC AACTGTATGA CACACTTAAT GCCTGGAAAC AAAATCTGAA CAAAGTGAAA 120
 AACAGCCTTT TGAGTCTTTC TGATACCTGA GTTTTATGC TTATAATTT TGTTCCTTGA 180
 AAAAAAGCC CTAAATCATA GTAAACATT ATANNCTAAA 220

SEQ ID NO:1140

LENGTH:219

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01286

SEQUENCE DESCRIPTION:

GATCTTGGGG CCTGTTTTCC CATGGGATTC AAGAGGGACA GCCCCAGCTT TTTTGTITT 60
 TAAGCTTAGG AATCGCCTTT ATGGAAAGGG CTATGTGGGA GANTCAGCTA TCTTGTNTGG 120
 TTTTTTGAG ACCTCAGATG TGTNTTCAGC AGGNCTGAAA NCTTTTNTNC TTATAAATG 180
 AGAAATGTAT ATTTTACTAA TAAATTATTN ACCGAGAAA 219

SEQ ID NO:1141

LENGTH:219

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01287

SEQUENCE DESCRIPTION:

GATCTAGAGA CAAAGGATAC TCAATGAGGA GCTTTTTTCC CCTCTTGGA CAGGTAAAAT 60
 GCTTTCCTT ATTAATATAA TTATAAACA GTATTTTATG TAACAGCTAT TCCCATATTC 120
 TAGGAGTGGC CTAAGAAATG CGTGTTTCAG TGACTAGATT ATAAATATNC TCTATTGTGA 180
 ATAGTTGAAT AAAACAGCTG TTTTCTCTG CTCCTAAA 219

SEQ ID NO:1142

LENGTH:219

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01288

SEQUENCE DESCRIPTION:

GATCTGTGAA ATGCTATCTC TCCTGANGCA ATACTGTTGA CCAGAAAGGA CACTCCATAT 60
TGTGAAACCG GCCTAATTTT TCTGACTGAT ATGGAAACGA TTGCCAACAC ATACTTCTAC 120
TTTTAAATAA ACAACTTTGA TGATGTAAC TACCTTCCA GAGTTATGGA AATTTGTCC 180
CCATGTAATG AATAAATTGT ATGTATTTT CTCTATAAA 219

SEQ ID NO:1143

LENGTH:219

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01289

SEQUENCE DESCRIPTION:

GATCCCTGGA CACTTACGTA CAATGCTTCG TNCTGCCTGA TGACAGCCGG GCCAGCCGCC 60
AGCNTACAAG GNTTGTNCGA CGCAGCCTCA GCCCTGTNTT CAATCACACC ATGGTGTACG 120
ATGGCTTTGG GCCTGCTGAC CTGCGCCAGG CTTGTNCCGA GCTCTCCCTC TGGGACCATG 180
GGGCCCTGGG CAACCGNCAG NTNGGGAGGC ACACGCNTN 219

SEQ ID NO:1144

LENGTH:218

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01290

SEQUENCE DESCRIPTION:

GATCTCGGTG CTTCTTCCTG TGCTGTGGTT TACCCCAAAC CTTAGGTTG TTTATTCATT 60
CAGATTAGAT AGACTGGAGC CATAAAGTTA ATTTGCACCT AGCTTTTGG AGAATAGCCA 120
TGATTAAGTG CTATTCGTGG TGGGGGTGGG GGGGAACCCT ATGATTTACT ATGCAGATGA 180
AGAGGGTAGG AACTAAATAA AGGACTTTGT AAGCCAAA 218

SEQ ID NO:1145

LENGTH:218

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01291

SEQUENCE DESCRIPTION:

GATCAAGAGG GAGTTCATGC AACACCTGAG AATCTGATTA ATGCACTGAA TAAGTCTGGA 60
TTAAGTGACC TTGCAGAAAG TCTAACTAAT GACAATGAGA CAAATAGTTA GCTTCTTTT 120
TTTTTCTTTT TATTAAANCT GNGATAGATT TTNTACCAA GCAGCATTG ATAAGAGGTC 180
CACTGGTTTT GGTAANCAAT AANCATTTT ATACCAA 218

SEQ ID NO:1146

LENGTH:218

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01292

SEQUENCE DESCRIPTION:

GATCCCCAGC TGTTTATGCA TAGATAATCT CTCCATTCCC GTGGAACGTT TTTCTGTTC 60

TTAAGACGTG ATTTTGCTGT AGAAGATGGC ACTTATAACC AAAGCCCCAA GTGGTATAGA 120
 AATGCTGGTT TTTCAGTTTT CAGGAGTGGG TTGATTTCAG CACCTACAGT GTACAGTCTT 180
 GTATTAAGTT GTTAATAAAA GTACATGTTA AACTTAAA 218

SEQ ID NO:1147

LENGTH:217

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01293

SEQUENCE DESCRIPTION:

GATCCTATCC AGTTGAGGAA TGCTTGCAAT GCTCATTGAA GGGATTGCT TTGGGACTTT 60
 GTCATCTTCC AGAAAGGAAA CATATTGTAT ATTTGGCCCA GTGTGATTGA TTGCTTTATC 120
 TTTGGTAACT TTTACTTGAA TGGGATTGTC TGAATTAATG ACTATTGAAT TTAATACTAA 180
 TTATGAGTTG ACAAATAAAT AAAAGGTAGT GTTTAAA 217

SEQ ID NO:1148

LENGTH:217

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01294

SEQUENCE DESCRIPTION:

GATCATAGTC AGAAAGTACT GCAGTTAACA GGAACCTTCT TGTTCAGGCT GTCATAGCCA 60
 CAGTTGCAAA AAGTGCAGTA TTGATTAATG CAATNAGTGC AATNAGTGAC ATCCTGAGTC 120
 TTTATCTGT TNAGCTTGCT NTNCTNTTCT NTCATACATC AGGATATTGC CTGTAATGTG 180
 GAGTGGACAG GATAAAAAATA AGNATTTTAC TTTCAA 217

SEQ ID NO:1149

LENGTH:124

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01295

SEQUENCE DESCRIPTION:

GATCTGAAGA AAGCTTTTGG TGCTTGCTCT CACAACCACC TCAGTCCTCC CTCCTGTCC 60
 TCCCCTGTCT CCTTTCCTCC TCCTGGGTTT ATGTTGTAAT AAAAGAAGAT TGTGGGTGTG 120
 TAAA 124

SEQ ID NO:1150

LENGTH:215

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01296

SEQUENCE DESCRIPTION:

GATCATAGCT TGTTTTATTT TGTGCTATAA AATTAACAGT ATTAAATGAC TTATATTCTT 60
 AGAATACATC GAGTGTCTTT TCTTAACAGA TTAGTGCCTT TTNATTTTGT TATTCCGTTT 120
 TACGTTACTG GTCCCAGCAT CAAAACCCTT GTTCCATGG CCTGTTTGTA TATTGTCTCA 180

ATAAACTTG CATCAGCCGG TGGTGGCGGC AGAAA

215

SEQ ID NO:1151

LENGTH:299

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01297

SEQUENCE DESCRIPTION:

GATCATAGTG TTTTGAATC ATTTAATGTC TGCAGCCAAA TTTTAAAGG TAATTTAGAC 60
CTAATACTGC TCTTGCTGTG TCTTATTAAG TTAATAATTA TGAATGANTN CTGGTAAAAA 120
TTCANNNGG CACTCTGTGA GTAGAGAGTA TCATTAAAGC TTATTNAGT CACATGTAGT 180
ATATATCTCC TAAAGCTGT CACTCTCACT TTNCTTACCA TTCTCTTGAT TTNNTCAGAA 240
NCCATCTAGT CATCATCTTT ATACTCTACC TGCTTCTGCA ATTGTATATC ANATNGNGN 299

SEQ ID NO:1152

LENGTH:214

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01298

SEQUENCE DESCRIPTION:

GATCAAAGTT TAATTGCTTC ATTTTGT TT AAAAAGGGAT ACTGATGTCA GAAAATCTGT 60
AATATGTTTT ATTCAAAAGA TGTAATAAT GTATACAGAC TTGTATGTGA TGGGATGGGA 120
AATATTTAAA TNCTAGGTGT TTTTTTTTTT TTNAANGNGG AACCNCAATG TTTATAGGAA 180
AAAANTGATT AANTNGTTCC GTTTGGCCNT GAAA 214

SEQ ID NO:1153

LENGTH:214

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01299

SEQUENCE DESCRIPTION:

GATCCCTCTC CTCGCTGCC TTCTGGAAGA CTTCAGAAGA TTGAGCCTCA CTGGTGCCAG 60
GAAGCCAAAG CTTACTTTGT AGAACTGACA CTAAGTACC CGAAGACTTA GGTGCTTTGT 120
GTACTTAACC CCAGGACCTN CTTACTTTTT AATATAAAGA GTGATGTTGT ATTTCGTGTT 180
CTGCACTTTT TAATATAAAG AGTGATGTTG TAAA 214

SEQ ID NO:1154

LENGTH:214

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01300

SEQUENCE DESCRIPTION:

GATCCCAAAG CCACGCTCAT CCAATCCTGG NGAATCATTT ATTTTGAATA TAGACCATTG 60
AATAGGTGAA AAATGGAAAA GTCACTTTTT GTACATTTGC ATTCCTTCAA TAATGATTAC 120
CATTTGTNCA CATATTTGTT GACCATTGGA ATTGATTTTA GCACAGTGCC TAAAATATAG 180

TAGGTGCTCA ATAAATATTT GTTAATTGAA TAAA

214

SEQ ID NO:1155

LENGTH:214

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01301

SEQUENCE DESCRIPTION:

GATCCAACT AATAAGAATA AGCTGTACAG GAACTAGTGC TCAATATACA TTGTATAAAT 60
 TTGTGGAAT CTCTTGGATG TNAATTGTTA CTTCAAGTGG CTTTATTAA GATTNCTCA 120
 GACTTACTTG GAGGTTAAAG CAAACCCAAA TGTGTATTAT TTTGTTACAG AGCTCTGCTT 180
 TATAATTTTG TAATAAAGTT TCAATACAGA CAAA 214

SEQ ID NO:1156

LENGTH:213

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01302

SEQUENCE DESCRIPTION:

GATCGCAGTG GAAGAAGATT AGTGCATCAT TGAGAGAGGA GAAGTGGAGT GTGGGGTGAG 60
 CAAAAGCCAA AATACTAATC ACTAGTACAC CAGAGATGCT CCACAAGGTA TGCTCCCCAC 120
 GGTTCCTTCT CAATTTCAAA GGTNAAGATG TTTTTTTGTG GTGATATAAA ATTTATTGTG 180
 AATACTTGGT CCATNAAATT GGTACTTGCT AAA 213

SEQ ID NO:1157

LENGTH:213

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01303

SEQUENCE DESCRIPTION:

GATCTTGTTG AGGCATTTAG CTGCCATGCA CCTGTCCCCC TTAAATACTG GGCATTTTAA 60
 AGCCATCTCA AGAGGCATCT TCTACATGTT TTGTACGCAT TAAATAAATT TCAAAGATAT 120
 CTGAGAAAAG CCGATATTTG CCATTCTTCC TATATCCTGG AATATATCTT GCATCCTGAG 180
 TTTATAATAA TAAATAATAT TCTACCTTGG AAA 213

SEQ ID NO:1158

LENGTH:212

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01304

SEQUENCE DESCRIPTION:

GATCTCATTT CAATTTCTTT ATTAGAGGGC CTTATTGATG TGTCTAAGT CTTTCCAGAA 60
 AAAAATATC CAGTGATTTA TATCCTGATT TCAACCAGTC ACTTAGCTGA TAATCACAGT 120
 AAGAAGACTT CTGGTATTAT CTCTCTATCA GATAAGATT TGTAAATGTA CTATTTTACT 180
 CTTCAATAAA TAAACAGTT TATTATCTCA AA 212

SEQ ID NO:1159

LENGTH:212

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01305

SEQUENCE DESCRIPTION:

GATCTGGTCT GTTCCTGCGT CTGCGGANGG CCCTTGTCTC CCAGCTATCT ATAACCTTAG 60
CTAGAGTGTC GCCTTGTTGG TTCCTGTTGC TGAGACTTCC TGGATGGAGC CGCCTCACCG 120
CCGGGCCCCG GGCCTGCNCG GANTGTGTCC AATAAAGTTC TTGGATGTGA AAACCTTAACA 180
ATTTTGTGTA ATAAAAATGG AGAAGCTCTA AA 212

SEQ ID NO:1160

LENGTH:211

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01306

SEQUENCE DESCRIPTION:

GATCCTTGGT GTGTAGTTCA GTCTTGCACT ATACAAGCTT TTGTGTATAA ATGTTTTATG 60
ATATGATTCC CTGTATTTTG CAGGGGTTTT TTTCTCTTT NCTTTTGA TAAATATGTA 120
TATCAATATT TTAAATNCAT CTTTGCTTT TTTAGAGGAG TTTGTAATCA CCTTATAACA 180
TGAAAATAAA CATTCCTTT TTAACATCAA A 211

SEQ ID NO:1161

LENGTH:210

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01307

SEQUENCE DESCRIPTION:

GATCCTGTAT ATGTGTGTTT TGGGGGAGCT ATGATAAGTT TTATGGCAAA CGGTTGGTAT 60
TGTTAACTTT TTATTGTCAT CAAAAGTTCA TAAAAGTCCT ATTAATCCCC ATATTCTNNN 120
NCTGCCCTTA ACTCTGGTAT ACACCAAAAA GAAATCTTGA CTTTCCTTGT TTTATCATT 180
TAAAAATAAA GTATTTTGCT AGTATGGAAA 210

SEQ ID NO:1162

LENGTH:210

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01308

SEQUENCE DESCRIPTION:

GATCCGCCCA TGTNAGCCTC CCAAAGTGCT AGGGTTACAG GCATGAGCTA CCATGCCTGG 60
CAACAGCTTT CATATTTGTA AGTTTTTTTT CCTAGGTAAC CCAAGGTCTA TTGAAATTNC 120
ATATAGCTTT CTTNCTATT ACATATTTAA ATAGATTNN CCTGATTNA GAAAAGCTGT 180
AGATTTTNAT ATGTNAATCT TGTNTCCNTN 210

SEQ ID NO:1163

LENGTH:209

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01309

SEQUENCE DESCRIPTION:

GATCTNGGAC TCTNCCTCTC ACGACTGCGC CTTAGTCACT CAGACATACG GCGCANTGCA 60
GGAAAAGCCT ACACAGACGA CCTGGGTGCT GTGGGTGGCG CCTGCNTGGA GGACGAGCCA 120
GCNTCCTGCN CTGGATGAGG ACAGCGAGCA CCCGCCATNA TTCTNCGGAC TGACTGAACT 180
TNACCTGTGA CCTCTTACCN GTGGAGCAN 209

SEQ ID NO:1164

LENGTH:209

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01310

SEQUENCE DESCRIPTION:

GATCACTNCA GGCCAGGNGT CCAAGACCAG CACGNCCAAC ATGGCAAAAC CCAGTCTGTA 60
CTAAAAATAG AAAAATTAGC TGGGCGTGGT GCGGTGTGCC TGCAATACCA GCTACTCAGA 120
AGGCTGNAGC AGGNTAATTG CTTGANCCTG GTAGGTGGAG GTTNCAGTGA GCTGANATCA 180
TGCCACTGNA CTCCAGCCTG GGTNACAGN 209

SEQ ID NO:1165

LENGTH:207

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01311

SEQUENCE DESCRIPTION:

GATCCTTACC GTCCTAGAGA GCAGACGCTT TCTGAAAAC ACTTGCTCCA AAAGACCCTC 60
TGAGTTAACG TTTCAGCTGT ATCATTAGAC TTGTATTAG AGCGTGTAC TTCCTCTGAA 120
CTGTACTGC CTGAATGGAG TCCTGGACGA CATTGGGTTT TTCCTCTAGG AGAATACAAG 180
CCTTAATAAA CAATACTATT TAGCAAA 207

SEQ ID NO:1166

LENGTH:207

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01312

SEQUENCE DESCRIPTION:

GATCTGAACA AAGTCTGCAT TTNGTTAATA GTGTGGTACC AATGTTGGTT TCATAGTTTT 60
GGCCATTGTG CTGTGTATTT ATAAGATGCT AACATTAGGG ATAGCTGAAT GTGGTATATA 120
TAGGAACTCT GTGCTGAGTT TATAACTCCT CTGTATGTCT AAAACTATTT CAAAATAAAA 180
NGTTTAAAGG TAAANAAAA GATTAAA 207

SEQ ID NO:1167

LENGTH:206

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01313

SEQUENCE DESCRIPTION:

GATCCAGCCA CCACTCTGAA ACTCATCACA TCTTCATTGA CAGGGAGGGA GCCCAGGACA 60
TATGTGTGGC TCATTGACCA GAAGGCTTTC TTAGTCCCAA CAGCCATGAA CCATGCACTT 120
ATGGATACCC AGCCTTTTAG GGCTACGTGA AATGCATCCT TGTANCATCA TTGTATTCTT 180
TCAATAAATA GCCTTCTGAG TTGAAA 206

SEQ ID NO:1168

LENGTH:213

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01314

SEQUENCE DESCRIPTION:

GATCTGCCTG CCTATNAGAG CTTTGAGAAG CTCCGCCACA TGCTACTGTT GGCTATCCAG 60
GAGTGTCTCTG AAGGCTTTGG GCTGGCCTAA TAAGGCCCTG CCCAACTCCG TGGGGTTTTT 120
TTAACCATTG TTGGACCTGG GGAGGGGGGA GTTAAAAAAA GAACCAGAAA GAAATTGTCA 180
AAAACCAATA AATGAAATCC ACCAACTCAC AAA 213

SEQ ID NO:1169

LENGTH:215

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01315

SEQUENCE DESCRIPTION:

GATCTAAAGT GACCTTGATG GACAGTGGA GAAATCACAA CATGGAATTC CTCGAATAAC 60
AATTTATTGA CTTTAAATAA TTTTGTCTAA TGCTACATAT ACACAATTAA AAAACCTTTA 120
CACTATTTCT AGAAAGTCAG CATGTATTTT TGGCTCGNNG TTTNCNCNG TGTTCCTGT 180
GGAAGGAATA AAAATTTGAG TTTCAGTTGT GTAAA 215

SEQ ID NO:1170

LENGTH:349

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01316

SEQUENCE DESCRIPTION:

GATCTGTGAC AGCAGCAGCT TCATGTTGTA TTTTITTTTAC TGAAATTGTA AAATATCCAT 60
CTTAAAGACA TCAACTATTC TAAAAANTGT TTACAGGATA TTCCTTTAGT GGTGGAATTA 120
AAATNTACGA NTACTTGCTT TTTCAAAAAA ATGTATTTTN TGTAAAAAGT TTAAAGATTT 180
TTGCTATATA TTATGGAAGA AAAATGTAAT CGTAAATATT AATTTTNTAC CTATATTGTG 240
CAATACTTGA AAAAAACGGT ATNGAAAGTA TTTTGAGTCA GTGTCTTACA TGTTAAGAGG 300
GACTGAAATA GTTTATATTA AGTTTGTATT AAANTTCTTT AAAATTAAA 349

SEQ ID NO:1171

LENGTH:205

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01317

SEQUENCE DESCRIPTION:

GATCCAAGCT GTATATACCA TATATAAACA TTTTACATGA ATCATTTAGT TTTTAAATC 60
ATTACTAAT GCTATAAAAT TTCCTATATT ACCCCAGTAA TTTGCATCAG CTGGTTTATA 120
TACTAAAGCA ACATGTTTTG ATGAGTTTCT TACATCCTTA TCGAGGAATT GGGTTAGGAA 180
AAAATACATA ATTGTAAAAC TGAAA 205

SEQ ID NO:1172

LENGTH:205

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01318

SEQUENCE DESCRIPTION:

GATCTTCAGG NTTCTACAAA TAGGGTAATT GTAAATTAA AGCATTAGCA TTTATTGGTG 60
AATAATGTAT ATATCCCCAT TCCAAGAAAT ATAAGTNAGT NANGTTGAAA TAAAATCTTT 120
AAAATTTACT ATATTGCCAG TGGTTTCACA NCAGTTCTCT TGTATTTATT TATCAATTAA 180
ATCAAATAAA AATGATTATG TCAAA 205

SEQ ID NO:1173

LENGTH:204

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01319

SEQUENCE DESCRIPTION:

GATCCCCTGA CCTGCATTAC CTTGGTAACC ATTTCATTTT TTAATTTAAT TTCATTTTTT 60
AATTTGGTG TACAAGCTGT AACATTCAT CTTTCAAAGT GTAACACGCT GATTCCTCA 120
AATAGAGATA CCCCTTTGAG TGATAAATT GCAAAATGCT GTCTTCATT TCTGTATTAA 180
AATTCATTC AGTTTAAAA TAAA 204

SEQ ID NO:1174

LENGTH:204

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01320

SEQUENCE DESCRIPTION:

GATCAGAGCT GCTGAGTTCA GGATGCCTGN GNGTGGTTAG GGTAGCTTCT TACATGGATG 60
TCAGGAGAGC TGCTGCCCTT GCGGTGAGTG CGTATTCAGG TGTTTTGCTG CTTGGCAGA 120
GAGTGGTTGA GTGTNGAATC GTTCAGCTCT NAGGTTCTGT NCCCTGTGGT GGAGAGGACG 180
CAGCAGCNAN NTCTGGGNTC TNAN 204

SEQ ID NO:1175

LENGTH:205

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01321

SEQUENCE DESCRIPTION:

GATCAGTGCT CTCTATTGAT GTTCTTGCTG GTCTCCAGNC ACATTCCTGT TGCATTAAGN 60
CTTGAAAGAC TTGTAGATGT GTGATGTTCA GGCACAGGAT GCTGNAAGTA TGTACTATT 120
CTNAGTTTGT AAATTGTCCT TTTGATACCA TCATCTNGTT TTCTTTTGT AGGTATAAAT 180
AAAANCACTG TTGNCANTAA GGAAA 205

SEQ ID NO:1176

LENGTH:203

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01322

SEQUENCE DESCRIPTION:

GATCTCAGCC ATAAAGTGCC AGTTTGCTTA GTTCTCACTG TCTCCTGGTC TGTGCTGCCC 60
TGCTCTGGGG ATGCACGGCG GCAGGGTGGG GGAGGGAGGT TCCTCGCAGG TCTCAGCCCG 120
GGACAGGGTC TTGCAAGCAG CCTCCTGGGC AGTCGTAAGG GTTGCGGCGT GATGTCTTCA 180
ATAAATTAAG TTTTATTTGG AAA 203

SEQ ID NO:1177

LENGTH:203

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01323

SEQUENCE DESCRIPTION:

GATCAAAATG AAACAAATAT ACCTTATCCT AAAGAGCTCA TAACAAATAA GTTACCTCCA 60
CTCTATAAAC TCAGACCTAC TTTTGAAGA TAACTGCTTT TAACCTCTCC TTACAAGATT 120
TTTGTGTTG ATGTATTTAA TTTTAGCCCA TGTCTCAATT CTCATTTTCA AAGAATCAAT 180
ATATTAATAT ACCTTTGGTC AAA 203

SEQ ID NO:1178

LENGTH:202

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01324

SEQUENCE DESCRIPTION:

GATCGCTCTT GTGTTTTTGC ACTATTAATT AACTTCAAGT GCAATTTTGG CAGGCAGGCC 60
AAGGGTCTCA ACAGGCTATT TGAATGAGT TCTCTTTTAA GGCCTTCAAC GTAGTNNAC 120
ATTTTCAAAT CAAAAAGTAC AGCAGGAGCC AGCCTTTATT TTGCTGTGT ACACAATAAA 180
ATATTCCGCT TCTATAGGCA AA 202

SEQ ID NO:1179

LENGTH:211

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01325

SEQUENCE DESCRIPTION:

GATCAGCTGA AGGTTTCATGG GTTTTAAGTG CTTGTGGCTC ACTGAAGCTT AAGTTAGGAT 60
TTCNTTGCAA TGAGTAGAAT TTCCCTTCTT TCCCTTGTC CAGGTTTAAA AACCTCACAG 120
CTTGATAAT GTAACCATTG GGGGTCCGCT TTAACTTGG ACTAGTGTA CTCCTTCATG 180
CAATAAACTG AAAAGAGCCA TGCTGTCTAA A 211

SEQ ID NO:1180

LENGTH:199

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01326

SEQUENCE DESCRIPTION:

GATCCCAGGG TGCAAAGTGG CATTGAGACA GCAGCAACAG CTCAAGAGAT ATCTCCTGCC 60
TACTTGCCCC TCCTTCCAGG CCGGCTCTAA GAGAAAGGCC CATCTACTCA GGAAGAGGGC 120
CAGGNCCTTG GGTTCCTGGG ATTGGCCCCT GAGAGGGCTA GTCCTGTGGC TGAATAATAA 180
GCATGTCCCG CCCNNTAAA 199

SEQ ID NO:1181

LENGTH:199

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01327

SEQUENCE DESCRIPTION:

GATCTTTTT TGGATATTTA TACTTTTGA TATATAGTAC CTTTAAGTAG CAGTATGGGA 60
CAAGGCTTGT AAATGTTTTG TCTAATGTTT TATTGTCACC TTTTATGCAT TTATCACTTC 120
CAAATCTAAC TTTGCACAAG TAACCCATGT AAAAAAAT GTACATTTTT CAAAAGTTGT 180
AAATAAAAAT AACCTTAAA 199

SEQ ID NO:1182

LENGTH:252

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01328

SEQUENCE DESCRIPTION:

GATCTGGACA GCTGTCCCTC CACTACAGAA ACCTCACAGA ACACAGCAAA GNATAAGTGC 60
ANGAAGGCTG CTTCCAGCTC CAAAGCACCT ANGAATGGAG GTAAAGCGAA GGATTCAGCA 120
ANGACAGCAG AGGAACTTC CANGCCAAAA GNTGACTAAA GNAGTACAGG TTANGGTATC 180
TGGTATCTGC ATGTAGANTC TTCAGCTGGT GGATGGTGAC TTTGAAGTA CNAAAGGCTT 240
TGGCAACNGN AN 252

SEQ ID NO:1183

LENGTH:197

DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME ____ DE ____

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

2153480

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THIS IS VOLUME 2 OF 8

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DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET
COMPREND PLUS D'UN TOME.

CECI EST LE TOME ____ DE ____

NOTE: Pour les tomes additionels, veuillez contacter le Bureau canadien des brevets

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JUMBO APPLICATIONS/PATENTS

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THAN ONE VOLUME

THIS IS VOLUME 3 OF 8

NOTE: For additional volumes please contact the Canadian Patent Office

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01329

SEQUENCE DESCRIPTION:

GATCTAGGGA GTTACCTAGC AGACCTTCCG GACTGACGTG ATGCTACAGG GGTCCCATCT 60
TTCCTTGCA TTGAGCTATT TTACAGTTCT GTGAATTGTA AAGAACTGAG GGTAATGCGA 120
ATNACTCTTG TTCATAGAGG CAAATGAATT TTGTCCCATG GAGATTTAAT TGATATTACT 180
CTGTGGATGT TGACAAA 197

SEQ ID NO:1184

LENGTH:146

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01330

SEQUENCE DESCRIPTION:

GATCATAGCT ACTACTTCAT TGCAACCTTT ATTAAGTGAC CACATCAGAC ATCATGCTAA 60
ATACCTGAAT GCATGAAAAA ACTCCAAATA AGAGAATCTC TTCAGGATTA TAAAAGTTGT 120
AAAATGCAAC TGTATTGCTG AGCAAA 146

SEQ ID NO:1185

LENGTH:197

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01331

SEQUENCE DESCRIPTION:

GATCCGGCTG CACACCAGGT GCGGAGGCTG AGCCATCCCT GCTGGACTCC CTACCGCAGA 60
CGGAGTCANG NACGCAGCCG CAGCCNCNTT CCTTCACACC CCCTCACAGA CTCCTTGTGT 120
CCAACGGGAA TAGGAAGAAT TAGTTACTGA CTTACCTGA GAAAAAATA AATNCTCTAT 180
GGTGGTTTCA CAGGAAA 197

SEQ ID NO:1186

LENGTH:196

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01332

SEQUENCE DESCRIPTION:

GATCTCTTTG TGAAGTCTGT GTTCTCTATA TTAGATTGCT GTTTATATGT AAGAATTTTA 60
TTGCTTATGT GGCATACAAT ATTTATACT ATAACTTTA TAGAAGTACA GTATTAAAGT 120
CAGTGGTACA CAGACATTCT GTACATATCC TGTGAAACGT GCTGTCATAT GAAATAAATA 180
TATCTGTCTT TACAAA 196

SEQ ID NO:1187

LENGTH:196

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01333

SEQUENCE DESCRIPTION:

GATCTTCCCC ATTGTCCACT CAAGTCGTGG CCTGGGGAAC ACAGACGGAG CTGTCCCCAG 60
TGTCCTCCGT CCCTCAGCCC CTGGCCTGGC TGAGTTTGGC AGGGCCTGGG CCATCCCTGG 120
GACAAAGGTG CGTCCCTTCA GCTCTTCTCC GTGGAGCTCG GGGCTTCTG TATTTATGTA 180
TTTGTACGAA TGTAAG 196

SEQ ID NO:1188

LENGTH:196

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01334

SEQUENCE DESCRIPTION:

GATCTTCGGC CTCATTCTGA ATACCTNTTC TTTGGACAGT NTTTTTCCTT TGGTGCTCTC 60
TTGCCTTTAG CTACCTTCTC TAATATGTAT GCTACCATCA CTAATAAAGT GATGGGAATG 120
GGTTTGAGAG TCGTAATTTA TATTAAAAAG TTGTTGGACT TTAAATACA TTTTNNCAA 180
TAAAAAATTA AGCAAA 196

SEQ ID NO:1189

LENGTH:193

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01335

SEQUENCE DESCRIPTION:

GATCATGTGT GCACAATACT TGTGGCCAC AAAATTTAC AATGACTGCT GAGGAATCAT 60
TCTTTTGGC TGTAATAATAT ACAAAGGGC ATCATTAAGT AGACCAGTA ATTACTGCTT 120
GTNTCTAAG GCTGCTGTCT TTATCAGCAC TAACTAAATA AATTGTTGG TTCAGTTGTA 180
CTGTCTCTGC AAA 193

SEQ ID NO:1190

LENGTH:192

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01336

SEQUENCE DESCRIPTION:

GATCCTGTGT CCTAAATTAA TATACACCAG TGGTTCCTCC TCCCTGGTAA AGACTAATGC 60
TCAGATGCTG TTTACGGATA TTTATATTCT AGTCTCACTC TCTGTCCCA CCCTTCTTCT 120
CTTCCCATT CCCAACTCCA GCTAAATAT GGAAGGGAG AACCCCAAT AAACTGCCA 180
TGGNCTTTTA AA 192

SEQ ID NO:1191

LENGTH:189

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01337

SEQUENCE DESCRIPTION:

GATCAGTGCC TTGATGCCAA CTAAGGAAAT TTGTTTAGCA TTGAATCTCT GAAGGCTCTA 60
 TGAAAGGAAT AGCATGATGT GCTGTTAGAA TCAGATGTGA CTGCTAAAAT TTACATGTTG 120
 TGATGTAAAT TGTGTAGAAA ACCATTAAAT CATTCAAAT AATAAACTAT TTTTATTAGA 180
 GAATGTAAA 189

SEQ ID NO:1192

LENGTH:189

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01338

SEQUENCE DESCRIPTION:

GATCAAATTT TTGTAATAAT TTTTAAGAAG AGATGGCTTA TTAACAGGGA AGAAGCTTGT 60
 NATATTCCAG TTGTAAGAAT AGCCTTAGTG TTTAGATTTT TTNATGATAG GNNAGATGCG 120
 GNCATCACTG GGATATTNC AAATCCCAAG GNCATCAGAG TGAAGTGCA GTTGTGAGAT 180
 GATTNNAN 189

SEQ ID NO:1193

LENGTH:188

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01339

SEQUENCE DESCRIPTION:

GATCCCAGCC AGGCCCTGGA GGTCTGACAG CCCCTCCCTC CCAGAGCTGG TTCCTCCCTG 60
 GGAGGGCAAC TTCAGGGCTG GCCACCCCCC GTGTTCCCA TCCTCAGTTG AAGTTTGATG 120
 AATTNANGTC GGGCCTCTAT GCCAACTGGT TCCTTTTGT CTCAATAAAT GTTGGGTTG 180
 GTAATAAA 188

SEQ ID NO:1194

LENGTH:187

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01340

SEQUENCE DESCRIPTION:

GATCTGAATG ATACTGTCTG CTGTGCTTT TTTCCATGAG AAATCACTGT TGCAAATTGC 60
 CTATAAATTG ACTCTACTAA AATAACAATG TTTCAGTCTG AAAATTTGAA TTGAAAAAAA 120
 TGTATAATAT AAAATTGTAA TACTCTCAA TGATTATAAA AGTAAAAGTT GGTAATTAG 180
 GCAGAAA 187

SEQ ID NO:1195

LENGTH:187

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01341

SEQUENCE DESCRIPTION:

GATCAGGGGG GAAATGGAAT GAGTGAGGCG GGCCAGGGAG CCGCTCAGCT CCAATCTTTG 60
TCACTGTGTG AAATGTGGAC TTGGTATGAC CTGACTGTCC AATTTTCAAG ATGAACCAGA 120
AATCCAGACC NTTATATAAA ATCTCCTGGA TTTTAAATG TTGGCAATTA ATCAGAATGT 180
TTTAAAA 187

SEQ ID NO:1196

LENGTH:186

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01342

SEQUENCE DESCRIPTION:

GATCACTTAA TTCCTTTCTT ATCTTCCCC TCACCTCCCT TTCTCCCACC CTCTTTTCCA 60
AGCTGTTTCG TTTGAATATA TTACTGGAAT GAGTTGCAGG NAATGCAGCA NACTTGTTTC 120
NCCTAGATTT GAGTCAAACCT CCTGNTCAAA GAATCGGTNG GGCATANAAG AAATNTTCTT 180
NTTAAAA 186

SEQ ID NO:1197

LENGTH:186

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01343

SEQUENCE DESCRIPTION:

GATCTTTTAA ATGACAGTAC AGACTGAGAT TTGAAGGAAA CATGCACAAA TCTGTAAAC 60
ATAGACCTTC GCTTTATTTT TGTAAGTATC ACCTGCCACC ATGTTTGTGTA ATTTGAGGGT 120
CTTGATTCAA CCATTGTCGG TGAAGAAAAT TTTCAATAAA TATGTATTAC CCGTCTGAAG 180
CTTAAA 186

SEQ ID NO:1198

LENGTH:186

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01344

SEQUENCE DESCRIPTION:

GATCTTCAGG TATTTTAAAT TTTAGTTACA TCAATTAATG TAAATNAATC CAAATGCTAA 60
TTTTTGTTGT GCAAGAAGTT TCTTATGTAA ATNCAGGGTA TGGATAAGCT AATTAAGATA 120
TCCATCTTTG GTGGCTCTAA GTGTATTATT TGTNTTTAAA TAAAGTGTAC AAATATAGAT 180
AACAAA 186

SEQ ID NO:1199

LENGTH:184

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01345

SEQUENCE DESCRIPTION:

GATCTAAACA CGAGGAAACA TTATTCATTG GAAAAGTGCA TGGTGTGTAT TTNAGGGATT 60

ATNAGCTTCT TTCAAGGGCT AAGGCTGCAG AGATATTTCC TCCAGGAATC GTGTTTCAAT 120
TGTAACCAAG AAATTTCCAT TTGTNCTTCA TGAAAAAAAAA CTTCTGGTTT TTTTCATGTG 180
GAAA 184

SEQ ID NO:1200

LENGTH:183

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01346

SEQUENCE DESCRIPTION:

GATCGCCCGC CCCAGCCCGG GGCCGCTCAG GTCTGCTTGG AGGATGCCTC CCCCAGGAGG 60
GCAGTGAGGG ATGCCGCAAC CTCGACTTCT CAGCCTCCTG GGGTTCGCC GGCCAACACT 120
GTCTGTNTCA AATACTGTGC TGTGAGTTGT TTCAATAAAG GGGCCCCAAG GGCTGGGCTG 180
AAA 183

SEQ ID NO:1201

LENGTH:184

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01347

SEQUENCE DESCRIPTION:

GATCTCTGCT CAGCTTCCCT TGCCTTTTAA GGCCTGCCCT AGCCAGGGTT CCCTCCTGCT 60
TCCAGTACCC TCTCATGGCA TAGGNTGCAA CCCAGCAGAG GGCAGCTAGA TGGACATTTC 120
CCCTGCTCGG AAGGGTTNGC CTGCCTGGCT GGGGNGGTCA GTAAACTTTG AATAGTAAGC 180
CAAA 184

SEQ ID NO:1202

LENGTH:183

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01348

SEQUENCE DESCRIPTION:

GATCCCCTTT GGTTTACTA CCCAAATCTA AATAGATACT TTTGATAATA GATAACTGCT 60
CTTTTACTAA GACATAGTCT CTACCTATAG AAATGTATTT TGAAAACACT TATTTTACAC 120
AGCAATTTTG TATCCATTTA AACTAACCTT TTATCAATAA AGCACTATTG TTTAGATATT 180
AAA 183

SEQ ID NO:1203

LENGTH:183

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01349

SEQUENCE DESCRIPTION:

GATCTCATTC TCCCTTTTAA TCCTGAGTTA CCATCAGTGC TAATGTTTCT CTTTTGGGTA 60
TAGTTCTCCA GGAGAACTTG TCCTATATTT NTTTGTGTGT GTTTTTTTCC TTCCAGCTTA 120

AACAAATTAA AACTAAATAT CTAAACCTTG TATACAGACA TAAAATTAG TGAGAGAAAC 180
 AAA 183

SEQ ID NO:1204

LENGTH:183

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01350

SEQUENCE DESCRIPTION:

GATCTGCTTT TNCATTTCT CCCAACCAAA TCCTCTTAAA GACCCTTTGC TATGTAGTCT 60
 CATGGTCTAG CATGCATCTT GTAGAAACAA GGCATNCTGG CAGATTGCAG GGTTGAGATG 120
 TGTTTTATCT GTTTTATATT TAAAAGATT CTGCCAGAAA ATAAAACCAG ACCTTGTCT 180
 AAA 183

SEQ ID NO:1205

LENGTH:183

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01351

SEQUENCE DESCRIPTION:

GATCTGAATA GAGAAATGCT TACAGATAAT CATTAGCCCA CATACCAGTA ACTTATACTT 60
 AAAGATGGGA TGGAGTTGTA AAGTGCTTTT ATAATACAAT ATAATTGTTA AAGGCAAGGG 120
 TTGACTCTTT GTTTTATTTT GACATGGCAT GTCCTGAAAT AAATATTGAT TCAATATGGC 180
 AAA 183

SEQ ID NO:1206

LENGTH:182

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01352

SEQUENCE DESCRIPTION:

GATCCTTGGG GGCCAGGGTG AAGGGTATTT TACGGGAACT CTATAAGCA GGAAGAAGCA 60
 AGTTTATTCT TTAGACCAGT AGCTCTCAAC CATGATGTGG TCGTATATTT ATGGGTCAAC 120
 ATGTGTTGTG GGGATATCCC AAGTAACTTG TTATTAATAA AAGTTAAGTT GCAAAATTTA 180
 AA 182

SEQ ID NO:1207

LENGTH:182

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01353

SEQUENCE DESCRIPTION:

GATCAAAATT GAAGACACAT TCAGAGGTTT GATTGGTTGA GATTAAGTGG TGTGGTGGTT 60
 GGTGTATGTA TGTTNATTT TNATGTCTTT GTATGTAGTT CTACATAATG CAAATTGTGC 120
 TTTCTGATGG ACAAGACCTC ATAAGTGTGA TTAATATCAA TAAAAGGGG ATGTTGTGGA 180

AA

182

SEQ ID NO:1208

LENGTH:183

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01354

SEQUENCE DESCRIPTION:

GATCCGTCAA TCTTGGGTGG AATNATTGTN CGCATTGGCG AGAAATATGT TGACATGTCT 60
GTCAAGACCA AGATTCAGAA GCTGGGCAGG GCTATGCGGG AGATTGTCTA AAAGTGTGG 120
TTTTCTGCCA TCAGTGAAAA TTCTTAACT TGGAGCAACA ATAAANAGCT TCCAGAACAG 180
AAA 183

SEQ ID NO:1209

LENGTH:180

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01355

SEQUENCE DESCRIPTION:

GATCATGTTA TATTCTATAT CAGACAACT ATTTNTTTT GACCTTTCTT CCCCTCCATC 60
CAGTATTTTCG GTTGATTTC TTTCTCCCC TCTCTCCCC TTCCACGAAC TGCAATACCA 120
GTAACCTTGG TATATATTTT TTGATACTGT ACACATGGAT GTNTTGTTTC TATGTGCAAA 180

SEQ ID NO:1210

LENGTH:180

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01356

SEQUENCE DESCRIPTION:

GATCAAAGAT TCTCCCATC TCACAGACAA GGAACTNAG GCCAGAGGGA GGAGAGAATT 60
GCTCATGGCT CCANAAGTGG TGGCAAGTTT CTCTGGACTC TTAGGTTTAT TTTNAATATG 120
AAATATAAAA NCAGTTTCAA ATATCTNATT GAGGGAGANG TAAACCTTA TTAAANCAAA 180

SEQ ID NO:1211

LENGTH:179

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01357

SEQUENCE DESCRIPTION:

GATCTATAAA ATGGAAGGTG ACCAATGTCA CTGCTTCTAA AATACTGTCC TAAACAACCC 60
AGAAGATTTT ATTCAGCTC ATGAATAGCT GTTCTAAATC TGTTGTATGT TAGACATACT 120
ATGAACTACC TCTTCACTTA TTATGGGGAA GTTTCCTTAA TAAAAGTGTG ACGATTAAA 179

SEQ ID NO:1212

LENGTH:179

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01358

SEQUENCE DESCRIPTION:

GATCCAAGAC CAGGGNGGTT GGGACGGCCT CCTNCCTAC TTTGGGACGC CCACGTGGCA 60
GACCGTGACC ATCTTTTGG CGGGAGTNCT CACCGCCTCA TTCACCATCT GGAAGAAGAT 120
GGGCTGAGGC CCCAGCTGC NTTGGACTGT TTTTNCNC CATAAATNAN GGCATTTN 179

SEQ ID NO:1213

LENGTH:178

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01359

SEQUENCE DESCRIPTION:

GATCTGAGAT GTTCCTTAAC ATGTAGCCAT GTAATTAGAA CTCACAAGGG GCATTGAAAT 60
NTTTTCCTTT TTCANATAGT CTGGGGCTAT TTAATTATTT NAAGTAAGCC AAGTCTACCA 120
TTTGAAAAAT GGTGCTTTAT TTCCATATCT GANGCCTGAN GTTATTTNNN AGTTTGTN 178

SEQ ID NO:1214

LENGTH:178

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01360

SEQUENCE DESCRIPTION:

GATCTGGCAT CCNAGGCTG CAGCTTTATT AGCTTATAAC TTAATCATCT CTATCTTTAC 60
CAGCAGGCTC TGTATTGTTG ATATTTGCAA CTNGNTTGC TTTCCCATG GTGGAATTGA 120
AATAATTAGT TTTAATNAC ATAAGANGCC TGTGCTAT TNGGNGGAAG ATAGATGN 178

SEQ ID NO:1215

LENGTH:176

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01361

SEQUENCE DESCRIPTION:

GATCAAAGAG GTTATCTCTG CCAGTCACAA GTGTGGCTGG TGTCATTCTG GGTCTGACTG 60
GAGCCCTCCT GGACTGTTTC TTTAATTCA AAAGCCCTGC AGACATAGTA CCTGGTCAGA 120
ACTATGCCTC GGTTTATTTA TCATTTTGAA ATAAATCAA AATTCAACC TGTA 176

SEQ ID NO:1216

LENGTH:176

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01362

SEQUENCE DESCRIPTION:

GATCAAAACA ATTACCTAAT TGCAAAAGAG AAAGTGAAT GGAACATAGT CTCANATTCT 60

NCTAATGTGT ATCTCACAAT GTCATGTAAT GTAAAGNAAA CCCTTTTGGA ATTAGAATTC 120
TTGTNCTGAA TGCTGAACTA TTTGGTAATA AAGTGCTTAT NTGCAGATAA CAGAAA 176

SEQ ID NO:1217

LENGTH:175

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01363

SEQUENCE DESCRIPTION:

GATCTGTGCT GGGGAACAAA GCTTTTGCAG TACCTTATAT TGTAAGTAAA ATTTTATTTA 60
ACATATCCTT CAGTGAGCTC ATTTCACT GTAGCCTCTT CCTTAAATTT TGTGGTGCTC 120
CTGTAACAGT AAGANCTAAT TCTGAAATAA AAGACATCTC CTAATGCTGT GCAA 175

SEQ ID NO:1218

LENGTH:174

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01364

SEQUENCE DESCRIPTION:

GATCAGGATA ATAATCTGCT TAGTAAGAGA AACAAATTTGA ATTTTAGAAG GAAATTGCCT 60
TACCATTGTC AAATTAAGGT AATTAATAA CAGTGAATTT CAAATGCCT TTTAATGAC 120
AATGTGTGAA CTTAATTTGT TTTAATAAAC CAAATTTGT GTTATTGTGT TAAA 174

SEQ ID NO:1219

LENGTH:174

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01365

SEQUENCE DESCRIPTION:

GATCTGAGCA GGCAAAGCTC AAAAGAGAGT TTGGAGGTTA AAAATAATTT ATTTTGCAG 60
TAGTGTGCTT TGAAATGTGT AAATCTTATT TCTAATGTAT ACAACCACAT TTCACATAAA 120
AATATGCAAT TTATATGCCA GATAAAAATA AAACAAGTGA ATTTGCAAGT GAAA 174

SEQ ID NO:1220

LENGTH:173

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01366

SEQUENCE DESCRIPTION:

GATCAACATG ATGGTGACTG GGAAAAAATT ACTTCAAGTA ACATGCTTAG CTTTCCCTCC 60
TTAATGTGAA AAATCAAGGG CTTACTGACA TAGGAACAAC AGAAATGCTC CTGGAACCTC 120
AAGTTGCTGA ATTATAAGTT TATTTTNNAT CAATAAATAT NNNNATACTN AAA 173

SEQ ID NO:1221

LENGTH:216

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01367

SEQUENCE DESCRIPTION:

GATCCATATT TAGTTTTATT AAGCTTTTCC CTGTTTTTAG TTTGTTTTG GGTTTTTTGG 60
CTCATGAATT TNATTCTGT TTGTCGATAA GAAATGTAAG AGTGGAATGT TAATAAATTT 120
CAGTTTAGTT CTGTAATGTC AAGAATTAA GATTAAAAA NCGGATTGGT TAAAAANTGC 180
TTCATATTTG AAAAAGCTGG GAATTGCTGT CTAAAA 216

SEQ ID NO:1222

LENGTH:173

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01368

SEQUENCE DESCRIPTION:

GATCGNCTCT GAACCATCCC NTTTCTGCTG CCCGGAGCTG GGGAAGCTCG CTGTGGAGCG 60
TCTCGCACGT GGCAGGCAGG CAGAGAACTT GCTGCACCTT CTAGGAAATT GCAATCGATT 120
TGTAATGCAC TTTCGCTAAT TGGGAGTTCA AAATTAACT TTAATAAAGC AAA 173

SEQ ID NO:1223

LENGTH:179

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01369

SEQUENCE DESCRIPTION:

GATCTTAAGA GCAGACTTAA AGTAGCTTG TACGCCTTAA TGTTCATTTT GATTATTTT 60
AAATCTTTAC ATTCAGAAAT NAGATACTGT ATTATCAGAC CAGGAGGCAT TGCTGTGAAA 120
GATAATNTCC TATTCTAAAA TATCAAATTT AAAATAAAGA TAATGAAAGA AAACATAAA 179

SEQ ID NO:1224

LENGTH:172

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01370

SEQUENCE DESCRIPTION:

GATCCAAAAA TGGTAGCCAC TCACCCTTCA CAACTGAAG TCCATGGACC ACGGAAGTCG 60
AGAATTAATG TACACCTGTA TCATGTGTAG GAAACCAGAA ATGTGTTTCT TATTNTTGT 120
TCCCAAACAG GATTAATGTT GAAGACTAAT TTATAAATGT GAACCTAAGA AA 172

SEQ ID NO:1225

LENGTH:179

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01371

SEQUENCE DESCRIPTION:

GATCAGCATG AGGACAGAAG GCAGGAGACT TTGGTCAGTT ACCTGGGAAT TCTGGGCTGC 60
CAGGAAACGA TTTGGGCCTC TGTCAGTTTC TTTTCCATGT ATGAGGAGGG GGAAATTTGT 120
ATATTAGAAA CTTATTCATC CCACTCAGGA CAATAAAAAAC GAATGTACAA AAAGCCAAA 179

SEQ ID NO:1226

LENGTH:175

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01372

SEQUENCE DESCRIPTION:

GATCACAGTG GCCACGNCCA GGCCACAGTC ATGGTGGCCA CGTCCACAGC CACTAATCAG 60
NAGNCCAGGC CACCCTGCCT CTACCCAACC AGGGCCCCGN GGCCTGTTAT GTCAAACNT 120
CTTGGCTGTG GGNCTAGGGA CTGGGGCCAA ATAAAGTCTC TTCCTCCAAG TNAAG 175

SEQ ID NO:1227

LENGTH:318

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01373

SEQUENCE DESCRIPTION:

GATCTTTAAT CTCATGAAGT ACGACAGCTA CAGCCGCTTC TTAAAGTCTG ACTTGTTTTT 60
AAAACACAAG CGAACCAGAG AAGAGGAAGA AGATTGCTTAT GATGCTCAA CTGCAGCTAA 120
AAGAGCTTCC AGAATTTATA ACACATGAGC CCCCAGGAG CCGGGACTGG CAGCTTTAAG 180
AAGCAAAGGA ATTTCTCTC AGGACCGTGC CGGGTTTATC ATTGCTTTGT TATTGTAAG 240
GACTGAAATG TACAAAACCC TTCAATGGGA TGTGTGTTTT ATTAAGTCTC TCACCAGTAA 300
ATTTTGCATG ATGGGCTN 318

SEQ ID NO:1228

LENGTH:171

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01374

SEQUENCE DESCRIPTION:

GATCTGGAAG AGGCTTGTNA CCTGAACTTC TGTGTGGTGG CAGTACTGTG GCCCACCAGT 60
GTAATCTCCC TGGATTAAGG CATTCTNAAA ANCTTAGGCT TGGCCTCTTT CACAAATNAG 120
GCCACGGCCT AAATAGGAAT NCCCTGGATT GTGGGNANGT GGGCGNAGT N 171

SEQ ID NO:1229

LENGTH:170

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01375

SEQUENCE DESCRIPTION:

GATCTGATGG TTTTAAAAAG AGGAGTTTCC CTGCTCAAGC TCTCTCTCTT TGCCTGCTGC 60
CATCCATGTA AGATGTGACT TGCTCCTCCT TGCCATCTGC CATGATGTGA GGCTTCCCCA 120

GCCACGTGGA ACTGTAAGTC CAATTAAACC TCTTTTCTTT GTAAATTAAA

170

SEQ ID NO:1230

LENGTH:170

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01377

SEQUENCE DESCRIPTION:

GATCCATGGT GTTAGAAGCC AGGGGAACAG TTAACAGGGG AGGGATACTG GGGAGGGGCA 60
TCCTGGAGTG CTGGTCTACC TCATCTGGGT GTTGATTTC A TGAGTATTGT CAGTTTGTTT 120
CCAGACTCCC TGTGAGAT GTGGAAATAA AAACCACCTA ANCANGNAAA 170

SEQ ID NO:1231

LENGTH:170

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01378

SEQUENCE DESCRIPTION:

GATCCATCAC AAAGCGAAGT CATGGGAGAG CCACACTTGA TGGTGGAATA TAAACTTGGT 60
TTACTGTAAT AGTGTGCTGT TCATGGAAAC CGAGGGCTGC ATCTTGTTA TAGTCATCTT 120
TGTACTGTAA TTTGATGTAC ACAACATTAA AAGTACTGAC ACCTGAGAAA 170

SEQ ID NO:1232

LENGTH:168

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01379

SEQUENCE DESCRIPTION:

GATCTGGGAT GGAATATGGT TTTCTTGATT CCCTTTCAGC CTTCATTCT CTCTCTCAGG 60
ACTACTACTT TTTAATTACT TTTCACTTAA TTCCCAATA CTGATGAAAT AAAGAAAAAT 120
GAGGGTTATT TATATACATT TCAATAAAAT CCAATTGAT TTTTCAA 168

SEQ ID NO:1233

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01380

SEQUENCE DESCRIPTION:

GATCTAGAGA ACATAACAAA TGAAACTCTA GAAATTTGAA AGAAAAAAA AACTTAGCT 60
GTAAGTGCTT TGACCTATTT TTTTAAAAA AAAAAAACC TGTNTTAATT CTGTGACTGN 120
ATTGNACCCT TCACCAGCAC TANGNGAAGT NGGANTGGAN GAAATTN 167

SEQ ID NO:1234

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01381

SEQUENCE DESCRIPTION:

GATCAAGCCA TCGGAGCTGC TAGAGTTCTG TCTGGACTTT CCAGAGACCA GTATCCCTT 60
TTGCTGCCTC TAAAAGGCCT GTCCCTGCAG ACATGAGAGA CAGCAGGTCT CATGGGGTG 120
ACAAGCTTTT TTTTTTTT TAAANGATTT TCNAAANNNA ANTNCN 167

SEQ ID NO:1235

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01382

SEQUENCE DESCRIPTION:

GATCTTTTGT CTTCCAGTCT TCTCTTAGTG TCCTGCTCCT AGGTTTCCCT CTCTTCTGGT 60
TCTTCTCCCA GGTATTCTCT TCCCAGGCCT CTCTGGCCAC TGCTTTGTAT CAGGGTTTTT 120
CACGCTTTTG TAGAACTGAG GTTCAATAA ACAGTTTCAG TTGCAA 167

SEQ ID NO:1236

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01383

SEQUENCE DESCRIPTION:

GATCCTCCAG CCCACCACCA CATAGTAATC ACTGACACTG TGGGGTGTCT CAGCTGGGGT 60
TCTGCTGTGT GTGTGTGTAT TTNACAAAAT ATGTATGGTT TCTGTTCAGC TCTTTTCAGT 120
TAACAGATGA ACTGNNNNTA TCATTAAATA TTTTGAAAA CATGAA 167

SEQ ID NO:1237

LENGTH:171

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01384

SEQUENCE DESCRIPTION:

GATCCATCAG TAATGTAGCT AGCTGTAGAG CTGCAACTT AATAGCAGCA GCTGCCCAAT 60
GCCATGTNAA GTAACAACT GGTTTTGGT TTTTTTTTC CCCTTCAGTT TAAATGTNAT 120
GTGNAATGTA TTAAACCCT TATTAAATA AANCTTGTT TCAGAAATAA A 171

SEQ ID NO:1238

LENGTH:166

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01385

SEQUENCE DESCRIPTION:

GATCTGGGGT TGGGTCTAG CACCAGCTAC CAATTTNAGA ATATTATCC TNGGTTTCTT 60
TATGAAAAAT GGGTGCTAGT GGTAATTCCT TNGTGGCTTA GTAACTACT CTNTGGATGA 120

TTTCCAAACA TTCAAAGCCA ATAGCCTNGT NATNAACAAG ANATTN

166

SEQ ID NO:1239

LENGTH:165

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01386

SEQUENCE DESCRIPTION:

GATCAAAACC CAGCAGAGTG CAAGCAGCAG TGAAGCAGGA TGGTCTACCT TCTGCTTCCC 60

TGGAAAGGAT GAATTACAT CATTTGACAA GCCTATTTTC AAGTTATTG TTGTTTGTTC 120

GCTTGTTTTT GTTTTGCAG CTAAAATAAA AATTTCAAAT ACAA 165

SEQ ID NO:1240

LENGTH:165

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01387

SEQUENCE DESCRIPTION:

GATCTGTCTG TGTGTTATA TATTCTTTTA TGCATACTTA AAGTTAAAGG GTTTTATCCA 60

CTGTCATTTC AATTGGATAA CATTTTGTCA AGTTTTTTTT TCCTGATTAT TTGATGTAGC 120

TGGATTCAAG AATGGATTGC CTNATCAATA AAGAATATTT AGAAA 165

SEQ ID NO:1241

LENGTH:166

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01388

SEQUENCE DESCRIPTION:

GATCCTATTT TGGGCCTGGG GTGGGTATAC CTGNGGCTGG TCTTAGGAGG GTGCTAGGCT 60

GCAGACTGCC TTGTACTCCC TGGACACCCT CAAATGGGGT TTTCTGTGTT ATTTCATAAA 120

ATTCTTTGAA GTCCAATAAA GCATGTAGGA GATTTTAACC ACTAAA 166

SEQ ID NO:1242

LENGTH:164

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01389

SEQUENCE DESCRIPTION:

GATCAAAGGN CAAAAGACCA AAAATCAGCG GGCTGAGGAT GGAGCACAGC CATGAACCTG 60

CTCAGACAA GACGCACCA TGCTTCTCAG GGTCAAGGCT TTATGTAAAA GCTTCCTGTC 120

GGGGCTGCTA GGTCAGCATT AAAGTAAGGC AACCAACAGT NAAA 164

SEQ ID NO:1243

LENGTH:163

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01390

SEQUENCE DESCRIPTION:

GATCTGCTCA GTAATATAAT TTGCCATTTT TATTAGAAAT TTAATTTCTT CATGTGATGT 60
CATGAACTG TACATACTGC AGTGTGAATT TTTTGTGTTT GTTTTTTAAT CTTTGTAGTGT 120
TACTTCCTG CAGTGAATTT GAATAAATGA GAAAAAATGC AAA 163

SEQ ID NO:1244

LENGTH:163

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01391

SEQUENCE DESCRIPTION:

GATCTGGATT TGCTTTACCT TGTTAATATT ATCTAGGGGA AAAAGTGCAA ATTGCTCCAT 60
GTTCTTCTCT CCCTTATGTA ACATCTCCTG AGGGTGTTTA GTTGCATGGC TGTTCAGAAA 120
GGTATTAAGG GCTTAGGCCA AATCTTACTT TGAGTATGTT AAA 163

SEQ ID NO:1245

LENGTH:162

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01392

SEQUENCE DESCRIPTION:

GATCGTCAAA AAGAGAACCA AGAAATTCAT CCGGCACCAG TCAGACCGAT ATGTCAAAAT 60
CAAGCGTAAC TGGTGGAAAC CCAGAGGCAT TGACAACAGG GTTCATAGAA GGTCAAGGG 120
CCAGGTCTTG ATATGATGCC CAGCATTGGT TATAGNGCA AA 162

SEQ ID NO:1246

LENGTH:197

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01393

SEQUENCE DESCRIPTION:

GATCTGGAAG TGAACACAGT TTATGTACAG GGAAAAGGAT TTTATTATCC TTAGGAATGT 60
CATCCAAGAC GTAGAGCTTG AATGTGACGT TATTAAAAA CAACAACAAA GAAGGCAGAG 120
CCAGGATATA ACTAGAAAAA GGATGTCTTT TTTTTTTTTT TNNCNCCTT TNTAANCNCT 180
GNTGCTGCCT NANTTN 197

SEQ ID NO:1247

LENGTH:160

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01394

SEQUENCE DESCRIPTION:

GATCTCAATG CCAATCCTCC ATTCTTCCTC TCCAGATATT TTTGGGAGTG ACAAACATTC 60

TCTCATCCTA CTTAGCCTAC CTAGATTCT CATGACGAGT TAATGCATGT CCGTGGTTGG 120
GTGCACCTGT AGTTCGTGTT ATTGGTCAGT GGAAATGAAA 160

SEQ ID NO:1248

LENGTH:160

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01395

SEQUENCE DESCRIPTION:

GATCTGAAAA TCGACCTCAA CTCAAGGGTG GTCAGCTCAA TGCTACACAG AGCACGGACT 60
TTTGGATTCT TTGCACTACT TTGAATTAT TTTTCTACCT ATATATGTTT TATATGCTGC 120
TGGTGCTCCA TTAAAGTTTT ACTCTGTGTT GCACTATAAA 160

SEQ ID NO:1249

LENGTH:159

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01396

SEQUENCE DESCRIPTION:

GATCTGCATG ACCTATAATC TTTGAACCAC TTTCGTACCT CATGTTTTTA TCCAGCACTC 60
TTATTGTAAT ATGTACTAGT CTGTGAACAA TGTCAAATAA AAGAGAACGA ACAGGTAGTT 120
TGGTGGAGCT GAGCTAGTGT ACAATACACT AGTTGTAAA 159

SEQ ID NO:1250

LENGTH:159

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01397

SEQUENCE DESCRIPTION:

GATCTTGGA TTTTGTNTG GATTTCACA GTTTTTAAAA TTAATCATGT CAGCCCAATG 60
CAGCTGTGTC ATTGCCACCT AGTGGAATAA CTAACATTAC TGTAAAGCTG TGTGATTTTA 120
AACTTGAATC CCCAGTAAAN GGTTCACGTG TCTGTGAAA 159

SEQ ID NO:1251

LENGTH:159

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01398

SEQUENCE DESCRIPTION:

GATCCCTCTG AGAGTTGATG AGGATGTGTA ACAAGTATTT NCTTCTATNG TGCCTGCCAG 60
GGCTGAAGCT GCCTGGTATC CAGGAGGGGA ATGCTGGTAT CCCCATATGN CTGTNTTTGT 120
TTGAGATTTT TAATAATAAA TAATAAATTT TTGAAGAAA 159

SEQ ID NO:1252

LENGTH:158

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01400

SEQUENCE DESCRIPTION:

GATCCTATTC TTGTA AAAAT ATTTGTATGT ATGCACAGAA ATCTGCAAAG ATGTACACTT 60
 AGTGAAGTGG TTACCAACGA ATGGTGGGAC TAACTAAAAT GGTCTTTTTA CTTATATGTG 120
 CATTCTTTT TATAATAAAA ATGGGTATA TGCCTAAA 158

SEQ ID NO:1253

LENGTH:158

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01401

SEQUENCE DESCRIPTION:

GATCTGCCCT GTGTTATCCA GTTATGAGAT AAAAAATGAA TATAAGAGTG CTTGTCATTA 60
 TAAAAGTTTC CTTTTTTATT CTCTCAAGCC ACCAGCTGCC AGCCACCAGC AGCCAGCTGC 120
 CAGCCTAGCT TTTNCCCNNTT TTTTTTTTTT NNNCNNTN 158

SEQ ID NO:1254

LENGTH:157

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01402

SEQUENCE DESCRIPTION:

GATCTCAATC TTCGGGGTGT GATGAATAGC GAATCATCTC AAATCCTTGA GCACTCAGTC 60
 TAGTGAAGAT GTTGTCATTA TGTACAATAC ATAAGTAGTT TAATTAAC TA TGATGTTA 120
 ACTATTATTA ATAAATTTTA ACATTTTCCA AAATAAA 157

SEQ ID NO:1255

LENGTH:157

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01403

SEQUENCE DESCRIPTION:

GATCCGGATG NGGGGAGCTC TGTACAGAGG GCTGGTGATT GTAAAAATTT CTTTGTAAA 60
 GTAGAAGTTG GGGGTGGGGT GGGTGCTGGC TGCAAAAATT TCTGGCTTCT CTTACCCCTA 120
 TTGCCCCCGG CAATAAATTG TTTCTATATG CCAGAAA 157

SEQ ID NO:1256

LENGTH:160

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01404

SEQUENCE DESCRIPTION:

GATCTTATTT GGAATTGACA TTCTCTATTG TAATTTTNTT CCTGTTTATT TTAAATTTN 60

CTTTTGTGTT CACTGGAAAG GAAAGATGAT GCTCAGTTT AAACGTTAAA AGTGACAAG 120
 TTGCTTTGTT ACAATAAAAC TAAATGTGTA CACAAAGAAA 160

SEQ ID NO:1257

LENGTH:156

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01405

SEQUENCE DESCRIPTION:

GATCTTTGTN CTTGACCTCT AGACCCAAG ATGTGAACAG TGCACGTTTT AATGTCATCT 60
 TTNCTCATGT GTTATAAGCC CCAAGTTGCT GTATATTNC ACAAGTATGT CTACACACTG 120
 GTCATGATTT TNATAATAAA TAACGATAAA TCGAAA 156

SEQ ID NO:1258

LENGTH:155

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01406

SEQUENCE DESCRIPTION:

GATCTTGCTC TGATTATAAT GCCAGTGAAT GTTGCTGAAC TCTTTGTATA TGCAAATTGC 60
 AAGATTTAAA CCATTCTGAT GCAAGGATAA ACCTTTACTT TGACTIONCAG CCTGTGTTTT 120
 TGTCTTTAAA TCTCTTAATT TCATTCCTCT GCAA 155

SEQ ID NO:1259

LENGTH:155

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01407

SEQUENCE DESCRIPTION:

GATCTGCACT CCCACTCCCC CCACACTTCC CAAAGTGCTG GGATTACAGG CATAAGCCAC 60
 AAGCCACCTC ACCCAGCCAA CATGTTACAT CTTAATTCTT GGATTTTCTT CACTGCAGGG 120
 CTTTGGGTGG AGAAATAAAA CTCTTCAAAT GCAA 155

SEQ ID NO:1260

LENGTH:155

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01408

SEQUENCE DESCRIPTION:

GATCTGGGAG TGCTGGACGT CATCTTCCAC CNCACCCAGC CGTGGGTCTT CTCCTCGGGG 60
 GCAGACGGGA CTGTCCGCCT CTTACCTAG CTGTTCTGCC TGCTGGGGC TGGGGTGGTC 120
 GTGCTGAAGT CAACAGAGCC TTTACCCTGT GCAA 155

SEQ ID NO:1261

LENGTH:158

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01409

SEQUENCE DESCRIPTION:

GATCTTGGAG GCCAGCCAGC TGAAGGAGAC ACTGCAGGCG GTGCCCAAGC CAGGGGCCTT 60
TGACCTGGAG CAGGTGAAGC GTTCCACCTA CTTNTTCAGC TGACACCCCG TGAGCCTTGT 120
CAGTGTGTAA ATAAAGCTCT TTTGCCACCC CCAGGAAA 158

SEQ ID NO:1262

LENGTH:151

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01410

SEQUENCE DESCRIPTION:

GATCCATCAT NGATGTAAAA GTTCACAATC ATGGTTCAAA TGTAACAGTG CAGAATTGAA 60
TATGGAGGCA TGCATAACCT TCCTCTTAGA AAATGGCAGG TGTGTAAATT TCAAATTTTT 120
GTGCAATTAG ATTAAATCAT AATGCAACAA A 151

SEQ ID NO:1263

LENGTH:154

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01411

SEQUENCE DESCRIPTION:

GATCTGATGG GTTTATCAGG GGTTCCTACT TTTGTTTCTT CATTTTCTCT TGCCACCAGC 60
ATGTAAGAAG TGCCTTTGGT CTCCTACCAT GATTCTGAGG CCTCCCTAGC CATGTGGAAC 120
TGTAAGGCCA ATTAAACCTC TTTTCTTCC CAAA 154

SEQ ID NO:1264

LENGTH:154

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01412

SEQUENCE DESCRIPTION:

GATCAGCACC TTGTATAGGA ATTCCCATGA ATTATGACTT CTCATTCTGT TTTATCAGAG 60
TGCATATATG TCCTACTTCA GGAAAAGTAA AACAGTCATT TACGAAAGAA AGTCAATCTG 120
TATCCTAAGC ATTTAATAA AAAGTTAAAA CAAA 154

SEQ ID NO:1265

LENGTH:153

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01413

SEQUENCE DESCRIPTION:

GATCCTGGCC TGAGAATTGA GGGGAGGTGG CCAGCCCGCA GAGGTGGGGT GCTGGGGCTG 60

CATGATTTTN GCCCTGCGTC CCTTCTCTTT GGGGCTCCTT TCCCCTCTCA TACATAAAAT 120
CGCTTTCAAA TTAAATCGC TGTTTTCTGG AAA 153

SEQ ID NO:1266

LENGTH:163

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01414

SEQUENCE DESCRIPTION:

GATCCGAGTG AAGCCCCAGG TCTCANAGAG CAAGCTGTAG CCAGATGGTA CCAGCTTCGC 60
CTGGGGCTTC AAGAACCCTCC CATCTATCCC CATTCTGAN ACAGGGAGTT ACAGTCCCTT 120
TTTGGCCCTC ACATNCAATA AANGTGACTG ATANCACTGG AAA 163

SEQ ID NO:1267

LENGTH:153

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01415

SEQUENCE DESCRIPTION:

GATCTGGCAA CACGTTTTNN TTGGAATATT TGTGTTTTCT TGAGGAGGTA TAATTACTGT 60
ATCCTAGGTG TGAATTTTGG AGTGCAGATG CACATTTTAA AGAAATNATG ATTAANCTGA 120
TAATGTTTTT NGGCTGAAAA TATAAANNA AAN 153

SEQ ID NO:1268

LENGTH:152

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01416

SEQUENCE DESCRIPTION:

GATCATAAAT CAAGGAATGC TGACAGCCAC TAAAGCTGGA GAAGGCCAAG GACAGATATT 60
CAATCCTCCC GTAGAAGTAC AGCCCTGCTA ATGCATTGAT TTTGGACTTC TGGCCTCAGA 120
ACTGTAAGAG AATAAATTC TATTGTTTTA AA 152

SEQ ID NO:1269

LENGTH:152

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01417

SEQUENCE DESCRIPTION:

GATCAGACCA ACAGTGCTGT TTCCCGGGAG GAACACTTTT TNATTNTTAC CCTTTGCAGC 60
TCCCACCTTT AATCTGTTTT ATACCTTGCT TATTAAATNN GCGCTTAAAT NATTGAAATA 120
ATGCTGNCTT AGTAGCAACT AAAATGTGNC TN 152

SEQ ID NO:1270

LENGTH:156

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01418

SEQUENCE DESCRIPTION:

GATCCCCCT ACCACCCCA GTCCCAAATC CAGTCCTCTG GCCCTTGCCT AGCCCTGAAT 60
TGCTTCTCTA AGCTGGTGT CCATGCACA GGGCCATTCA GGAAGGGCTG GGGGAGTGTG 120
TGTGGCAATA AAGCTTGAAG GCACCGTGGG AGCAAA 156

SEQ ID NO:1271

LENGTH:151

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01419

SEQUENCE DESCRIPTION:

GATCCTCTTC TCTCCAAATG TTAGCCATCC TGAAGTAGCC GAACAGTAGA AACTTTGGTG 60
GGGATTAACC GGGAGCTTGA AAATTTGTNT TTGGTAACCT GATACTGGAC AGCTGAACTG 120
AATGGCTGCA AAATAAATAC CTCACATGAA A 151

SEQ ID NO:1272

LENGTH:93

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01420

SEQUENCE DESCRIPTION:

GATCTGGAG GACCCTGGGC CCCAGGCCAG CTCCCATCGC TGGGGGACGG TGAACGGCCA 60
TGTGTTAATG TTACGATGTT TTTAAAAGAC AAA 93

SEQ ID NO:1273

LENGTH:149

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01421

SEQUENCE DESCRIPTION:

GATCCCCTTT GTCAGTGGGG AAACCAAGGC AGAGCTGAGG GGACAGGGAG GAGCAGAAGC 60
CATCAAGATG GTCAAAGGGC CTGCAGAGGG AGATGTGGCC CTTCTCCCC CTCATTGAGG 120
ACTTAATAAA TTGGATTNAT GACACCAA 149

SEQ ID NO:1274

LENGTH:151

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01422

SEQUENCE DESCRIPTION:

GATCTCAACG TGCTGATATG GAAAGTGCTT CAGAATGTAT TAAGGACATA AATTAAGTGT 60
ACAATAATGT GTGTGTGTGT ATATATGTAT ATGCTTACGT GTGTATGGAA AGTATCTCAG 120

CAGATACAAT AAAA ACTTAA TTGTGATTAA A

151

SEQ ID NO:1275

LENGTH:149

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01423

SEQUENCE DESCRIPTION:

GATCCTCCCT CTATTTTGCA AACAGTCTGT AAGTAACTNA TAAAACTTTA AAATATGCAA 60
ATTTTAAAAT TATATAGTTT GATTACTCA TCAAATTATC ATGTATGCTG TTATTTAAGT 120
ATGAATAAAG GCTTTTTTAA ATNGGGAAA 149

SEQ ID NO:1276

LENGTH:254

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01424

SEQUENCE DESCRIPTION:

GATCCTACTC CTTGGAGTA AAAC TAGTGC TTACCAGTTT CCAATTGTAT TTAGCTTCTG 60
GTTGGAATTT GAAAAAAAAA GAAAAAAGA AAAAGAAAAC CTAAATAAAA TAGGTGAAAG 120
TTCCCTGACT ATTCAGGTGA ATACACAAAG TTTGAAGTGT TAACTTTTTC TTTCCATTTC 180
ACTGATGTTA CTGGTCACCT TAGAGAATTA TTTCATAGTC TGTGGCTAAA TAGTAAATTC 240
AGANGAAAAA TAAA 254

SEQ ID NO:1277

LENGTH:148

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01426

SEQUENCE DESCRIPTION:

GATCCTACTG TTGAGTTAGG AAAATATGGT TAGACAGACT CACATTACTT TTTTCAGAG 60
GTAAACTCTA GATTACTGTG TCAACCCAAT ACTATTGGC CATAGATGTA AAAACTACCA 120
AATAAAAGTG GATTTTGTGG TCTACAAA 148

SEQ ID NO:1278

LENGTH:148

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01427

SEQUENCE DESCRIPTION:

GATCCACAGT GGAGTCTCAG TAATTATATC TCCTTGATT CTTCATTNC TCTTCTGCTA 60
TAAAAGTAGA GATAATGTGT AGTCACTNCT CATTAGTGA ACCAATTGTN ATANTTCTGG 120
AAATCTNTTN TCTTTAAGTG TAAATANN 148

SEQ ID NO:1279

LENGTH:124

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01428

SEQUENCE DESCRIPTION:

GATCCCAATC AGATTCCCGC TAATGGAAGA AGTTTAGAAT CTTTCAGGTG GAATAAAGTC 60
ACATGAAAAC AAAACACAAC TATATATATT TCCAGTTTTT TTGCCTTATT GATTTTTTNC 120
CAAA 124

SEQ ID NO:1280

LENGTH:147

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01429

SEQUENCE DESCRIPTION:

GATCTTTGGG GAGATACATC TTATAGAGTT AGAAATAGAA TCTGAATTC TAAAGGGAGA 60
TTCTGGCTTG GGAAGTACAT GTAGGAGTTA ATCCCTGTGT AGACTGTTGT AAAGAAACTG 120
TTGAAAATAA AGAGAAGCAA TGTGAAA 147

SEQ ID NO:1281

LENGTH:147

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01430

SEQUENCE DESCRIPTION:

GATCCTGACA CTAAGGAATG CTGAAGCTTT GGACTTCGGC AGTCTTCAC CTCAGTCAT 60
CAGCTACAGT TGGAATGAAT TTNAAAACGC TCGGGACCTG TTAATNTNTC CTGTAGNCTG 120
TATTATNTNA AAAATCTGGG CAACAAA 147

SEQ ID NO:1282

LENGTH:147

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01431

SEQUENCE DESCRIPTION:

GATCTCGCTC CCCCTTCGG TTCTTTCGAC CGGTCCCCC TCCCTTTTT GTTCTGTTTT 60
GTTTTGTTTT GCTACGAGTC CACATTCCTG TTTGTAATCC TTGGTTCGCC CGGTTTTCTG 120
TTTTCAGTAA AGTCTCGTTA CGCCAAA 147

SEQ ID NO:1283

LENGTH:146

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01432

SEQUENCE DESCRIPTION:

GATCTCAGTT CCTGGCTTTC CCCCCAGCCT TCTCACCCCTT TGTGTCTGTG TAGTGATTG 60
GTGAGAAATC GTTGCTGACC CTTCCCCAGA CCATTATGA GTCNAAGTTT ATTATTCAAT 120
AAAAGTGCTN TATGCGCTTT CTCAA 146

SEQ ID NO:1284

LENGTH:146

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01433

SEQUENCE DESCRIPTION:

GATCCAAAGA TGAGGGGATT NTTTCAGAAA GACAATCTCG GCATGCATTA TTTCTTNN 60
TTGAAGATTC ACTCATGTTG CATGCATCTN TAGCTTGTC CTTTAAATT CCTAGTAGAT 120
TCTGTCATAT GCCTATCTNC AATTNN 146

SEQ ID NO:1285

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01434

SEQUENCE DESCRIPTION:

GATCCCCATG CTAAGAAAAT GCCCAAAAAA ATAGGCAAAA CACGAGAAGA GCTAGGGTAA 60
GAGAAGGACG TAAACAGAAC CTGACACCAG CTCCTTTTCC TTCTATACAT TATTTAATAC 120
CTATTAAATA AAATNATTTT TGAATAAAG CTTGTGGGAA CATTAA 167

SEQ ID NO:1286

LENGTH:179

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01435

SEQUENCE DESCRIPTION:

GATCAAAAAG GCTTATAAAA CAGAGTAATC TTGTTGGTTC ACNCTTGNGA CCGTGAAGAT 60
ACTTTGTATT GTCCTATTAG TGTATATGN ACATNCAAAT GCATCTNCA TGTGTTGTTT 120
TTGGCAACAA ATTTGAAAA GTAATATTTA TTAAATNTTT TTGTATGCAA ACATGCAA 179

SEQ ID NO:1287

LENGTH:145

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01436

SEQUENCE DESCRIPTION:

GATCCGATGG GAGTGTAAT GTGAGACACA ATGTCTTGAT TATACCTGTT TGTGGTTTAG 60
CTTTGTATTT AAATAAGGAA ATAACTTGA AAATNATTTG TCATCATAAA AATGAAACAA 120
ATNAAAATAT TTATTGCCAG GCAA 145

SEQ ID NO:1288

LENGTH:145

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01437

SEQUENCE DESCRIPTION:

GATCAGGGCA TGCAACCAAA AGCAGCTTAA ATGAAATATT TAAAAATAAA ATATCAGGAA 60
GCTATTTTGA GATTCTNCT GGCTTATGTT TCTACTTTAG GACCCTCATT GTNCTCTTAT 120
TAAAAAAAAT TATTCCTGT GCAAA 145

SEQ ID NO:1289

LENGTH:145

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01438

SEQUENCE DESCRIPTION:

GATCAGATTT TTTTGTACC TACGTAAGAG TACTTGAAGT TTTATTAAA ATAAAATGTT 60
GTGAAAAGG TAGCATTCTT TTTTAGGAG TGTTATTTT CACTATGTGT GGCACGGATA 120
CAATAAAGA CTTTACAAA CTAAA 145

SEQ ID NO:1290

LENGTH:145

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01439

SEQUENCE DESCRIPTION:

GATCCCAGGG CTCCTGCCA TTTTAGTGTC TTGGTGTAGT GTAACCATTT AGTGGTTGGT 60
GCCATTTTT TTTTGTNCA AATGATTAA ATNATTGGAA TNCACAATTT TTAAATATN 120
CAAATAAAN GTTAAACC TTAAA 145

SEQ ID NO:1291

LENGTH:145

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01440

SEQUENCE DESCRIPTION:

GATCAGGAAT TCTAAATAAA TTTCCAGTT AAAGATTATT GTGACTTCAC TGTATATAAA 60
CATATTTTGA TACTTTATTG AAAGGGGACA CCTGTACATT CTTCCATCAT CACTGTAAAG 120
ACAAATAAAT GATTATATTN ACAA 145

SEQ ID NO:1292

LENGTH:144

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01441

SEQUENCE DESCRIPTION:

GATCTGCCAG CACCCTGTGG GGCCAGACT ACAGGCTGAT GGCGGAGGCT TCGAGTGACC 60
 CGGGTGCCGA GGAGCGGGAA GAGTTGCTGG GGTAAGGGTC TCGGGCGACG CCGGCGCCCT 120
 GTGCCGTGTC CACGGGTGCA TAAA 144

SEQ ID NO:1293

LENGTH:144

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01442

SEQUENCE DESCRIPTION:

GATCTAAATA TTTNNAGCT GAGTTATTAG GGAGTCATTA TTCTGTGGTA CAATGCTGCA 60
 AAAAGCATCA TGTGAAGAA TGGGAACAT GCTTACTTTA TGAAGTGATG TATAACACAA 120
 TGAAATCTGT TTTACAATA CAAA 144

SEQ ID NO:1294

LENGTH:372

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01443

SEQUENCE DESCRIPTION:

GATCTTGGA GTATCCCTGG CTGCTAAGCC TATGGCAGGG GTGGTCCTTT CTACATTCCC 60
 ATTCACTTAA CAGCTCTTTT GGGATTGGGT GTTTCATTCC ATTTCTGCCC ACTCCCTCTC 120
 CTCTCCTCTC TGGTAGGTTT AATTTTATGC TTTCCCTGAT TCCAGCTTTC TGCTTCCTGA 180
 GGACTCCCGC TCCCNCCACC CCAAAGTTTG TCTGTGGGTG TTATAGTGGT AACTGCAGTT 240
 CCCTCCTCTG GGAATNGTAG GCTGTAATAG GNTTAATAAA CTCNACNTNC TCTAATCNTT 300
 GCTNAAAANG TGGGGGTAAN GGGGATGGCN TTGNCCCGG GTGGGAAANT TAAANNTGGT 360
 GTTTANGGNA AA 372

SEQ ID NO:1295

LENGTH:145

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01444

SEQUENCE DESCRIPTION:

GATCTTCTCT GTGGGGGAAA AGGAAGAGGA GGGTCTTGTT CTCCANTNT GTTTATCTT 60
 TGGGCTCTGG GAACAGGGGA CTACTTTGGG GCTTCTCCA ATNCTNTTGT ATGNTGTTAT 120
 TAAAAGCGAG CTATTGCATT TCAAA 145

SEQ ID NO:1296

LENGTH:141

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01445

SEQUENCE DESCRIPTION:

GATCTTATAT CCTGTGACCT GTCTAAATTC AATCTGTTAG TTTTATCATT TTTAAAAA 60

ATGTCCCGTGT GTGTCTTCCT TGAGATTTTC TACATTATCA TGTCATCTGC ANATAAAGAC 120
ATTACTTCT TTCTTTCCAA A 141

SEQ ID NO:1297

LENGTH:141

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01446

SEQUENCE DESCRIPTION:

GATCCAGTTG TACTAAGGTG TACAGGATAT TTGCAGATAT AGGTAACTG AATGAAGCAT 60
ATTAATAACT GCATTNCCT AACTTTGAAA AATTTNCAA ATGTCTAGGT GATTAAAAA 120
ATGAGATTGG GCTATTGCAA A 141

SEQ ID NO:1298

LENGTH:140

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01447

SEQUENCE DESCRIPTION:

GATCTAAAAT AGATATGTTG GATTGATATT CTCACGTGTT CGGTGTGGAA AACAAAACAA 60
GTACATGCTT TAGAAGCAAC AACAAATGAAA TCCTTTTGAA ATNTGTGTTA ATATCGTTA 120
NTAAAATACC TAGTTTGAAA 140

SEQ ID NO:1299

LENGTH:140

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01448

SEQUENCE DESCRIPTION:

GATCCATAGA AGGGCTTCCC AAACCTTGTT TTGCAACATC CCAAATTGTC TCCAGTTGAA 60
GGAAGGCCTT TATCAGATTC ATAGATGAGC TTTCATTGTA AAAATAAATG TACTTTGCAC 120
CACTTCATGA TGGAGGGAAA 140

SEQ ID NO:1300

LENGTH:140

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01449

SEQUENCE DESCRIPTION:

GATCTGAGGT TTTTAGATTT TAAATATTTA TGTGGAATTA ATTAAAGGTA GTTGGCTATA 60
TCGCTATCAT TTCATTCTTT TGACATTATT TGAATATTTT ACTGGAAAAA AAGACTAATA 120
AATTGTAAAA AGTTTTTAAA 140

SEQ ID NO:1301

LENGTH:139

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01450

SEQUENCE DESCRIPTION:

GATCTTCACA AAGTTGTCTT TTCACTGTGT TTTGTCAACG TGAAATTAAA TTGTAGTTAT 60
AAGCAAAAGT TGGTTGCCTA GGGAAACAATT GTATATNCAG TTAAACAGAA ATAAAAGAAT 120
ATTTGTCTTA AGATGCAAA 139

SEQ ID NO:1302

LENGTH:138

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01451

SEQUENCE DESCRIPTION:

GATCGNCACA TTTCCCAAAA ATAATAAAAA AATCACTAAC CTTTTTTAAG GAAAATATTT 60
AAAGTTTAC AAAATTCAAT ATTGCAATNA TCAATGTAAA GTACATTNA NTGCCTTATN 120
AAAACTTTCC CAATTTAA 138

SEQ ID NO:1303

LENGTH:137

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01452

SEQUENCE DESCRIPTION:

GATCATTTTT TCGGTCTCCG AGGTGAAATG ACTTATTAAT TAAAATTTGT AAACACAT 60
ATGCATATTG TATATGTGA GAAATGTAAT CACACTTTGT CTGGAATTA CATTAACTG 120
TTTGAAATCA CTGTAAA 137

SEQ ID NO:1304

LENGTH:136

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01453

SEQUENCE DESCRIPTION:

GATCTTTTTG TGATTGCTTT CCCGTCTCTA AGTAGTATTC TGTGTGTCT AGAGAACTGA 60
TTTTTTCCTA CATACGCAAA TTGTACATTT GTAAGTGAAA ATNTCAATAC ATTAAAAGCA 120
TTANCCTAAA ANCAAA 136

SEQ ID NO:1305

LENGTH:136

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01454

SEQUENCE DESCRIPTION:

GATCAGCTGG GTTTTGCCA GGAAGTTGTC TTTGTGGACT CTGCCTGCAT GGCTTAGTAG 60

TTGAAGGAAA TTTTTTTTG GTTTTGTTT TTATAATTCA GTTTAATCAA TAAACATGTA 120
TTTATTGACT GTTAAA 136

SEQ ID NO:1306

LENGTH:136

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01455

SEQUENCE DESCRIPTION:

GATCCCTTTA TGAGTTTGC TATTTTGCCA TGCTACATGT AAGTTTGCT TAATGTTTTT 60
ATGTAAAGCA TCTTCCTCCT TTTACTTCTT TTATTGTGAT AAAACTCATA TAAATTGAC 120
CGTTTGAAG TGTAAG 136

SEQ ID NO:1307

LENGTH:136

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01456

SEQUENCE DESCRIPTION:

GATCTGGGCC CGACCCTCAC TACCCCTGAG ATATTAGTTC CCAGGCCTGT TTTCCACAG 60
GATTGTGGGC TCTCTGCTTC CTTAGTCGGA AGTNTTTTCA ACTAATCAAA TAAATGAATG 120
AATGATGAAT AAGAAA 136

SEQ ID NO:1308

LENGTH:135

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01457

SEQUENCE DESCRIPTION:

GATCCCAAAG ATATTAAATA TATGCAAATA TTCCAAAGTC TGAAAAAATC CAACATCCAA 60
AAACACTTCT GACCCAAGCA TTTCAGATAA GGGACCAGAA TTATTAGATT AAATAAGGTA 120
TATTATTAAG TTAAA 135

SEQ ID NO:1309

LENGTH:135

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01458

SEQUENCE DESCRIPTION:

GATCAGGCCA AGAGTTTGCA CAGGGCATGA TACTGCACCC TGCCTGACCC AGCTGGGCTC 60
ACAGGTCAGG GGAGAGTTGG GGCAGGTGAA TGTCAGCATC AGGCTTCTNN TTTTAACTT 120
TTAAANAAAT ACAA 135

SEQ ID NO:1310

LENGTH:135

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01459

SEQUENCE DESCRIPTION:

GATCCTGCCT CAAAAAAAC AAAAAAATTC TTTATTTTCT CCATAAACTA CAGTTTATAT 60
AAGCAAAAGT TTCAGTACTA AGCAATTNA GTCTCTGCAG TCTCTNGTNT TGANTTAATA 120
CAACTTNGT NAATN 135

SEQ ID NO:1311

LENGTH:139

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01460

SEQUENCE DESCRIPTION:

GATCTACCTG TGGCCCGGCC TCCCTAATGT NATTCACATT GAATGGGGAT GAGGTCCGAC 60
AGTGGCTCAT AGAGCGAGTA TGAGCCCTAG CTGTGGGCTA GAAATNTCCT TAATAAACAT 120
CCTTATTTTC NTNTTTAAA 139

SEQ ID NO:1312

LENGTH:134

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01461

SEQUENCE DESCRIPTION:

GATCCTAGTA TGTTGATAGC TTTNATTTTG TGAGTGGTTT ACTAGTCATT TATTATGATT 60
CCCATGANCT CTGATATGAT TCATTGTGGT TTAACTCAG GTTGAATAAA AGCATCCATT 120
TCTTTTATAG GAAA 134

SEQ ID NO:1313

LENGTH:237

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01462

SEQUENCE DESCRIPTION:

GATCTCAAGG TTGATAGTGG TGTTCACTAG GAGACGTGGA ATTGAGACTA ATAACCTGGA 60
TGTTAAACT GTTTACTGTT TTTTCACATG TAGAAATGTT CTTGTGTAT TTTTCTACA 120
GAGGATTTTC TCTGATTTTA TTTTCTTTGT TTCTGACTCT AATAATTAGT TGGAACTCA 180
TATAAAATGA GCTTTCCTAA ATTAAATCTA TTTTAAATAA AGGTTATTAC TATTAAT 237

SEQ ID NO:1314

LENGTH:134

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01463

SEQUENCE DESCRIPTION:

GATCTATAGG TTTATTAGAA NCCTNACCAC AGNATCCAGA TTATCTTCAG TATTCTNTCA 60
GTACAGCTCT CTGCAGCTTA AACTCGGTGG TACATAAAGA AGATGATGAA CCCAAAATGN 120
TGGNCACTGT ATAN 134

SEQ ID NO:1315

LENGTH:133

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01464

SEQUENCE DESCRIPTION:

GATCAGAAAA TCCCTCTGAC ATCTCCACTG CCCCCAAAGA CCTCCGTTGA ACATTCTGTA 60
TGGAAAAGAG CCCTGGAGCA TCAGGTTCCC CAGATAGGCC CCCAAATAAA GACCTGTCTA 120
TGGCTCTCCC AAA 133

SEQ ID NO:1316

LENGTH:132

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01466

SEQUENCE DESCRIPTION:

GATCTAGCTG GCTGTAGTAT TGCNTTGATA ATTTTTTCT TTAAATTAC CTAATATATA 60
TAAGGAAGGG GTTTGGATAT ATTAAAATAG GTGTTAATTT TATCTATTTA CCAATAAATT 120
CATCTCTTTA AA 132

SEQ ID NO:1317

LENGTH:130

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01467

SEQUENCE DESCRIPTION:

GATCCAGCCA TTCCTGAAGC CCACCCTGCA CCTCATTCCA ACTCCTACCG CGATACAGAC 60
CCACAGAGTG CCATCCCTGA GAGACCAGAC CGTTCCCAA TACTCTCCTA AAATAAACAT 120
GAAGCACAAA 130

SEQ ID NO:1318

LENGTH:130

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01468

SEQUENCE DESCRIPTION:

GATCTAAAAG CCAACTTTT CTCAGTNTTA CTCAGTGGAA AGATAAACTA AGTTTAAATG 60
TTATNTTTT AAATNTAAGC AAAATTATT TCTGTNCTNT AATAAATAAG AAAATGTGGT 120
CCACTGCAAA 130

SEQ ID NO:1319

LENGTH:129

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01469

SEQUENCE DESCRIPTION:

GATCCCCTGC TCCTGTTGTG TTCTGTTGTA AATCATTGG CGAGACTGTA TTTAGTAAC 60
TGCTGCCTAA CTTCCCTGTG TTCTATTGA GAGGCGCTG TCTGGATAAA GTTGTCTTGA 120
AATTTCAAA 129

SEQ ID NO:1320

LENGTH:128

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01470

SEQUENCE DESCRIPTION:

GATCAGAATT TTTAAAGCAG AATTTGTCA AAAGGGTCAT TTTTTGTCT ACCCCTTTA 60
CACTTTTCAG ATTCTCAAAG TGTCTCATCT CAACTTTTAA AAGAATAAAG AATATCTGC 120
TGGGCAAA 128

SEQ ID NO:1321

LENGTH:128

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01471

SEQUENCE DESCRIPTION:

GATCCTTGTC AGATGAAAAT GGATTCACAG CTCTGGCAGT TCCCAATGTC TGGGGAGGGG 60
TATAGGTTTG AAAGGCTGTT TGAAAGAGGA ATGTTTAATA AAGGCTTTGA TTAAATCTTG 120
AAAAGAAA 128

SEQ ID NO:1322

LENGTH:128

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01472

SEQUENCE DESCRIPTION:

GATCTCGAAG TNACTCCGGG CTGAGCAGTG GGGCGGCTGG GGGAGGGGTG ACGATTCTCC 60
TCAGGCTTTG GCCCTGCAAG CAAACCCACA TATCTNCTCT GTATGTAATA AATNTNTTAA 120
CGTCGAAA 128

SEQ ID NO:1323

LENGTH:129

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01473

SEQUENCE DESCRIPTION:

GATCCTGAAG CNGCACTTAC CTNTGAANAG TCTTCAAACCT TTTAAACCTT GCCAGTNAGG 60
ACTTTTNCCTA TTGCAAATAG AAAACCCAAC TCAACCTGCT TAAGCAGAAA ATAAATTTAT 120
TGATTCAAA 129

SEQ ID NO:1324

LENGTH:127

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01474

SEQUENCE DESCRIPTION:

GATCTGTGAA GTTATTTTGT AAGGACATAC ATTTGGTAAG TAAGTTTGTG TCCCAGGAAA 60
TGTATGTNTT TTTAAACCCT TTCTAAATAT GCAGGCCATT AATAAATAAG ATTGTTTCTT 120
CCCTAAA 127

SEQ ID NO:1325

LENGTH:127

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01475

SEQUENCE DESCRIPTION:

GATCAGAGAG ATTTTNTTT TAACTACCA TGGTCCCAGG ATTCCATCCT GAAATNAATT 60
TTCCTTTGTA TGAATATGTG TAAATAATTT AAAAATAAAA CTGTAAAANA TTTGTNCGAA 120
GAATAAA 127

SEQ ID NO:1326

LENGTH:137

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01476

SEQUENCE DESCRIPTION:

GATCCCCCTT CATTTGATGT TTGGAAAATN CCAGTAATTA TCATTTTTC AACGAATATG 60
GATACCACAT AGTACTTTGG TGTACCTGC TTTTGAAAAA TAAAGTCTTT GGTTCACCCG 120
GTGAACTATT TATGAAA 137

SEQ ID NO:1327

LENGTH:126

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01477

SEQUENCE DESCRIPTION:

GATCCTCAGC CTCCCAGTGG TCTTTGTAGA CTGCCTGATG GAGTCTCATG GCACAAGAAG 60
ATTAACACAG TGTCTCCAAT TTTAATAAAT TTTTGCCCAT TTCTTATTAA AAAAATTGT 120
TGTAAT 126

SEQ ID NO:1328

LENGTH:129

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01478

SEQUENCE DESCRIPTION:

GATCCATCTG TGTAGTTTCT GAACAGTCAG CGATTCCAGG TTTTAAATAG TTTGTAAATT 60
TTCAGTTTCT ACACACTTTA TCATCCNCTC GTGATTTTTT AATTAAAGCG TTTTAATTCC 120
TTTCTCAA 129

SEQ ID NO:1329

LENGTH:125

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01479

SEQUENCE DESCRIPTION:

GATCCATGCT TTA CTGTGTT TAATGGGGGT AACAGGGGTC CCTACAGCCC TCCCAGCTAA 60
ACATTTGGAA CAAAACACCA GCCCTTTTGT AGTGGATGCA GAATAAAATT GTTAATCCAA 120
TCAA 125

SEQ ID NO:1330

LENGTH:124

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01481

SEQUENCE DESCRIPTION:

GATCTGTGTT GAAAGTNGTA TATTTTATC TGTNCGGTGC TGAGTGCAGG CCACCAGCTC 60
CTAAATAGAG GTTCCCTATA TGC GCGTATG ACATGGTGAA TAAACACAAC TCTCTCCACT 120
CAAA 124

SEQ ID NO:1331

LENGTH:124

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01482

SEQUENCE DESCRIPTION:

GATCGTTGTA ATTNNTTGAC ATTCCTTTNA GAAGTTGTGA AATGTTACAA CTTGTNCTTA 60
TG TAGACACA ATCTCCTGTC TCAGTACAGA GGCAGTACT TCAATAAAGT CTATTTATAC 120
TAAA 124

SEQ ID NO:1332

LENGTH:129

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01483

SEQUENCE DESCRIPTION:

GATCAAAAAA TGGAAATGTA TAATTAAATC ATACTTAGCA AATCTAACAC ATGAAATGTA 60
 ACATCTGCAT ATGGAGAATC GTGTTACTTT ATTGAAAAAC ATTAAANGTT TGAGANCTTA 120
 AGTTGGAAA 129

SEQ ID NO:1333

LENGTH:122

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01484

SEQUENCE DESCRIPTION:

GATCTGCCAA GATTCTTTGA ATACAGATAA TTAATGTAAA CAATTATCAT AAGTATACTA 60
 ACATGTTATN CTTTTTAAAT AAGAAGGTAT AATAAAATAT CCCATTGGTT TNATGTATTA 120
 AA 122

SEQ ID NO:1334

LENGTH:122

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01485

SEQUENCE DESCRIPTION:

GATCGGGCCN TTGGCTGTAA GACCCGACCC TTCGAGAACC CGANACGAAA CGCTCCATTA 60
 CCACTGCNCA GTGAGATGAG GGA CTCACAG TTCCAAGAGG NTTCTTTCCC GTGGNCCCCT 120
 NN 122

SEQ ID NO:1335

LENGTH:121

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01486

SEQUENCE DESCRIPTION:

GATCCAACCC TGTACTGATA GTACTTCCCA GTATGATATT GTGATGTTTC ATACAATGCA 60
 GTGAACATAA CCAACTTGTT ACCTAAATAA AGANTTGATA AAAACAGTGT GACATATTAA 120
 A 121

SEQ ID NO:1336

LENGTH:120

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01487

SEQUENCE DESCRIPTION:

GATCAAGGTC TGCAAGGGAA TTCTTGTTGT CTGCTTTCCA TTTGACACCG CAGTTCTGTT 60
 CAGCCATCAG AAGAGAGACA AGGNATTAAA AATTCTTTT TAATCNGTT ACCAAATAAA 120

SEQ ID NO:1337

LENGTH:119

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01488

SEQUENCE DESCRIPTION:

GATCTAGTAG GCACGTCTGT CAACAGGACA CATGCCTCCT CTGACTATAA CCTCTTAATA 60
GTTGTGTATA ATGAAACTG TAACTTTTT TAAATAAACN GTGTATATAC CTTGGCAA 119

SEQ ID NO:1338

LENGTH:120

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01489

SEQUENCE DESCRIPTION:

GATCTGAAG CCATGGTTTC TTCCCTGCCA GAAATGAAAG GTTCAGTTAT GAGGCAACCC 60
TCTAGTAAGG CATTGTAAAA GTTACTGGAT TTGGTTTAAT AAAAGTTGAA ATAAAGTAAA 120

SEQ ID NO:1339

LENGTH:322

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01490

SEQUENCE DESCRIPTION:

GATCTTCCGA GTGCTTGGGG CCCACAGAGA CATCATCCTG GAGAGCATTG CCACTGACAA 60
CCCAGAGGCG CACAGCAACC TCTACATCCT CACGGGCCAC CAGAGCACCT ACTAAGAGCA 120
GCGGGCCTGT CCAGGGGCTC CCCGNCCCAC CCCACGCCTT AGCTGCAGGC CCTTTTGGGC 180
AAAGGGGCCC ATCTGGGGC ATCCATTCCA TTTGTTCCA CATTTCCTTT CTACTCTTTC 240
TGCCAAGAGN CTGCCCTGC ATTTGTCCTG GGAAACACGG TATTTAAGAG AGAACTATAT 300
TGGTATTAAA GNTGGTTTGT TN 322

SEQ ID NO:1340

LENGTH:118

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01491

SEQUENCE DESCRIPTION:

GATCTTTGGA GCAAAAGCCA ACGGCAGGAA AAAATAGTTT GTACCAGTTT CATGAAGTAT 60
GTCTTTGGGT TTTGTAAAT AATTTTAACT CAAATAAAAT TGCTACTTTC AATACAAA 118

SEQ ID NO:1341

LENGTH:118

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01492

SEQUENCE DESCRIPTION:

GATCAGAATN AAATNTGTAT AGAGCAGAGT TTAAAAATGA ATGTAAATAG CACTAAACGT 60

NTNCTTTCTG CAACCTGTAC TTACAGATTC TCCCTGTAAA CTAAATAAAA AAAAANTN 118

SEQ ID NO:1342

LENGTH:118

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01493

SEQUENCE DESCRIPTION:

GATCACA AAA TGTGCATGAG NGTTATTNAC TTTATTCTNG TACAGTACTA GGATTCCTGT 60

AACCACTCTT TTTTCTTC GNNGTATTGA AACTGGTTC AGTGTTAACC AGGCAAGN 118

SEQ ID NO:1343

LENGTH:118

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01494

SEQUENCE DESCRIPTION:

GATCAATTCA CTAAAAGNA TGGCCCANAT AGCACNNATA GGACCAAGGG ACACATGTAG 60

TCANTTTTAA AAAACATGA CTTGGTCTTT TGTGTGTGTC TGTATATTC CATTAGAN 118

SEQ ID NO:1344

LENGTH:117

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01495

SEQUENCE DESCRIPTION:

GATCCAGGA GAGTG GGGCT ATGACTGCAA TAAGGAGTTG TTCCTTCACC TGAGATGTGC 60

TTCTTTTGGT TCATTCTGG CTTGACAACA AGAAATAAAC GTGGTATGTT CCTGAAA 117

SEQ ID NO:1345

LENGTH:119

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01496

SEQUENCE DESCRIPTION:

GATCTTGAGG GACCAACAT TTGTAGGGGC ACTAATCCAG CCCTTAAATC CCCCAGCTTC 60

CAAACTTGAG GCCCACCATC TCCACCATCT GGTAATAAAC TCATGTTTTT TCTGCTAAA 119

SEQ ID NO:1346

LENGTH:116

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01497

SEQUENCE DESCRIPTION:

GATCAGATTT GGGTGGGAGA AAGAAGTGGG TATCAAGGGT GATTGAATT TTCTGCAGCA 60

TTAAAGTGGC GTTAATAAGA TAAGTAATAA TAAAGAATTC TAACATCCAT GTCAAA 116

SEQ ID NO:1347

LENGTH:116

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01498

SEQUENCE DESCRIPTION:

GATCCGGTGG AAATCCAAGC TCTGGGCTGG TAATTTTAT GAGCATTTC AGCTTTTGCA 60
AATACAAAT ATAATNCTT ACAAAAATAA ATTTTATNC TAATCTAAAT CTGAAA 116

SEQ ID NO:1348

LENGTH:115

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01499

SEQUENCE DESCRIPTION:

GATCTTCTCT ATGATTGATA CATGGCACAG TGAGAGATTA ATGGGCATTG TGTACAAATT 60
GCTTCTCACC ATCCCCATTA GACCTACGAA TAAAGCATCC GGTCTAAAA TTAAA 115

SEQ ID NO:1349

LENGTH:118

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01500

SEQUENCE DESCRIPTION:

GATCTTTTG TAAAGGACC AAATGTTCTT TTATAAATGT AATAAGGAAT ATCTTGCTCT 60
TTAAATTTA TTAGGNNTT AATGAGTAAT TTNATTAAA AGATTCTTT TTTTGAAA 118

SEQ ID NO:1350

LENGTH:192

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01501

SEQUENCE DESCRIPTION:

GATCCTATTT GTTTCATTT ATTGTAAATN CCCATTTGCA TCAAAACCTA ATNATAGTGA 60
TNGGTAAGTA AAAACAAATG GTGTATTGCT TTTCATACAA GTGTTTTCAC AAAAGCCATT 120
TGCCTAGGCA GCAAAAAATA TTAATTTGTT AAAAAAATT TTCCTTCGTG TCCATCCNCA 180
NAAANTNGNG NN 192

SEQ ID NO:1351

LENGTH:115

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01502

SEQUENCE DESCRIPTION:

GATCTGTGGA CTTTCATCAN ATTATGAGAC TNNCTCAATT TCATGACTGT ACTACCTGAA 60
 ACAAAGTGAG AAAGGACAGG TGTATTTTNN TAAGTCATCA AGATAAATCC TTAAN 115

SEQ ID NO:1352

LENGTH:150

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01503

SEQUENCE DESCRIPTION:

GATCTTAGTT TGTAGCTTAT GACTTATTTA ATGAATGGAT GCCCAGCCAA GCTCAGAGTA 60
 GCGGCCCAAA GCATTGTGGA TTATTTTCCT GTTTTGTCTT TTTTTTTTTT TTTTTTNAAG 120
 CCATGNCANC CCNGANGGGG CCAGNGANTN 150

SEQ ID NO:1353

LENGTH:113

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01505

SEQUENCE DESCRIPTION:

GATCGNNAAG AGGTTACCCA GACCACACAC AGTTTGAGAA AACATNCCCA TTATNACCCA 60
 TCTAGCAAAG AGGCACCCTA AGTGGTCCAT GAAGAGTTTA ATTTTATNTT AAN 113

SEQ ID NO:1354

LENGTH:113

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01506

SEQUENCE DESCRIPTION:

GATCGGGTTT AGACGNNAAG TCATTCAGTG AAGCAAGCCA AAAGCNCACA TTTGTATGCC 60
 TTAGGTCTTC TTAAGTGGT ATCTGTAAAC ATGTGTCCAA TATAAANCT ATN 113

SEQ ID NO:1355

LENGTH:411

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01507

SEQUENCE DESCRIPTION:

GATCCTCCCT GCCCGCGAAG TGNACAGTTT AAAAAATTAT TTTCTGCAAA AAAGAAAAAA 60
 AAGTTAGGTT AAAAACCAAA AAACATACATA TTTTATTATA GAAAAAGTAT TTTTCTCCA 120
 CCAGACAAAT GAAAAAAG AGGAAAGATT AACTATTTGC ACCGAAATGT CTTGTTTGT 180
 TGCGACATAG GAAATAACC AAGCACAAAG TTATATTCCA TCCTTTTAC TGATTTTTTT 240
 TTCTTCTATC TGTTCATCT GCTGTATTCA TTTNTCCAAT CTCATGTCCA TTTTGGTGTG 300
 GGAGTCGGGG TAGGGGTAC TCTTGTCAA AGGCACATTG GTGCATGTGT GTTTGCTAGC 360
 TCACTGTCC ATGANAATAT TTTATGATAT TAAGGNAAT CTTTGA AAAA A 411

SEQ ID NO:1356

LENGTH:112

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01508

SEQUENCE DESCRIPTION:

GATCATGGTG TAATAAGACA TAACGTTTTT CCTTTAAAAA AATTAAAGTG CGTGTGTAGA 60
GTTAAGAAGC TGTGTACAT TTATGATTTA ATAAAATAAT TCTAAAGGNA AA 112

SEQ ID NO:1357

LENGTH:112

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01509

SEQUENCE DESCRIPTION:

GATCAAGTGC ATTTGACAGA AAAGTTCAGT TTCTTGGGAA GAAACACCTT TTAAGCTGAA 60
TGGAGAAAAT NCCAAAATAA ATTATATCAC CACAATGGTG TATACTCAGA AA 112

SEQ ID NO:1358

LENGTH:112

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01510

SEQUENCE DESCRIPTION:

GATCTGGGAA AAAACAAGA GACTCAATGG AGACAGAAGA AAATCCCAAG GTTCTAATAA 60
CTNCNTTCTN AAAAANTATC TACCCCATTT GGTGAAGTGA AAANCAGAAA AN 112

SEQ ID NO:1359

LENGTH:112

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01511

SEQUENCE DESCRIPTION:

GATCCTGGTT GGAGTAAACA TTCCATGGGA ACTCGGGCTG TNAGAATNTC CTAACCACCT 60
GANTGCAGAA ACATCCTTAT CACATCCTNC TGGGAAAGNC CAACAGCCTG AN 112

SEQ ID NO:1360

LENGTH:112

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01512

SEQUENCE DESCRIPTION:

GATCCATCAC CTGNGCAGCA TAACTGGCTT CNNCTCAGTC ATCCACACAA CACCAGGACT 60
TAAGACAAAT GGGACTCCCT GTCATCTNGA GCTATNCATT TATTAAACT GN 112

SEQ ID NO:1361
LENGTH:111
TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01513
SEQUENCE DESCRIPTION:
GATCCCTTCA TTGATGTTTG GAAATTCCAT ATTACATTTT GCACGATATG GTACACATAG 60
TACTTTGGTG TACCTGCTTT TGAAAAATAA AGCTTTGGTC ACCCGGTGAA A 111

SEQ ID NO:1362
LENGTH:111
TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01514
SEQUENCE DESCRIPTION:
GATCAGAGAA TGCAGCAGCA GTTTTTTCC TNGTTTNCCTT ACCACTTTAT TCTTTCANAG 60
TTTAAAGAAA ATGGACTCAT GCACAGAACA CTATGCATTT NAAAACTNGT N 111

SEQ ID NO:1363
LENGTH:111
TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01515
SEQUENCE DESCRIPTION:
GATCGGGGGC GTANATNCAT AGTAGTTTTT ACAGCTGTGT TATTCTTTGC GTGTAGCTAT 60
GGAAGTTGCA TAATTATTAT TATNATTATN ATAACANGTG TGTCTTACGT N 111

SEQ ID NO:1364
LENGTH:110
TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01516
SEQUENCE DESCRIPTION:
GATCTCAAAA CAGTGCTAAA ATCAAAGNTG TNGACTGTAA AGAAAAACAT GTATATATAT 60
TGCACCTNAA AGTTGTCAGA AGNTAGAAAC TNAATAAAAC TAACTTAAA 110

SEQ ID NO:1365
LENGTH:109
TYPE:nucleic acid
TOPOLOGY:linear
CLONE:HUMGS01517
SEQUENCE DESCRIPTION:
GATCCCACGC CACAGCCTTT TGNTNTGCAA CTGCCTTCTT CGGAAAGAAG AAGTGGGAGG 60
ATGTGAATTT TAGTTCTGAG TTTACCAAAT AAAGAGATAT AAGACGAAA 109

SEQ ID NO:1366

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01518

SEQUENCE DESCRIPTION:

GATCATGTAC TGAAGTAGTT TAAGCAGGCT GGCTAACTTA GACTNATTGA TTCTGCNTTT 60
GTACTNNAAT AGGGGTTATA ATTGTAAGAT AAAAATGTGT GTGTNCAAN 109

SEQ ID NO:1367

LENGTH:236

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01519

SEQUENCE DESCRIPTION:

GATCTGGGGG TTTCTTCATA TTCCTGCTGT TGGAAGCAGT TGACCAGAAA TGCTTGNCAG 60
NACTGCCAAA GCACTGCTGT GAAATGTGAA GTACTTTGTT TTTTATTTT TAATNATTTT 120
CTTTTGTGA TTAATATTTT TCTCTGTTCC TTTGTTATTA CTTGCATGGT TTGGCGTCAG 180
AAGTCCTTAC CTCTTTATAT TGTTCAGG TTAAATAAA ACAGTGTGGT GCCAAA 236

SEQ ID NO:1368

LENGTH:108

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01520

SEQUENCE DESCRIPTION:

GATCTGAAG TTATTTTAA GACATACATT TGGTAAGTAA GTTGGTCCCA GGAATGTATG 60
TNNTNAAAC CCTTCTAAA TATGCAGNCA TTAATAAATA ANATTGTN 108

SEQ ID NO:1369

LENGTH:107

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01521

SEQUENCE DESCRIPTION:

GATCCAACCC AAATCAAAT GTTAAATGCC CTCTGAATT TTTTGTCTG TTATTTAATT 60
ATATGGTGGG ATTAATAATA AAATAAACTT CATGTCTCTG ATTCAAA 107

SEQ ID NO:1370

LENGTH:107

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01522

SEQUENCE DESCRIPTION:

2153480

GATCTNGAGC TCTGTCTTCA GCAGATTTC A GGTGTAACAT TTGTAACTC GTACTNGAAG 60
GTGTGTCCTC AAGAAGAAAG TTTCAAATT AAAAAAGCTG CTGCAAA 107

SEQ ID NO:1371

LENGTH:107

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01523

SEQUENCE DESCRIPTION:

GATCATGTAC ATTGTAACGT GTGTCGTCAG TACTGCAGTT CCTCAACTTT NTTTGTCTNT 60
NATTACCATG ACATTTTTAA AGATACAGCT ATTTNTCGA TGTNAAA 107

SEQ ID NO:1372

LENGTH:286

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01524

SEQUENCE DESCRIPTION:

GATCACATCT AAAGCTTTAT CTTGTGTAA TCTAAGTATA TGTGAGAAAT CAGAATTGGC 60
ATAATTTGTC TTAGTTGATA TTCAAGGCTT TAAAAGTCAT TATTCCTGGG CTGGTAAGT 120
GAATTTATGA GATTACTGC TCTAGAAAGT ATAGATGGCG AAAGGACCGT TTTGTATTGC 180
TTCCTGATTA CCAGTCTGAT TATACCATGT GTGCTAATAT ACTTTTTTTG TTATAGATTG 240
TCTTAATGGT AGGTCAAGTA ATAAAAAGA GATGAAATAA TTAAA 286

SEQ ID NO:1373

LENGTH:107

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01525

SEQUENCE DESCRIPTION:

GATCCGCGCA CTAAGCCTC CCAAAGTCT GGAATTACAG GCATGANCTA CCATNCCTGG 60
CCTTCTAATG TTTTCNTAA TTAAGGCTCT NAACTTCAA GACTGTN 107

SEQ ID NO:1374

LENGTH:106

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01526

SEQUENCE DESCRIPTION:

GATCTAGAGG NGAGAAAAAG ATGANTTGCT CTTACATTC GATAATCAGT GACCACGAAA 60
CACTCAGACC AGAGCCTGGC TTATCAAAAA CCTTNAGTGA GNNCTN 106

SEQ ID NO:1375

LENGTH:106

TYPE:nucleic acid

00643

TOPOLOGY:linear

CLONE:HUMGS01527

SEQUENCE DESCRIPTION:

GATCCACGTG CCATTGTGGA GGCAGAGAAA AGAGAAAGGN TTTATATACG GTACTTATTT 60
AATATCCCTT TTAATTAGA AATTAACA GTTAATNCNC TTCAA 106

SEQ ID NO:1376

LENGTH:117

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01528

SEQUENCE DESCRIPTION:

GATCCTGAGC TCCCTTGCA GTCTGAAAA GGTATTGCAG TCAGAACTGT GTACTGATGA 60
TAAANGCCTC TGGTAGCAAT AAAAAGTTGT CCCTAACAAA AGAGGCAAAA AAATAAA 117

SEQ ID NO:1377

LENGTH:105

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01529

SEQUENCE DESCRIPTION:

GATCCAGCAA ACAGTTCTN TTTAAGAAAA ATAATTATA CTAAATTNAG TAAAATGGAC 60
TTCTTATTCA AAGCATCAAT AATTAAAAGA NTTATTTNAA TGAAA 105

SEQ ID NO:1378

LENGTH:105

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01530

SEQUENCE DESCRIPTION:

GATCAGCAAA ATGAGATAAA TGTTTCTNTT TTCCTTTCTG ACTGCATTAA ATCAGATACA 60
ACTCAGCATT AAAAGCTAT CTNTGTAAAT NTNGTNACTA ATAA 105

SEQ ID NO:1379

LENGTH:105

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01531

SEQUENCE DESCRIPTION:

GATCTAACAC GAGGAACATA TCATGGAAAG TGCATNGTAT NTATTTTAGG GTTATGAGTT 60
CTTTCAAGGG CTAAGNTGCA GAGNATTTCC TCCANGAATC GTGTN 105

SEQ ID NO:1380

LENGTH:105

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01532

SEQUENCE DESCRIPTION:

GATCAGGTTA CATGAGGGNT CACTCTTCTT GTTGACANN CTGTGAGTTC GGGCAAATNT 60
GTAATGGCAT ATCTCCACTA TTACAGTNTC ACACAGAATT ATTTN 105

SEQ ID NO:1381

LENGTH:332

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01533

SEQUENCE DESCRIPTION:

GATCGGTGCG TTCTCCTGAT GTTTTNCNT GGCTTGGGGA TTGTACACGG GACCAGCTCA 60
CGTAATGCAT TGCCTGTAAC AATGTAATAA AAAGCCTCTT TCTTTTGGG GTGGNNNTTG 120
TCCTTCTGTC AGCTAAATG GGAGCTCATG AGAGAAGGAC GTCAGGGAAA CGGGGTTGAG 180
GGTGGTCTCG GTGCAGAGAG AAGGGTGTCA GGGAAACGGG GGGTGAGGGT GGTCTTGGTG 240
CCAGACGTAG GGAATGGTGT TGGGAGTGGC CCGAGTGCCT GGCACAGTTG TCTNGTTCAT 300
TCATGTAACA TGATAATTTT TAAATCATTAA AA 332

SEQ ID NO:1382

LENGTH:157

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01534

SEQUENCE DESCRIPTION:

GATCCTGCTG CTGTAATGGG AACCCCTCCC CCATTACTT CTCCACCTCC CGTCCTCCCC 60
ATCATTGGTT TTTTTTGTG TGTCAACTGT GCCGTTTTTA TTTATTCTT TTTATTTTCC 120
CCCTTTTCAC AGAGAAATAA AGGTCTAGAA GTAGAAA 157

SEQ ID NO:1383

LENGTH:103

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01535

SEQUENCE DESCRIPTION:

GATCTACTGT TTGTTGAAGT GTGGGAAAAT AGCCTCTCTA AGGCAGCCCA GATGGGACCA 60
AAATCAGTAC AAACATATTT AAGTAAATTT TAAATGCGT AAA 103

SEQ ID NO:1384

LENGTH:284

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01537

SEQUENCE DESCRIPTION:

GATCCCCTTG TCCCTGGAGT AGGGACTAAC TATAGCACAA AGTAATATGT GCCAATGCTA 60

TTTGTGAAAT GTTTGGGCTT TCTAAACGAC TAAAGGATTT GTNGGGTTTT TNCTTAAGTT 120
 TTGAACCAAA TCCTAGAGCC AGCTGATAAT ATTTAATAAT CTAGAGGAGA GAATAATGAT 180
 GTACCANTAA GTGGAGATTC CTCCTTATGA TGTATGCTAG GTTATGGAAG ATGTAAAATA 240
 TTCAACTTTT TCCTNCGTTT TTTGGACTTT GTATTTTACT GNAN 284

SEQ ID NO:1385

LENGTH:103

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01538

SEQUENCE DESCRIPTION:

GATCTGGAAC TCCTAAGCCA TCTACTCCTA CACCAACCNN TTCATCGAAC NCACACCCTN 60
 CTNATGCTCA GAGCTCAACT CCTAGTACCC CTCAGCCAC CCN 103

SEQ ID NO:1386

LENGTH:104

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01539

SEQUENCE DESCRIPTION:

GATCGCCGTT CTGTTTNGCA TNNTCCCACC GGGAGTTGCC NGGCAGGAGC ATGGGGTGCT 60
 TGGTTGTTTC CTCCTAATA AAATAAACGC GGGTCGCCAT GAAA 104

SEQ ID NO:1387

LENGTH:102

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01540

SEQUENCE DESCRIPTION:

GATCTTAGCC TTAGGGTAAG TAAATGGGT CTTTAAATAT AANAGTGTGA AAACATTTTC 60
 NATCTAATAG TACTCTTTN AATAAAAGTC AGTAGTNGGA AA 102

SEQ ID NO:1388

LENGTH:378

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01541

SEQUENCE DESCRIPTION:

GATCCTNGGT TTTTGTGGTT TGACTTCTAT GGNGTTTAA AAAACACAG ATTTTtagTG 60
 TTAATATTGT GTAAATGTAC TCACCTTAGG GATTCATTG AATGATGGTN TTATACCATG 120
 ATTGTNTACA GTTTGTGAAA TTGTTGCAAG GGCAAAGATA ACTCTTAAAA AACCGTCGAG 180
 ATTACAATGC TCTAGAATCA GCATATAAGA AAATAAATGA TATCTNCATG TNGANTNNGG 240
 GTGGATGGGG GGAGCACGCA TAATTTTAA GTGTGAAGCT TTGCATCANA GAAATTATTA 300
 AAANGCTTTT TTNCTCCNGT ATNTTCCTGT ATTAATCCTT AATGTTTATG GCAAATAAAA 360
 TGTAAAGGGGN ACATGAAA 378

SEQ ID NO:1389

LENGTH:102

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01542

SEQUENCE DESCRIPTION:

GATCGTAACC GTAACCGTAA CCGNNAAGCA CAAACGGGGG GAGCGGGGCA GTGAGCGGGG 60
CAGGNATGAG NCCCGAGGTG GGGTCGGTGG CCAGNACAAC GN 102

SEQ ID NO:1390

LENGTH:102

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01543

SEQUENCE DESCRIPTION:

GATCCAGAGG TCCNNGTCAC TTGGAGAAAG NCCAGTCCCT GNGACGGGGC AGCCCTCTNT 60
GTCCCTCGGG CAGCTCGTGT GAATCCTGGG ACCTCTTCCG GN 102

SEQ ID NO:1391

LENGTH:101

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01544

SEQUENCE DESCRIPTION:

GATCTCAGCA ATTTGAACAC TAACCTCTCC CCTCCTGGCT CAAGAATTAC TCCGAAGTCA 60
GTCTGCAGAA AATAAATATT TAGTATGACA TGACACTTAA A 101

SEQ ID NO:1392

LENGTH:101

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01545

SEQUENCE DESCRIPTION:

GATCTACTCA GGCAACNACC AATCTTCTAN TCTGTCACTA TAGATTAATT TGCATTNTTA 60
AAGAAATNNA CATACATGGA ACCATACATC ATCTATGCTT N 101

SEQ ID NO:1393

LENGTH:101

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01546

SEQUENCE DESCRIPTION:

GATCCTAGGA AGTNTGTCCC TGTCTCCCT GTGCAGGGTA TCCTGTAGGG TGACCTGGAA 60
TTCGAATTCT NTTTCCCTTG TAAAATATTN NTNTGTCTCT N 101

SEQ ID NO:1394

LENGTH:100

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01547

SEQUENCE DESCRIPTION:

GATCCACGTG CCATTGTGGA GGAGAGAAAG AGAAGTGTTC ATATACGGTA CTTATTTATA 60
TCCCTTTTAA TTAGAATTAA AACAGTTAAT TTAATTCAAA 100

SEQ ID NO:1395

LENGTH:100

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01548

SEQUENCE DESCRIPTION:

GATCTTAGGT TACATAAAGT TTCTAAAGTT TCAAAGAGTC TTGATACAAA ATCAGTTTAT 60
ATTCTGAAAA TATTTATAAT AAAGTATTCT AATTCTCAA 100

SEQ ID NO:1396

LENGTH:98

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01549

SEQUENCE DESCRIPTION:

GATCAATTCT TCAATTTGAT TGAAGTGTTC AGCCTTTTCA AGATTTCTTT ATTTACAAAT 60
GATTACATTT AAATGAATGT ACATTCTTCT CACTGAAA 98

SEQ ID NO:1397

LENGTH:98

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01550

SEQUENCE DESCRIPTION:

GATCTGTAAC ATTTGTTTCA AAATGCTGTT TCATTTTAT AAAGTACCAG TGTTCAGCTG 60
CTTTTATAC ATTAAATTAG CAATTTGAAA AACTCAA 98

SEQ ID NO:1398

LENGTH:98

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01551

SEQUENCE DESCRIPTION:

GATCCTCAGT GTCCTTACCC CCTCCTACCT CTTTCTGTG CCACCTGCTG TGGGTCCAGC 60
AGGCNTTAC TTGAGTACAA TAAAAAGTCT GAGTCAA 98

2153480

SEQ ID NO:1399

LENGTH:98

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01552

SEQUENCE DESCRIPTION:

GATCCAAGTG TAGTGGGACC CCCTACTAGG GTCAGGAAGT GGACACTAAC ATCTGTGCAG 60
GTGTTGACTT GAAAAATAAA GTGTTGATTG GCTAGAAA 98

SEQ ID NO:1400

LENGTH:104

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01553

SEQUENCE DESCRIPTION:

GATCTCCAAA GTGGTGAGTT TATGTGTGAT TTTATTTTGT TTTATGCTCT TCTGTATTTT 60
CCGAATTCA TACAATAAAT ATCTGTTACT TTTACAATAT GAAA 104

SEQ ID NO:1401

LENGTH:94

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01554

SEQUENCE DESCRIPTION:

GATCCAGAGA GTTCAAGGGA TTGGGGAAAG AGAGGCGTCA AGTCATTTC ACTTTGTACC 60
TGTAAGTTAG GTAATAAACT ATTATACTCG TAAA 94

SEQ ID NO:1402

LENGTH:92

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01555

SEQUENCE DESCRIPTION:

GATCTAGTNT CTNGCATTTC TATTATGTTG CTATATACTT TTGTTATCCG TATACTAAAA 60
AAAAAGAATA AATAAATGTT TTGATTGTAA AA 92

SEQ ID NO:1403

LENGTH:92

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01556

SEQUENCE DESCRIPTION:

GATCTNTACA TTCTTCAGAC TCATCGTGTG TTTGANACTT TTTATAATGA ACATATATCA 60
TTTTNNTTAG AAAAGAATAA AGTTTTTGAA AA 92

00649

SEQ ID NO:1404

LENGTH:119

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01557

SEQUENCE DESCRIPTION:

GATCCTCTGG GGAAGCCAGG ACCAGGAGAG AAGCAAGGTC AAGAAATCCC ACAGTTTGAT 60
GTATTAAAGA AATNACTTAT TTCTACTCAA AATAAATGGC ATTGAAGTCT TTCTTTAAA 119

SEQ ID NO:1405

LENGTH:90

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01558

SEQUENCE DESCRIPTION:

GATCTGTGT CTCCTCTCCA TCTCTGCCTT TGTACCAGT GTGCATGTGT TTGTGTGTTT 60
TTTAATAAAA TATTGACTCG GCCAGTTAAA 90

SEQ ID NO:1406

LENGTH:90

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01560

SEQUENCE DESCRIPTION:

GATCTGTTAT GGCATTCACT TCCAGATTAA TTTCCCGTGT TTGAAGTATG TNCATATGTN 60
CTTTACAGAA TAAACATCT GAATTTTAAA 90

SEQ ID NO:1407

LENGTH:87

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01561

SEQUENCE DESCRIPTION:

GATCCATTTT CTTTCAAAAT TTTCTTTATT GTAAAGTATG CAAAATATAT ATTCATACGA 60
TTTATTAAAT CAGAATGTTT ATACAAA 87

SEQ ID NO:1408

LENGTH:85

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01562

SEQUENCE DESCRIPTION:

GATCTGGAAT CCTTTTCTG CATTGACAAG GACCACAGCT AAAGGACAAT AATATGAATG 60
ACTCATTAAA ATCTCAAAAC TTAAA 85

SEQ ID NO:1409

LENGTH:85

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01563

SEQUENCE DESCRIPTION:

GATCCAAGTT ATNTTNAGAA GAAAAACCTA ATTGAACAGG TATGGGTTGG GAGCATAATA 60
AATGTGTTTT GAGAATTGTT CTAAA 85

SEQ ID NO:1410

LENGTH:84

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01564

SEQUENCE DESCRIPTION:

GATCATTATT TCATGACTGG TGCCTTCCTA AACTCTGAAA TCAGCCTTGC ACAAGTACTT 60
GAGAATAAAT GAGCATTITT TAAA 84

SEQ ID NO:1411

LENGTH:84

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01565

SEQUENCE DESCRIPTION:

GATCTAAGCC CATGAGCACA GGGACTGGCT ATCCCAAGAC CTGGCAGATG TGGCTGCTCA 60
ATAAACACTT GTTGAACCAT CAAA 84

SEQ ID NO:1412

LENGTH:86

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01566

SEQUENCE DESCRIPTION:

GATCACCCAA GGGTTTTTTT GTGTCGGACT ATGTAATTGT AACTATAACC TCTGGTTCCC 60
CATTAAAAGT NCCCATTTNA GTTAAA 86

SEQ ID NO:1413

LENGTH:83

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01567

SEQUENCE DESCRIPTION:

GATCTGTGTT TGTATCCCTT TATGTAATGT AAAATTTAAG GGTATTTTGA TTCTAAATAT 60
GATAAAATAA TTTCTCACCT AAA 83

SEQ ID NO:1414

LENGTH:83

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01568

SEQUENCE DESCRIPTION:

GATCAGCAGT CCACCACAAA AGCTTCTGTT AAAAGACCCT ACACAAATGC ACAAATTCAG 60
ATTAAACAAG GAAAAGACGG AAA 83

SEQ ID NO:1415

LENGTH:83

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01569

SEQUENCE DESCRIPTION:

GATCTTGGTG TTCAAACAG AACTGTATTT TTGCCTTTAA AATTAAATAA TATAACGTGA 60
ATAAATGACC CTATCTTTGT AAA 83

SEQ ID NO:1416

LENGTH:82

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01570

SEQUENCE DESCRIPTION:

GATCCTTCTG TAAAGGTTTT TGGAATTATG TCTGCTGAAT AATAAACTTT TTTGAAATAA 60
TAAATCTGGT AGAAAAATGA AA 82

SEQ ID NO:1417

LENGTH:86

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01571

SEQUENCE DESCRIPTION:

GATCTGCATA TTTCTGTATA TTTGTCATGA CAGTGCTTGC ATCCTATTTG GTGTACTCAG 60
CAAATAAACT TTTCAATTTA AACAAA 86

SEQ ID NO:1418

LENGTH:81

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01572

SEQUENCE DESCRIPTION:

GATCCCAACA TGGTCCTAGC ACTGCACACT CAGTTTTNCT CTAAGAAGCT GCAATAAAGT 60
TTTTTNAAGT CACTTTGTAA A 81

SEQ ID NO:1419

LENGTH:81

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01573

SEQUENCE DESCRIPTION:

GATCTTCANT TAATCNCAC TTA AAAATGA CCAAAACATG TCTTTCTTGA ATTAAC TTG 60
AATAAAAGTT TGTATATTAA A 81

SEQ ID NO:1420

LENGTH:81

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01574

SEQUENCE DESCRIPTION:

GATCAGAGCT CAGTTCCTGT AGAAAACGAA CTGTAAAAGA CCATGCAAGA GGCAAAATAA 60
AACTTGAAGT GAATGCTTAA A 81

SEQ ID NO:1421

LENGTH:80

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01575

SEQUENCE DESCRIPTION:

GATCTTGGGT TTGGTCTACC CACCCAAGAG AAAAGACTGT TAACTGGAAG AAAAAATATA 60
TATATNNAAT TTTATGTAAA 80

SEQ ID NO:1422

LENGTH:79

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01576

SEQUENCE DESCRIPTION:

GATCACAATT ACCTTTAGTT GTTTTTTTTG TAATAATTGT AGCCAAGTAA ATCTCCAATA 60
AAGTTATCGT CTGTACAAA 79

SEQ ID NO:1423

LENGTH:79

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01577

SEQUENCE DESCRIPTION:

GATCCTTATG AATGACAGGT TACTGTTTTG CTTATTGCT TAACTTAATG TAGTGAAATA 60
AAGCAGACAA AGCTTGAAA 79

SEQ ID NO:1424

LENGTH:79

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01578

SEQUENCE DESCRIPTION:

GATCTTCTGC ATGAGACCTG GAGTTGGGGA AGCAAGGTTA CATTGTATT NGTTTATCCT 60
ATGAATACTN TTCTCAAA 79

SEQ ID NO:1425

LENGTH:78

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01579

SEQUENCE DESCRIPTION:

GATCAGGCAG TCTGCTCAGA TACATTGAGT GCGGATTTTA AGTTTTGTTT TGA AAAAATA 60
AACAGATTAA CCTGCAAA 78

SEQ ID NO:1426

LENGTH:78

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01580

SEQUENCE DESCRIPTION:

GATCTAAATT TCTAATGTGT TCTATGGGTT TCAATTCTGA AAAAAGAAAA TGAATAAAGA 60
TTTAAATAAA TATTGAAA 78

SEQ ID NO:1427

LENGTH:78

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01581

SEQUENCE DESCRIPTION:

GATCTTCATT GTGCTGGGTG CCAGGNCAGT NATCCATTTT AAAATTGTA ATTCAATAAA 60
GTTTTTTTTG TTNTAAA 78

SEQ ID NO:1428

LENGTH:77

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01582

SEQUENCE DESCRIPTION:

GATCTCCAGG CTGCGCTCC AGAGCAGCCC ACACCAACNC CAAAATAAAA AAATGTATAT 60
ATTCCTTTAG CTCTAAA 77

SEQ ID NO:1429

LENGTH:76

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01583

SEQUENCE DESCRIPTION:

GATCCCAGGG ACCTCAGTCG GCTTAATCAG AGTGTGGCAT AGAAGCTATT TAATGATTAA 60

AGTCATTGTC AGTAAA 76

SEQ ID NO:1430

LENGTH:76

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01584

SEQUENCE DESCRIPTION:

GATCAAACCTT TTATGTTCT TAATAAGCTT GCAATTGANT AAAATAGAAT ATAAAATAAA 60

GGTGAAATAA TATAAA 76

SEQ ID NO:1431

LENGTH:79

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01585

SEQUENCE DESCRIPTION:

GATCCCAAGT ACAATGAAAA GTTGCCTG TATGCTGGAC GGCATTCTG CTTATCAATA 60

AACCTGTTTG TTTTACAAA 79

SEQ ID NO:1432

LENGTH:75

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01586

SEQUENCE DESCRIPTION:

GATCTCCAAC NTTGGAAAA ATACATGATG TGAACTGNG GGTNCTATGT TAAAAATAAA 60

TGTATGATAA CTAAT 75

SEQ ID NO:1433

LENGTH:74

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01587

SEQUENCE DESCRIPTION:

GATCCAAACA TTTTGTGTG TGTGTATGGC ATTGATGCAG AATAGAATAA AATTATACTT 60

AGTTCTTTT TAAA 74

2153480

SEQ ID NO:1434

LENGTH:73

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01588

SEQUENCE DESCRIPTION:

GATCCCGGCG CGGGAAAGTC ACAGAGCTGC CTGGGCTTGT ACCTGGNCAC ATAAAGCCCC 60
ANTTTAAAGC AAA 73

SEQ ID NO:1435

LENGTH:73

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01589

SEQUENCE DESCRIPTION:

GATCCCANAG CNATAAAATA AAATTTTATT CAAAATAAC AAAACAAATT NATCTACTGT 60
ACACAATCTG AAA 73

SEQ ID NO:1436

LENGTH:72

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01590

SEQUENCE DESCRIPTION:

GATCCCAGGC TTCTGCGGAC CGACGATACG TTTAAATGTT GTTCTAGTAA AGTTTTCGAT 60
ATGTTTCTGA AA 72

SEQ ID NO:1437

LENGTH:71

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01591

SEQUENCE DESCRIPTION:

GATCCCTTGG NGGNTAGTT CGTATTTTGG TTTAAACTA TTTGTTAGAA TAAAGTAATT 60
TTGCTAATAA A 71

SEQ ID NO:1438

LENGTH:70

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01592

SEQUENCE DESCRIPTION:

GATCTTAAGT ATAAAAATTG TGTAATTGGG CCTTTACTCT CTCAATAATA AAGTATTTTG 60
TTTATATAAA 70

00656

2153480

SEQ ID NO:1439

LENGTH:68

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01593

SEQUENCE DESCRIPTION:

GATCTGTATT TTCTAAGTCC CCAGTTCTCC TGGCTCTCCT TTCTGAAATA AAGGATTGAA 60
AACNGAAA 68

SEQ ID NO:1440

LENGTH:67

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01594

SEQUENCE DESCRIPTION:

GATCTGTTTT TAAAAATCAT AAAGTGTGTG CAGACTCAAT AAAATCATGT ACATTTCTGA 60
AATGAAA 67

SEQ ID NO:1441

LENGTH:71

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01595

SEQUENCE DESCRIPTION:

GATCAACAGT TACTGTNACT GAGTCGGCCC ATTCTGTTTA GAAATATATT TNAAATGTTT 60
AGTAATTGAA A 71

SEQ ID NO:1442

LENGTH:66

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01596

SEQUENCE DESCRIPTION:

GATCTGCCAT TTCATGCCNT GTGACTACNN ATCATTGGCC CTGCAATAAA ATCATTTATT 60
TTTAAA 66

SEQ ID NO:1443

LENGTH:64

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01597

SEQUENCE DESCRIPTION:

GATCCTGCAT GCTACTCTTA GATAGAAGAT GGCAAAACCA TGGTATTAAA ATATGAATGA 60
TAAA 64

00657

SEQ ID NO:1444

LENGTH:64

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01598

SEQUENCE DESCRIPTION:

GATCAAGTCA CTNTTGACAA CATCCAGGNG AATATAAAAA CTTAATAAAG CTGTGGAAG 60
GAAA 64

SEQ ID NO:1445

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01599

SEQUENCE DESCRIPTION:

GATCAATTGG TTAACTTCT TTTATGTAAG TATGGTATAT AAATTTCAAG ACGAACACTA 60
AA 62

SEQ ID NO:1446

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01600

SEQUENCE DESCRIPTION:

GATCACTTTT CACTTTTGG AATGTTTGT ATTGAACTT AATAAACTT TAACATGGCA 60
AA 62

SEQ ID NO:1447

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01601

SEQUENCE DESCRIPTION:

GATCGNTCTC AGGCCCTCCC CCCGGAGTAC TTCAGAATGC AATAAATCAA AATAATGGCA 60
AA 62

SEQ ID NO:1448

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01602

SEQUENCE DESCRIPTION:

GATCTGTATG TGTTCTATTC AGCACAAGGA AATAAAATTT TAGTTGAGGA TTCAGCACTA 60
AA 62

SEQ ID NO:1449

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01603

SEQUENCE DESCRIPTION:

GATCCCCATT CTTTCAAAA AAAAAATAAA ACAATAAAGA CTGCAAGGAA GACTGANGGA 60
AA 62

SEQ ID NO:1450

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01604

SEQUENCE DESCRIPTION:

GATCCAGTCT GGAATAACAT TTTGTAAAAA AAAAATATAT ATATATATAT ATATNGCTGA 60
AA 62

SEQ ID NO:1451

LENGTH:61

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01605

SEQUENCE DESCRIPTION:

GATCGGGGGC ACCAGAGGGG CAGAGGCACC AACATCTGAA TAAAGCCATT GTTCTCCCAA 60
A 61

SEQ ID NO:1452

LENGTH:61

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01606

SEQUENCE DESCRIPTION:

GATCTTGGAC NTCTCGCATT CAGAACTGTG AGAAATAAAT ATCTATTATT TACAAATTAA 60
A 61

SEQ ID NO:1453

LENGTH:60

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01607

SEQUENCE DESCRIPTION:

GATCTCCGTC TTGTATGGCT GAATGTTGGC CTAAAATAAA GATTACTGTT GTAAAATAAA 60

SEQ ID NO:1454

LENGTH:62

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01608

SEQUENCE DESCRIPTION:

GATCTGTGGA GAATGTACAC AGTTTAAACA CATCAATAAA TACTTTAACT TCCACCGAGA 60
AA 62

SEQ ID NO:1455

LENGTH:72

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01609

SEQUENCE DESCRIPTION:

GATCAAGAAT CCTGCTCCAC TAAGAATGGT GCTAAAGTAA AACTAGTTTA ATAAGCAAAA 60
AAAAAAACCA AA 72

SEQ ID NO:1456

LENGTH:59

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01610

SEQUENCE DESCRIPTION:

GATCTAGATG TTTCTTTAAC CAAGATGAAT TAAAATATAG TAGAGTTCCA CTGTNCAAA 59

SEQ ID NO:1457

LENGTH:63

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01611

SEQUENCE DESCRIPTION:

GATCAAATTG TACCTTTTGA GAGAAAAGGA CCAAAATAAA AGAAAAATGA ATTATGAACT 60
AAA 63

SEQ ID NO:1458

LENGTH:59

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01612

SEQUENCE DESCRIPTION:

GATCAGCAGT CTTGGATGGN AGGNAACAAA GCTAAATAAA TGTTAGTTTG GTGAGCAAA 59

SEQ ID NO:1459

LENGTH:65

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01614

SEQUENCE DESCRIPTION:

GATCTCCCTT ATATTCTTAT GATGAGGCTA AATAAAAGTC TAATAAAAAT GTTAAATATG 60
TGAAA 65

SEQ ID NO:1460

LENGTH:56

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01615

SEQUENCE DESCRIPTION:

GATCAAAATC AAGTTTAAAG TTTTGTGAC CAGATAAATT TAATGATTTT GGCAAA 56

SEQ ID NO:1461

LENGTH:58

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01616

SEQUENCE DESCRIPTION:

GATCTTAATT ACTTTCAGAA TATTTTCAAA ATAGATATAT TTNAAAATC CTTACAAA 58

SEQ ID NO:1462

LENGTH:55

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01617

SEQUENCE DESCRIPTION:

GATCGTTCTT CTCTCCGTAT TGGGGAGTGA GAGGGAGAGA ACGCGGTCTG AGAAA 55

SEQ ID NO:1463

LENGTH:55

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01618

SEQUENCE DESCRIPTION:

GATCCCTGAG ACGGGGTAAG TTATAATAAA CAGAAATGTA TTGGCTCAGA AGAAA 55

SEQ ID NO:1464

LENGTH:55

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01619

SEQUENCE DESCRIPTION:

GATCTGTTAT GTATTTCAAC ATAATCATGT TTCATAAAGA TTTAGTCTTC TGAAA 55

SEQ ID NO:1465

LENGTH:56

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01620

SEQUENCE DESCRIPTION:

GATCCCACCT TTGCTCCTGA CAACCCTCAT TTCAATAAAG ACCAGTGAAG ACCAAA 56

SEQ ID NO:1466

LENGTH:54

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01621

SEQUENCE DESCRIPTION:

GATCAGAATC CTGCTCCACT AAGAACGGTG TAAAGTAAAT TAGTTATAAG CAAA 54

SEQ ID NO:1467

LENGTH:63

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01622

SEQUENCE DESCRIPTION:

GATCTTGAGC CTTAACTGGA CATGAGGGGC ATGAAAATAA AGCTGAACTG CAGCCTCCTG 60
AAA 63

SEQ ID NO:1468

LENGTH:54

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01623

SEQUENCE DESCRIPTION:

GATCTTTTCT AAATGTTATT ACTTGTAAT AAAGTCTATT TTTCTCCCGT GAAA 54

SEQ ID NO:1469

LENGTH:54

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01624

SEQUENCE DESCRIPTION:

GATCTGTATA TTTTTTCTA AGAGAAAATG TAAATAAAGG ATTTCTAGAT GAAA 54

SEQ ID NO:1470

LENGTH:54

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01625

SEQUENCE DESCRIPTION:

GATCTGCGCA TATATATATA TGTATAAAAA ATAATAAAAT AATGGAAGNT GAAA

54

SEQ ID NO:1471

LENGTH:54

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01626

SEQUENCE DESCRIPTION:

GATCCTAAAT NCACGCACCC CGTGGGAGCN CAATAAAGAT TTACTGAATT GAAA

54

SEQ ID NO:1472

LENGTH:53

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01627

SEQUENCE DESCRIPTION:

GATCCGCCAT CTGTAATGTC CTTGGCACAA TAAAACCAA TGTCAGTTTC AAA

53

SEQ ID NO:1473

LENGTH:52

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01628

SEQUENCE DESCRIPTION:

GATCCCTAGT GATTACAGCC CTGAAGAAAA TTAAATCTGA ATTAATTTTA AA

52

SEQ ID NO:1474

LENGTH:52

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01629

SEQUENCE DESCRIPTION:

GATCCAGTGT GGATTCTNG AGTAATAACG TTGGTTTAT TTATCATATA AA

52

SEQ ID NO:1475

LENGTH:52

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01630

SEQUENCE DESCRIPTION:

GATCTTCAAT GTTTATTTTA AAATAAAATA AAATAAGTTC TTGACTTTTA AA

52

SEQ ID NO:1476

LENGTH:56

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01632

SEQUENCE DESCRIPTION:

GATCTTGAAT GAAAGTCTTC TCAGGCTGTA GGGTGGTTCC TACAACCACA GCCAAA 56

SEQ ID NO:1477

LENGTH:51

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01633

SEQUENCE DESCRIPTION:

GATCTCATCT GAATCCCCAA CACCCAATAA AGTTCCTTTT TAACACACAA A 51

SEQ ID NO:1478

LENGTH:55

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01642

SEQUENCE DESCRIPTION:

GATCAAAATC CTATTAGAA AAAATAAAAC TACTTTCTGT TTATCTCTTT AGAAA 55

SEQ ID NO:1479

LENGTH:34

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01671

SEQUENCE DESCRIPTION:

GATCCAAAAA CATCCGTGAA CCTCTGTCTG TAAA 34

SEQ ID NO:1480

LENGTH:305

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01673

SEQUENCE DESCRIPTION:

GATCAAAATA AAGGATGATA ATAGATATTA TTTTNCCTTA TGACAGAAGC AAATGATGTG 60
 ATTTATAGAA AACTGGGAA ATACAGGTAC CCAAAGAGTA AATCAACATC TGTATACCCC 120
 CTTCCCAGGG GTAAGCACTG TTACCAATTT AGCATATGTC CTTGCAGAAT TTTTTTTTCT 180
 ATATATACAT ATATATTTTT AACCAAAATG AATCATTACT CTATGTTGTT TTAATTTTGG 240
 TTTGACATAT CAGTATATCT GAAACACCTT TTCATGTCAA TAAATGTTCT TCTCTAACAT 300
 TTTAAA 305

SEQ ID NO:1481

LENGTH:734

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01686

SEQUENCE DESCRIPTION:

GATCCAGCCC ATTCTCTACT CTTACTCCTT TCATGGGCCA CCAGAGCCAG TACTCTTGGA 60
 TAGCAGCAGC ATTCTAGCTG ACAGAATTTT GCTGATGGAT ACTTTCTTTC AAATTGTCAT 120
 TTATCTTGGT GAGACCATAG CCCAGTGGCG TAAAGCTGGC TACCAGGACA TGCCCGAGTA 180
 TGA AAACTTC AAGCACCTTC TGCAGGCACC ACTGGATGAT GCTCAAGAAA TTCTGCAAGC 240
 ACGCTTCCNG ATGCCACGTT ACATCAACAC GGAGCATGGA GGCAGTCAGG CTCGATTTCCT 300
 TTTGTCCAAA GTGAACCCAT CTCAGACACA CAATAACCTG TATGCTTGGG GACAGGAAAC 360
 TGGAGCACCC ATCCTAACTG ATGATGTTAG CCTGCAGGTG TTCATGGACC ATTTGAANGA 420
 AGCTGGCTGT CTTCCAGTGG CCTGTTAAAG CTGAGGATAC AACCAGGGAA ATGCAAACGG 480
 TNTCAAGATT TGGTGGTTCA AAATTGTCTA GAAAGGGTTT GATAACCATT CCNGGTTACT 540
 TTTTCTTNGG ANGTTTAAAC CAAATAATCA ANGGCNATTT TATTATGGAA CCTCTTTAGG 600
 TTATAATTNA TTNGGAATNC CGNCNTTGGC CTTTCTTGN CCTTTAAATT TTAAGGGAAN 660
 AAANNTTGG GCNTNAGGNG GTTNNGGNTT TTTGGNNCNA ACTTNGGGN TTAATAAANC 720
 NGGGGNNTNT TAAA 734

SEQ ID NO:1482

LENGTH:731

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01687

SEQUENCE DESCRIPTION:

GATCAACCGG AGCGCTCCG AGCCATCCTT GCATCGGGCA GCCCAGCTG AGGATATCAA 60
 TGCTTGACAG CTGACCACGT CCCCGAGGCT GCCTGTNTTC TAGTTGACTT TGCACCTGTN 120
 TTCAGGCTGC CAGGGGAGGA GGAGAAGCCA GCAGGCACCA CTTTTCTGCT CCCTTTCTCC 180
 AGAGGCAGAA CACATGTTTT CAGAGAAGCT GCTGCTAAGG ACCTTCTAGA CTGCTCACAG 240
 GGCCTTAAC TCAATGTGCC TTCTTTTCTA TCCCTTTGGG CCCTGGGAGA AGGAAGCCAT 300
 TTGCAGTGCT GGTGTGTCCT GCTCCCTCCC CACATTCCCC ATGCTCAAGG CCCAGCCTTC 360
 TG TAGATGCG CAAGTGGGAT GTTGATGGTA GTACAAAAAG CAGGGGCCCA GCCCAGCTGT 420
 TGGCTACATG AGTATTTAGN GGGAAAGTAAG GTAGCAGGCA GTCCAGCCCT GANNTTGGAG 480
 ACACATGGGG TTTTGGAAA TAAGNTTCTT GNGGGATGAA TGTAACAGGN GGGNTTCTT 540
 CANGGAGTGG TNCAGCNCAG ACATTTNNAC ATAAGGACCA AACAGCCCAG NNTNCCGNAT 600
 TTTGNCNCCC AAGNCCTTT TTTGGACTTG GANCTTTNTT NGGGGAAAGC CNCTTNAANG 660
 TTTAAGNGCC AGNATNGGTG TTTGNGAAG NATTGCCATC CGATTTAGCC TTTANGGGAN 720
 GTTCCANAAG N 731

SEQ ID NO:1483

LENGTH:687

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01688

SEQUENCE DESCRIPTION:

GATCGGTGGC TCCATCCTGG CCTCACTGTC CACCTTCCAG CAGATGTGGA TTAGCAAGCA 60
 GGAGTACGAC GAGTCGGGCC CCTCCATCGT CCACCGCAA TGCTTCTAAA CGGACTCAGC 120
 AGATGCGTAN ATTN TGCTGC ATGGGTTAAT TGAGAATAGA AATTGCCCC TGGCAAATGC 180
 ACACACCTCA TGCTAGCCTC ACGAACTGG AATAAGCCTT CGAAAAGAAA TTGTCTTGA 240
 AGCTTGTATC TGATATCAGC ACTGGATTGT AGAACTTGT GCTGATTTN ACTTTGTATT 300
 GAAGTTAACT GTTCCCCTTG GTATTAACGT GTCAGGGCTG AGTGTCTGG GATTCTCTA 360
 GAGGCTGGCA AGAACCAGTT GTTTGTCTT GCGGGGTCTT GTCAGGGTTG GAAAAGTCCA 420
 AGCCGTAGGA CCCCAGTTTC CTTCTTAAG CTGATGTCTT TTGGCCAGAA CACCGTGGGC 480
 TNGTTAATTG CTTTAAAGTT GGAAGCGGT TTGCAATTAC GGCNCTAAAA NGTATTCATC 540
 CTNAATTNAA GGAAAGGGTT TTTTGTGAC CGAAANNNG ATTCTTTGAA GNGNTGNCAC 600
 CAAATTTTGG GTTTCANCC GGTAAAGGGN GACATTAGN CCCAGNACAA GGNATTNTGA 660
 AAGGGAANAN AANGGCNNCC GAAAAAN 687

SEQ ID NO:1484

LENGTH:649

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01689

SEQUENCE DESCRIPTION:

GATCAAACTG TATTGCCCAG GCCAGCTCCT GAAGAACTGT GAACTATGAA CGTCTCAGCC 60
 TAGAAGGATA ATGTGACCTT CAATTTGCAC ACCATCCATT GTCTCTTCA AACTAAGAGC 120
 CTCTCTAAGC TAGATAGGCC AAGGATTATT TTTTAACTT TTATTTTAGG TTCAGGGGTA 180
 CATATACAGG TTTGTTACAT AGGTAACCTC ATGTCATGAG GGATTTTGTA TAGATTATTT 240
 GGTGACCCAG GACTAAACC TAGTACCCAT TAGTTGTTTT TNCTGCTCCT CTCCCTCCTC 300
 TCACCCCTCA CCCTCAGTTA GTTCCCAGTG TGTGTTGTTT CCCCACATCT ATCCATGTGT 360
 TCTTATTATT TAAGCTCCCA CTTATAAGTA AGAATGCA GTGTTTGTTT TTCTGTTCCT 420
 GATTAGGTAA TGCTGAGGGA TAATGGCTC CAATTNCCAT CCATNGTTT TGCAAAGGAN 480
 CATGNCTCA TTNCTTTAAA TATGGGCTNG CATAGNNGT CCATGGGNGG TGAATGTACC 540
 ACATTTTCCT TTNANCCAGG TCTNATCAAT TGGNGGGCCA TTGNGGGTGA TTCCAAGGCT 600
 TNGGTAATGG TGAANAGGGC ACAATAANCC AGTACCATGG GGCATGAAA 649

SEQ ID NO:1485

LENGTH:549

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01691

SEQUENCE DESCRIPTION:

GATCCTCTGA TGGGAGCTGA AAGGATGAGA GGTGGGCATC TAGATTTAGG GAGGCTGTTC 60
 AGGCTTTGCA GGTCCCTTAC CTGAACACAT AGAAACCCTG GAGCTGTGAC TGTGTCCATG 120
 TGTGTGTGTT TGTCTGTGTG TGTGCGGGG GATGGGCACC TGCATGAATG TGGTAGAGAA 180
 AATGGCTCTG CTCAGAGGGA AGATACGCAT AGCAAGGCAG GGACCAGAGG AATCAGAGG 240
 GCCTGGAGAG CAGCCGGGCA ACGNCTCCAG GGACCTGCCG GCTTCCCTCA GTCCTCCAGG 300
 GGCCAGCAC TCTTCCTTA GGCCCTGTGA GCGTCCCTTG TCAGGATACA TTCTCTCATT 360

TTGCTGAAGC TGATTTGATT GGGTGTCTGT TTCTCGCAGC CAAAAGAGCT CTGAAATGAG 420
 GAAAGTGCTT CTGTGCTAAC TCCCCGGGTC TCCTGAATTT CAGTCATTCA TGTACCCGCC 480
 TCGAAATTTT TTGCAATATC TGTGTACCCA ATGTCCATTT AATTAATAAA GAAGTTTCT 540
 TAAATTAAA 549

SEQ ID NO:1486

LENGTH:543

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01692

SEQUENCE DESCRIPTION:

GATCGANGTT TACCTTGTGT CAGGAAAAA TGTGGGGTAT GCCAAGTATG CCGATAGAAT 60
 AAGTNCATAT GATGCCACTN GCCACTCTAC ATNGAAAGAT TCTGAATGGG GTGAGACTTA 120
 AAGTTATGCT GGCAGATTCG CCAAGAGAAG AATCTAACAA ACGGCAAAGA ACTTACTGAT 180
 TCTTGAGAAC ACCCGACTAA ATAATGACAT ANTCCTCAGC TGACTGACTG AAAATGTGAC 240
 TGGACGCATT CCCTGTGGAC AGTTGACAGC TTTTTTTTTT TCCATATACC TGNTAGTCTG 300
 TGTCCAGCAT TGTTTTGTCT GGGAAGCAGG GTTTGCTGNC ATGTATTTN NATTCATAC 360
 ATTANTGCTA AACCGNTTAT AGTAGTTGTN CCTAGNGCA NTATGTTGTT ACGTGTAGCA 420
 GAANTAAAGT TTTCTTTGCT TTANCTAAAT CATGNCTTA TTTNTGNGAA GGCCAGGACC 480
 GGGAAATTTT ATTNNGCAGT CTTTGNTTT TGCCTAATGN CATTGNCATG NNTTTGGGGT 540
 NCN 543

SEQ ID NO:1487

LENGTH:533

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01693

SEQUENCE DESCRIPTION:

GATCCAGAGT TGCATACAGA CCAATTTCTG CATCAGTGTT ATCTCGACCA GAGGCTAGTA 60
 GGACTGGAGA GGGCTCTACG GTATTTAATG GGGCCCAGAA TGGTGTGTCT CAGCTAATCC 120
 AAAGGGAGTT TCAGACCAGT GCAATCAGCA GAGACATTGA TACTGCTGCC AAATTTATTG 180
 GTGCAGGTGC TGCAACAGTA GGAGTGGCTG GTTCTGGTGC TGGTATTGGA ACAGTCTTTG 240
 GCAGCCTTAT CATTGGTTAT GCCAGAAACC CTTGCTGAA GCAGCAGCTG TTCTCATATG 300
 CTATCCTGGG ATTTGCCTTG TCTGAAGCTA TGGGTCTCTN TTGTTTGATG GTTGCTTTCT 360
 TGATTTTNTT TGCCATGTAA CAAATTACTG CTTGACATGT TGGCATNCAT ATTAATTACG 420
 GATGNAATCC TGGGNANCTA CCTGTNCCTC CGAAAACCTG TAGGTANTTG GGGGTCANGG 480
 GGAATTGNCC GGTAATTCCC AAAGCCATTT NATTAAGGN GGAAACCTTT AAA 533

SEQ ID NO:1488

LENGTH:531

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01694

SEQUENCE DESCRIPTION:

GATCCAAAAG ANCTGCTTTC TGAAGCAAGT TTCCAAGANG CTCTTCAGGA AAGCATTCTT 60

GACATTCAAG CGCACGAGTG GGTGCCGCTG TGGCTACTGC GGTATTCCGGT CATTGTGAAA 120
 AGTAGAGGAA TTATCAAATC AAAAGGCTAC ATTTTACAAG CTAAAAGAAG GGGTTCTTAA 180
 CTGACTTAGG AGCATAACTT ACCTGTAATT TCCTTCAATA TGAGAGAAAA TTGAGATGTG 240
 TAAAANTCTA GTTACTGCCT GTAAATGGTG TCATTGAGGC AGATATTCTT TCGTCATATT 300
 TGACAGTATG TTGTCTGTCA AGTTTTAAAT ACTTATCTNG CCTCCATATC AATCCATTCT 360
 CATGAACCTC TGTATTGCTT TCCTTAAACT ATTGNTTTTC TAATTGANAT TGTCTATANG 420
 GANATNCTTG CAATATATTT NNNCNTTANT TTTTATGNCT AATATNAATN CAGGNNAATT 480
 TGTGTTTGG TATTTTGGG CNNGGGTTCC GGGGAATGNT TNTNCANTTT N 531

SEQ ID NO:1489

LENGTH:526

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01695

SEQUENCE DESCRIPTION:

GATCGGCGTG ACCANCCCTT GCCGGAGGTG GCCCATGTCA AGCACCTGTN TGCCAGCCAG 60
 AAGGCACTGA NAGGAGAAGG AGAAGGCCTC CTGGAGCAGC CTCTCCATGG ATGAGAAAGT 120
 CGAGTTGTAT CGCATTAAAGT TCAAGGAGAG CTTTGCTGAG ATGAACAGGG GCTCGAACGA 180
 GTGGAAGACG GTTGTGGGCG GTGCCATGTT CTTTCATCGGT TTCACCGCGC TCGTTATCAT 240
 GTGGCAGAAG CACTATGTGT ACGGCCCCCT CCCGCAAAGC TTTGACAAAG AGTGGGTGGC 300
 CAAGCAGACC AAGAGGATGC TGGACATGAA GGTGAACCCC ATCCAGGGCT TAGCCTCCAA 360
 GTGGGACTAC GAAAAGAACG AGTGGAAGAA GTGAGAGATG CTTGGCCTNC GGCTTCAACT 420
 TCGGGCTGGC TCTTTCACCG CCATGCAAAC TCCATGCCTA TTTACTNGGA AACCTGTTAT 480
 NCCAAACAGT TGTNCNCTGC TAATAAATTG NCCAGTTTAC CTGAAA 526

SEQ ID NO:1490

LENGTH:525

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01696

SEQUENCE DESCRIPTION:

GATCAGCAGA GGNATCAAAC CAACACCTTC TTTGGCTCCC CTCCCGCAGC CACAGAGGCA 60
 ACCCAGCTTG TCAGCACCAT CCCTGAGTCA TTACAATAGC ACCCTGCAGC TATGCTGGAA 120
 AACTGAGCGT GGGACCCTGC CAGACTGAAG AGCAGGTGAG CAAAATGCTG CTTTCTGCCT 180
 TGGTGGCAGG CAGAGAACTG TCTCGTACTA GAATTCAAGG AGAAAAGAAG AAGAAATAAA 240
 AGAAGCTGCT CCATTTTTC TACTCTACCC ATCTATTTGG AAAGCACTGG AATTCAGATG 300
 CAAGAGAACA ATGTTTCTTC AGTGGCAAAT GTAGCCCTGC ATCCTCCAGT GTTACCTGGT 360
 GTAGATTTTT TTTTCTGTAC CTTTCTAAAC CTCTCTTCCC TCTGTGATGG TTTTGTGTTT 420
 AAACAGTCAT CTNCTTTTAA ATAATATCCA CCTNTCCTTT TTGCCATTTC ACTTATTGGN 480
 TCCATAANGT GAATTTTAAT TTAAGGTTAT GCCACACATG CATGN 525

SEQ ID NO:1491

LENGTH:522

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01697

SEQUENCE DESCRIPTION:

GATCAGCTGT TTGTCATAGG GCAGTTGGAA ACGGCCTCCT AGGGAAAAGT TCATAGGGTC 60
 TCTTCAGGTT CTTAGTGTC CTTACCTAGA TTTACAGCCT CACTTGAATG TGTCACTACT 120
 CACAGTCTCT TTAATCTTCA GTTTTATCTT TAATCTCCTC TTTTATCTTG GACTGACATT 180
 TAGCGTAGTA AGGTGAAAAG GTCATAGCTG AGATTCTCTG TTCGGGTGTT ACGCACACGT 240
 ACTTAAATGA AAGCATGTGG CATGTTCATC GTATAACACA ATATGAATAC AGGCGCATGCA 300
 TTTTGCAGCA GTGAGTCTCT TCAGAAAACC CTTTCTACA GTTAGGGTTG AGTTACTTCC 360
 TATCAAGCCA GTACGTGCTA ACAGGCTCAA TATCCTGAA TGAAATATCA GNCTAGTNGN 420
 CAAGCTCCTG GTCTTGAGAT GTCTTCTCGT TAAGGAGATG GGCCTTTTGG GGGTAAAGGN 480
 TAAAATGGAT GAGGTCTGNC ATGNTTCACT ATTCTAGGAC TN 522

SEQ ID NO:1492

LENGTH:509

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01698

SEQUENCE DESCRIPTION:

GATCCCAACA ATATCCCAA GGCCTCAATG ACAAGTGGTT TGGTTCAGCA GTTCCAACAC 60
 ACAGTCCTTC CCTCAGTGAC TCCCTTGGNN CCCTCATCTG CACACTGATT GCCATATTGC 120
 CCTCTATTTT CTGTCTTTGG TTTAAACCCC AAGGGCCCAG AGGCTTTCTC CGATGTCTAA 180
 CTCTTTGTGC CTTGAGCTCC TTTATGTTG GGTGGCATGT TCATGAAAAA GCCATACTTC 240
 TAGCAATTCT CCCAATGAGC CTTTGTCTG TGGGAAAAGC AGGAGACGCT TCGATTTTTC 300
 TGATTCTGAC CACAACAGGA CATTATTCCC TCTTTCCTCT GCTCTTCACT GCACCAGAAC 360
 TTCCCATTA AATCTTACTC ATGTTACTAT TCACCATATA TAGTATTTTCG TCACTGAAGG 420
 ACTTTATTCA GAAAAGGAAA AACCTCTTTT TTAATTGGGA TGGGAACCTT CTANCCTGCT 480
 TTGGNCNGGG GGCCTCTGGG AAGGNCTTN 509

SEQ ID NO:1493

LENGTH:497

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01699

SEQUENCE DESCRIPTION:

GATCCTGTCA AAATAGTCCG ATGCCATGAA CATATAGAAT CTTACAGTA AATGGAGAAT 60
 TACTCTTTTT TAGACAAAGA GAAGGGCCTT TTTATCCAAC CCTAAGATTA CTTACAAAT 120
 ATCCTTTTAT CCTGCCACAC CAGCAGGTTG ATAAAGGAGC CATCAAATTT GACTCAGTG 180
 GAGCAAATAT CATGTGTCCA GGCTTAACCT CTCCTGGAGC TAAGCTTTAC CCTGCTGCAG 240
 TAGATACCAT TGTGCTATC ATGGCAGAAG GAAAACAGCC TGCTCTATGT GTTGGAGTCA 300
 TGAGATGTCT GCAGAGNCAT TGNGAAGTCA CCAAAGGATT GGCATTGAAA ATATCCATTA 360
 TTAAATGAT GGGCTGTGGN TATGAGGCAT ATAAATGNGC TCAGAGGGAT GCACTTGGGT 420
 NAATATGGNT ATTGTGCTGT ATCTGTGTTG TGNCTGTGTG TGCANCTGAG GTATGCCCTGT 480
 GGTNTGCTGA TAAATCN 497

SEQ ID NO:1494

LENGTH:472

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01700

SEQUENCE DESCRIPTION:

```
GATCAAAATA TCATGGATTG AACCTCATCA ATTGATAGCA GTGAGTGACT GANGCTTCCA 60
AATCAAGAAA AGCCGGCACC AAGAACTTCC ATTCTAATCT AGAGCTGACC AGTTTGAGCT 120
GATTCTNTCT TTGAAGAGTC CTTCTTGATT GCAGTGCAGT ACTGGCATTG CTGAATGGAT 180
GTANGNGGAG TATTTTAGTC TAAAGGCTTT TCAAATTACT TGAATTTTTT TAAAAATTGA 240
GGAGCTTTAT TTCTATTAC CCTTCCATTG TTGTATATCA AATTTCATN GTCATTAAAA 300
ACTGTATCTT GAAACTTTGT GAACTGACTT GCTGTATTG CACTTTGAGC TCTTGAAATA 360
ANTGTGATTG TNGTGTGATT ATCTGGTTTC CNGTTTAAAC CATTACCTGT CACCNTTNAT 420
CCTTAACCTT GAAAGTCCAG AAACCATNNN ATTATTAAGG TNGTCCAATA AA 472
```

SEQ ID NO:1495

LENGTH:496

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01701

SEQUENCE DESCRIPTION:

```
GATCTGTGTG GATGGCAAAC TCCCAGGCC ATTCTGGGAC CTAAGTTTAA GAAGTGCCGT 60
CCTCGAACTT NCTGACTCTA AGCTCCTGAG CGGGAGTNAG ACTTAGCCCT GAGCCTGCAC 120
TTCCTGTTCA GGTGCAGACA CTGAACAGGG TCTCAAACAC CTTCAGCATG TNTNTGTGT 180
GCTCACGTGC CACACAGTGT CTCATGCACA CAACCCAGTG TACACACCAC CTACATGCAC 240
ACAGCGTCTT TNCACACTGT GTATGTGAAC AGCTTGGGCC CTGCAACACA ACCATCTACA 300
CACATCTACA ACCNNNAGGA CACACACATG GGTCCGTGCC ATGTCACCTC CNTAGGGGAN 360
GGNTTCTTT CCAAGGTGTN GCCAGGCCAG GCAAGCCTTC CAGGCCATGA ATTCCTTACT 420
TAGGTACCTN GGGGTTTGGG GTGGGNGNCC CAGNCAAAT TCTNNGGTTN CGTNCNCTTT 480
GGTTNNGNCC AGNTTN 496
```

SEQ ID NO:1496

LENGTH:492

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01702

SEQUENCE DESCRIPTION:

```
GATCCTGTAC AGCCAGTGTG GGGATGTGAT GAGGGCCCTG GGCCAGAACC CTACCAACGC 60
CGAGGTGCTC AAGGTCCTGG GGAACCCCAA GAGTGATGAG ATGAATGTNA AGGTGCTGGA 120
CTTTGAGCAC TTTCTGCCA TGCTGCAGAC AGTGGCCAAG AACAAGGACC AGGGCACCTA 180
TGAGGATTAT GTCGAAGGAC TTCGGGTGTT TGACAAGGAA GGAAATGGCA CCGTCATGGG 240
TGCTGAAATC CGGCATGTTT TTGTCACT GGGTGAGAAG ATGACAGAGG AAGAAGTAGA 300
GATGCTGGTG GCAGGGCATG AGGACAGCAA TGGTTGTAT CAACTATGAA GAGCTCGTCC 360
GNATGGGTGC TGAATGGCTG ANGGACCTTT CCCAGTNTTC CCCAGATTNC CGTTGCCTTT 420
CCNTNGTGTG AATTTTGGTN ATCTAAGCCT AAAAGTTTTT CCTAAGGCTT TCTTGTCTTC 480
AAGCAACTTT CN 492
```

SEQ ID NO:1497

LENGTH:490

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01703

SEQUENCE DESCRIPTION:

GATCCAAATA CACAGAATCA AGGGAAGGAG TTGCTTCTTC TAAGAGTGAT GCTTAATCTT 60
 TTGGGTCATG GATGAATTGA AGATTGATT AAAGTTACAA TAAAAAGAGN CCCNTCAAA 120
 GCACGTACAN NCTGTATCAC GAACGGTGCC TGGCCTACTT TTCTCTTTTC TACCCACCCC 180
 ACCCCAACCC CCCCTGTCTC AGTGAAAACC TGGTTGTTAC TAAAGTGAAA CTTTAATAAG 240
 GATATTGCCT AGGGAAGATT AGTTGTTTTC CTTGTCATTC AAGTTCATTC TGGACCTCTT 300
 CCTCTGAGCT GTTAATCAGT GTTGCTAAAC AGACAGGGAA AGACAAGGGA GAGAAAAATG 360
 CTGATTCAAT CTTCAGAACT TTTAACCNNT TTAACCNCTA ATTCTTCTCC TTGAGAAGCT 420
 ATTCTTTGAT TGTGAAAGCT TTGTTGTTCA GGGNAATATG GGGTAATAAA AATAGCTAAC 480
 CATTTTTAAA 490

SEQ ID NO:1498

LENGTH:477

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01704

SEQUENCE DESCRIPTION:

GATCAAACTT CCATATTTGC CTTGGGAATA ATGGACAAAG GGAAATACTC TTAATTCATG 60
 AATAAAAACCT TTGCAGAAAA TTAGACAGTG TTTAATTTTC GAAAACCTCC CTCTCTAGAC 120
 AGTAGATACC ACCTACTGAT GGTACATAT ACTAGGGAAA TTTTAAATTT AGGAAATGCT 180
 GATAGCTCAT ATTATAAATT TCTAAATCCT AGGAAGAAAC GCTTGGAGTG CTTCTGAATA 240
 TACAGAAGTT CCATTTAAGG GCAAGTTTCC CCGTAGATGT ATCAAAATAC TACCAACTGT 300
 AAATTGAGGT TTAATTCCTA AATGTATTCT ACTTGTTCTA AAACAATCTG TCCNCAAATA 360
 TANAACATA AAGTAATAAA TTGTTATTTT CCGCACCAAT GGGGNATCTC TAATGGTGGA 420
 AAATGGTAAT CCTATGAAAA ATTAATTTT TTTAANTAAA ANGGTNATTT TAATAAA 477

SEQ ID NO:1499

LENGTH:476

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01705

SEQUENCE DESCRIPTION:

GATCCCCGAG TCTTCACAAA TNCTCACTGA AGAAAATTCC TGGAACAATT CAGGGTCCTT 60
 TCATAACCTC TACTCTGAGG TGTTANTAAA AAACCTTAGT AACTTAAAAA AAATGAGCTG 120
 TACACAAATA CTGAACAATA ATGCTNCNTA TGTTAAGTAT GTANGAAAAA TATATACTTT 180
 GACATANATA AGAAACGGTG AGTTGATAAT TGGATAGAAT GGTGGATAGA GTGATAGATA 240
 TGTAAGTAAAG CAAATATAAC AAAATGATAA TTGTACAATC TAAGTGTTTG GACTATAAAT 300
 ATGCACTTCC CACAACNTTT TTATATGNTT AAACAGTTTT ATAATACCAT ATTANGGGAA 360
 ACTGTTTGTC TCAAGGAAAT AGAGNTTGTG ATATGTTCTA GTNCAATGNA GGTGTAATCA 420

TGGTNAAATT AAAAGCTTTT ACTTCCTGGG CAATTAAAGG TAATCCTGGT AGGAAA 476

SEQ ID NO:1500

LENGTH:488

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01706

SEQUENCE DESCRIPTION:

GATCCTGACT GCTGTCATGG CGTGCCCTCT GGAGAAGGCN CTGGATGTGA TGGTGTCCAC 60
 CTTNANAAG TACTCGGGCA AAGAGGGTGA CAAGTTCAAG NTCAACAAGT CAGAACTAAA 120
 GGAGCTGCTG ACCCGGGAGC TGCCAGCTT CTTGGGGAAA AGGACAGATG AAGCTGCTTT 180
 CCAGAAGCTG ATGAGCAACT TGGACAGCAA CAGGGACAAC GAGGTGGACT TCCAAGAGTA 240
 CTGTGTCTTC CTGTCCTGCA TCGCCATGNG GTNTAACGAA TTCTTTGAAG GCTTCCCAGA 300
 TAAGCAGCCC AGGANGGAAA TGAAACTCC TCTGATGTGG TTTNGGGGGG TCTGCCAGCT 360
 GGGGGCCCTT CTGNGTNGNC CANTGGGGNA CTTTTTTTTT TTTTCCACC NTGGGNTCCT 420
 TTNANGANA NGGGCTTNGA TTGCTTGAGC AAAGTTCAA ATAAAAGNTT TNTNGGGAAG 480
 NTTTTAAA 488

SEQ ID NO:1501

LENGTH:472

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01707

SEQUENCE DESCRIPTION:

GATCCAGAAG CTGATGGATG TGGGTCTGAT TGCAATTCGG TGATGACTTG TTCATACCCC 60
 CTTCCCTTCG CCCTCATGTG GAAAGAGGAG CTGGGACCGC GGCAGCAGC ACGGAGCGGA 120
 AGGGAGAGCA GGGGAGAGAA GGCCTCATNT CTCTATATTT ATACATAACC CCGGGGAAGA 180
 CACAGAGACT CGTACCTGCG CTGTTTGTGC CGCCGCTGCC TCTGGGCCCT CCCAGCACAC 240
 GCATGGTCTC TTCACGCTG CCCTCGAGTT CCATGTCTCT TTCCCCTGCC CCTAGTTGCT 300
 GTCTCGGCTG CTCTCCCATG GTTGGTTTTT TTTTNNATT GGGGCAGTGG GCATGTTAAT 360
 GGGGGAGGGG AGGGGGTTCT TCCAGCCTNA GGTCCCAGTT GGTCTNACGT NGTTTAATTC 420
 TTGGGTCCCC TTTTCCAAT TAAAACAAGC CANTNGGGGC GTGGGTNTA AA 472

SEQ ID NO:1502

LENGTH:469

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01708

SEQUENCE DESCRIPTION:

GATCGCAAT TGCTNGAGCT GTTGTGGAAT AAATACTGGG TGAATACGTT GAGTTCTTCT 60
 AGCTTGCTTA CTAATGCAGA CTATACCACT GGTCAAGTCT TTGATTGTC TGAAGGTTA 120
 GAGCAGTCAG AAGCCCAGCT GGGACGAGGG AGTTTCATGT TGGGTTTGA AACGCATGAC 180
 CGAAAATCAG AAGACAACT TGCCAAAGCT ACAAGAGACA GCTGTAAAAC TACCATAGAA 240
 GCTATCCATG GATTGATGTC TCAGGTAAAT TAAGGATAAA CTGTTTAAATC AAATTAACAT 300
 CTCTTCACA GTCTCTGAGA AGGGCTNTAC CTGAAAGACA GTATGNGGGA AAATATTCAA 360

.GGTAACACTT TTAAANCCAG TTNCCNAAAA TCTGATTAGG ANGNTANGG TTCTCTGAAG 420
TGGTCCTAAA TATTANTATC CCTGTAATAA ANGCTCTTTA AANTGGAAA 469

SEQ ID NO:1503

LENGTH:466

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01709

SEQUENCE DESCRIPTION:

GATCTGCAGT GGCTGTTTGA CCAGACCACA AAGTTCACAT CTCCTGAGCT TAGTGTCCTG 60
GGCTGTCCAC CTCCCAGCCA TACTTGACTG TCCCCAACT CTCCTGCAG CCACATGTTT 120
CCCATGACCT GTGGGCTCTG CAGATGGACC TCTCTCGCT AGAGATGCCC TTCTCCCAA 180
TGGCTTCCCT CCTGGAAGGC CCAGCCTGAG TCCTCGTCTC CTTCCAGTG CTTCTGCCAG 240
AAGCATCCCC ATGATGTTGT GACCGCACAG CACTTTGTGT CTTGCTTTGA GCACTTGCCA 300
CTCTGGCTGG TGCTGCTGCC ACTGATTGTG TACTGTCTTG CTGCCCTTC TAGACTGTGA 360
GCTCCTCGTG GGCAGGGACC GCCTGTGTTT TCTGTATTTC CCACGGAGCC TAAGNACAGT 420
GCCTTGCACT TGATAAGGTG CTTAATAAAT GTCTGNTCAA CTGAAA 466

SEQ ID NO:1504

LENGTH:465

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01710

SEQUENCE DESCRIPTION:

GATCACTGTG TTCAGTGTG TTGGAATGGA TTCAGACTGG CTAATGGGGG AAAGGGGAAA 60
CCAGAAGGGG AAGGTGCCAA TTACCTACTT AGAACTGCTC AATTAAGTAG GTGGACTATG 120
GAAAGGTTGC CCATCATGAC TTTGTATTTA TATACAATTA ACTCTAAATA AAGCAGGTTA 180
AGTATCTTCC ATGTTAATGT GTTAAGAGAC TGAAAAATACC AGCCATCAGA AACTGGCCTT 240
TCTGCCAATA AAGTGCATG GTAAATATTT CATTACAGAA TTTATGTTAG AGCTTTCATG 300
CCAAGAATGT TTTCTTACAA AATTCTCTTT TTATTGAGGT TTTACTAATA AGCAGCTTCT 360
ACTTTTGAGC CTCAACTTAA AGCAGANCTG TTTTCTACTG GGATTTTTC TTAACAGCAA 420
GCCTTTTCCT TTTATGTAAA ATTAATCTA TTGTGGAATT TGAAA 465

SEQ ID NO:1505

LENGTH:462

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01711

SEQUENCE DESCRIPTION:

GATCTTGTCT TTAAACATG ATAGTCCTTT CAGTATAATG TCTTAGATTA AAGACGTTGC 60
CTTTAATATC TGTTGGGAAG GAAATGTCCA GACTTTTCAA ATCTCTTATT ATATGTTTCC 120
TTTTNTTGT TACATAGGGA ACAATGTTA TAGTCGTGTG TACAGTGGGG GTCTACANCN 180
NGAAGTGAT ATTTTCAAAC AATTTTTTAA NGATTTAACA ATTTTTGTAA ATCATTTTCA 240
GGCTTCTGCA GCTGTAGATT CTCAGTGTGA ATCCCTTGCT TGCTCATGCA TAAGTGTATT 300
TGCAATACCA NATATACAGG TTTAGTATTT TTGCCTGTTA GTNGATTGTT TCACATGNGT 360

AACGNTTGG GTGAGATGTT ANATGGTTGG NCGAGGTACT GTGGANGTGA ATGTGGGNAG 420
TAATTTTAAAN NCATATGNAA TTGGTCACCA GGGCCNAATT TN 462

SEQ ID NO:1506

LENGTH:459

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01713

SEQUENCE DESCRIPTION:

GATCCCAAGC AGGCTCACAA ATTTAAATGA GGGCTTTGTG TGCAGAAAGA GGAATAAGTA 60
CAGATTATTT TCCTACCACT AGATTTTGG GGAGAGTCAC CATGGAATGT TGACAATTAC 120
TTAAATATT TTAAGTCCC TTGCTGAATT CCTGTCCTGT CCCTGAGGAA TCAGATGGTC 180
ATACAGCCAT AGGCACCCAC CCGAAATTC CCTAGGAGTT GGAGTAATGC TAGAATTGAA 240
GACCTTCTGA GTAAAGGGCT TCTCTGCCTT CTCAGAGGCA GGAGAATTG CACTGGTTGT 300
GTAAATGTA TAAAAAGCTA TATGTTCCAG AGTTTACTCA TTTCCAATGT GTAGATGAAT 360
AAAATGTAGT GTACAAATTA TTTGAAAATC CCAGAAGGGA AGGTACTTTT CAAANACAGT 420
ATTTTTTTTA ACAAATAAAC TTACGNTTTT TACAGCAAA 459

SEQ ID NO:1507

LENGTH:454

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01714

SEQUENCE DESCRIPTION:

GATCTCCTGT CCATCAGCCA GGACAGTCAG CTCTCTCCTT TNAGGGCCAA TCCCCAGCCC 60
TTTTNTNGAG CCAGGCCTCT CTCACCTCTC TACTCACTT AAAGCCCGCC TGACAGAAAC 120
CACGGCCACA TTTGGTCTA AGAAACCCTC TGTCATTGCG TCCCACATTC TGATGAGCAA 180
CCGCTTCCCT ATTTATTNAT TTATTTGTTT GTTTGTTTTA TTCATTGGTC TAATTTATTC 240
AAAGGGGGCA AGAAGTAGCA GTGTCTGTAA AAGAGCCTAG TTTTAAATAG CTATGGAATC 300
AATTCAATTT GGACTGGTGT GCTCTCTTTA AATCAAGTCC TTTANTTAAC ACTGAAAATA 360
TATAAGCTCA GATTATTTTA ANTGGGNATA TTTATAANTG NGCAAATATC ATACTGTTCA 420
NTGGGTTCTG GAATAAACTT CACTGGAGGG NAAA 454

SEQ ID NO:1508

LENGTH:453

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01715

SEQUENCE DESCRIPTION:

GATCGAGCAG TGTGACTACC CCCCCTCCC CGGGGAGCAC TACTCCGAGA AGTTACGAGA 60
ACTGGTCAGC ATGTGCATCT GCCCTGACCC CCACCAGAGA CCGACATCG GATACGTGCA 120
CCAGGTGGCC AAGCAGATGC ACATNTGGAT GTCCAGCACC TGAGCGTGGA TGCACCGTGC 180
CTTATCAAAG CCAGCACCAC TTTGCCTTAC TTGAGTCGTC TTCTCTTCGA GTGGCCACCT 240
GGTAGCCTAG AACAGCTAAG ACCACAGGGT TCAGCAGGTT CCCCCAAAGG CTGCCACGNC 300
TTACAGCAGA TGCTGAAGGA GAGCAGCTGA GGGAGGNGGN GCTGGCCACA TGCTACTGNT 360

GGGTCAGNTT CCAAAGTCCT TTNNTTANCA CTGTTGTGGA CAATNTNANN TNGGGTCAAN 420
TNAAGGGCAG GTNGGTTNAA GNGGNGCCNN GGN 453

SEQ ID NO:1509

LENGTH:450

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01718

SEQUENCE DESCRIPTION:

GATCCTGGGG AAGGTGGGGA ACATGCTTGC AGTATCTNTC CCTGTNTGTN TGCTCACATA 60
AGCATTCCGT CCATCTGAGC TCATCGTGCT ACTGGTATGT GTATGTNCAG TTACACAGTT 120
TTNTGTATCA TAGATTCTAG TGTGTTTATA CAAGGNGACA TCTGTGGTTT CCCCAACCGT 180
TCCAAAAGGC TATTTCAAAG GAACCAGCCA ACGTATGAGA AATGANTGTA AACTGTGGA 240
CATTGACTTC CCGCATAAGG CAGGGTGACC CCCTGAACTC CAGATGTNTG CACAGTATCT 300
NATGTGTGT TTTCCGTTGT GACGAATGTG NATTGAACA TTTGGGGGAG CACCCAGAGG 360
GATTNTNAG TGGGAAGCAT TACACTTTCG TAAATCANGT ATTNNTTCC TGNTAAACC 420
AACCTANTTA ANTNTTANC CCTTGGCAAA 450

SEQ ID NO:1510

LENGTH:449

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01719

SEQUENCE DESCRIPTION:

GATCCATGGA TGAGTGGGG AGTGGAAAAT GGCACAATAT CAAGTGTGAG ANAGGNGATA 60
NACTTCGACT CTNCTGCCTT CAACTGAGAN CAGTTGACCG CAAGCTGAAA CTGGTGTGTG 120
GNAGTCACAG CTTCAATCAAG GTCATCAAGG CCAAGAAAAA CAAGGAAGGA CCAATGAATG 180
TTAATTGAAA TATGAAAGCT GAAATGCAAC AAACAACCTC CGCTTAAAC AATTAAGTTG 240
TTAATAACTG TGATTTTGTA AATTCAGTA ATTCATTTAA ATGATGTTTC AGTAGATATA 300
TTCTAGCATA TTANGAGCTT TTATAACTGA GTTATAGATT AGTTTGCTTT CTGGAATAAA 360
ATTTTCTTCT TATACTCTTC CTTTTTTTA GATATNACAT TTTGCTTTTA TGNCATTCAC 420
GGGGGCAAAA ANTAAAATAT CTTTTTTN 449

SEQ ID NO:1511

LENGTH:464

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01720

SEQUENCE DESCRIPTION:

GATCAGAATC ATGGTCTCCC GCAGTGAAGT GGACATGTTG AAAATNAGGT CTGAATTCAA 60
GAGAAAGTAC GGCAAGTCCC TGTACTATTA TATCCAGCAA GACACTAAGG GCGACTACCA 120
GAAAGCGCTG CTGTACCTGT GTGGTGGAGA TGACTGAAGC CCGACACGGC CTGAGCGTCC 180
AGAAATGGTG CTCACCATGC TTCCAGCTAA CAGGTCTAGA AAACCAGCTT GCGAATAACA 240
GTCCCGGTGG CCATCCCTGT NAGGGTGACG TTAGCATTAC CCCCAACCTC ATTTTAGTTG 300
CCTAAGCATT NCCTGGCCTT CCTGTCTAGT CTCTCCTGTA AGCCAAAGAA ATGANCATTN 360

CAAGGGAGTT TGGAAGTNAAGTCTATGANT GTGAAACAAC TTTNNCCTC CTGTNGTNCT 420
GTGTTAATAA ANCAGGTGNA TTAACTGGN TTTNGTACTT TAAA 464

SEQ ID NO:1512

LENGTH:445

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01721

SEQUENCE DESCRIPTION:

GATCTTGCCA TGGAAGATAC TAGCCCAGCC TAGCAGAAAA GTGCAATATG TATAGCATAC 60
TTTGACATTT TAAACATGAT AGTCCATAAC CATTTTGAAA TGCTGGGCAA ACTACATGAA 120
GTTATTATA ATTAATTCAC AGCTAATCAG GCATTTTGAA AGCTTAATG GATTCAAAAA 180
CCATAATGTT GGAATTTGGT AAAATTTTAA TGTGATTTT TACTGTGAAA AGGTTTTTAT 240
AAGATATACA CACCCTAGTT TAATGTTGTG TCTTGGTGTG GATTACAGA TTTACTACAG 300
GTATTCTGAA CCAGGAACAC ANTCAGGTTT TCAGGCCAGT TTGAATACTG GCTGGCCTTA 360
AATTCTAATT ATNNGGAGTA GGGACATCAT ACCTAAATNT TTATGTCAGT GGGGNCCTGA 420
CTTGTCTGTG GGANCTTAGC AAATN 445

SEQ ID NO:1513

LENGTH:435

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01722

SEQUENCE DESCRIPTION:

GATCAATCGG ATTGAGAAGA ACATCCTGAG CTCAGCGGAC TACGTGGAAC GTGGGCAGGA 60
GCACGTCAAG ACGGCCCTGG AGAACCAGAA GAAGGCGAGG AAGAAGAAAG TCTTGATTGC 120
CATCTGTGTG TCCATCACCG TCGTCCTCCT AGCAGTCATC ATTGGCGTCA CAGTGGTTGG 180
ATAATGTCGC ACATTGTTGG CACTAGGAGC ACCAGGAACC CAGGGCCTGG CCTTCTCTCC 240
CAGCAGCCTG GGGGCAGGGC AGAGCCTCCA GTCGGACCCC TTCCTCACAC TGGCCCCTAT 300
GCAGANGGTN AGACAGTTCT TCTGGGGTTG GNAGCTGCTC ATTCATGATG GCCTNCTCCT 360
TNAGGCCTCA ATGCCTGGGG GGANGGCTGC ACTGTCCTAT TTGGNCGGGA CANACGGTTT 420
TNTAAAAATT TAAA 435

SEQ ID NO:1514

LENGTH:434

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01724

SEQUENCE DESCRIPTION:

GATCTAACCT AGACTAAAAT TGGGAACCTA TTTGCAATTT TTGACCCNGN CCACTAACTA 60
GTGATTCTNC TCCAAAATTG AGAAAGACAG CACCCATTGA AGCAGATATG TGTGTGAAAG 120
TATATTTTTC AATTCAGAT TTTTAATTTT AAGGCTCCAG GAAAGAAAGG AGAGTAGAAC 180
ATTTTCTCTC ATTTTATCAA ATCCTCTCTT GCCCTCCCTC AATTCCTCTG TAACATTCCT 240
GAAGCTGTTT CCACTCCCAG ATGGTTTTAT CAATAGCCTA GAGGTAAAGA ACTGTCTTTT 300
TCTCTGATTC TTTAATAAAT TATCTTTATA GGAATATGCA CAAGTTTTTT TTACACTCAG 360

TGTTAAAAGT ATTTATTAAT NGGGAAGTCA ACTTAATGTT TTGAAATAAA NTATATGNCT 420
CTGGTTAATG CAAA 434

SEQ ID NO:1515

LENGTH:423

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01726

SEQUENCE DESCRIPTION:

GATCCAGTGA TTCANTCACT TAAATNAAGT CTTTTGGTCA GAAATNACCT TTTTGACACA 60
AGCCTACTGA ATGCTGTGTA TATATTATA TATAAATATA TCTATTTGAG TGAAACCTTG 120
TGAACCTTT AATTAGAGTT TNCTTGATA GTGGCAGAGA TGTCTATTTG TGCATTCAAA 180
AGTGTAATGA TGTACTTATT CATGCTAAAC TTTTATAAA AGTTTAGTTG TAAACTTAAC 240
CCTTTTATAC AAAATAAATC ANGTGTGTTT ATTGAATGGT GATTGCCTGC TTTATTTTCA 300
AGGACCAAGT CTTTGATTTT GATTATGCTA TGTNATAACT GACCCNAAAT AAATNCAAGT 360
NCAAATTTAT GTNGNCTGTA TAAGGTTTGT AATAANCCAT GNCTGAGGNC AAAAAAGGNN 420
AAA 423

SEQ ID NO:1516

LENGTH:419

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01727

SEQUENCE DESCRIPTION:

GATCTGTAAT CTCCACTGCT TGGATGCTG CCCTCTACCC CAGAGGAATT TACAGAAACT 60
TGCCCTGTGC CTGTGTCCCC CATGCTAGGG GCGGAGGGGT CTTTCCTTC TTCTTTCCTA 120
CCTACCCCTT TTCTCTGGC CAGGGGCCTC GTATCCTACC TTTCTTGTC CCCTGGGCTG 180
GCTGCACAGA GGATTGCCCC TTCTCTTTTC AGAGCTGGCC CTCGATGCCA AATTAGCATT 240
TAGTATTTTG CACAAAGTCT AAGGGACCAT GGCTGCCTGC CTGGGGGAGG AACCATAGCT 300
CCNTCTGGGC CGCTTCTGGC CTCTGGAGC CATGGGCCAA AGGCAAGGGG ATGGGCAGAG 360
GTCTGTGTTT GGTCTGGCCC AGTCCNCAT CATTAAACTC AGCCTGACTG CTGCCTAAA 419

SEQ ID NO:1517

LENGTH:419

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01728

SEQUENCE DESCRIPTION:

GATCCTCAGT AGANCAGTCC AGAAGCCTGA NAGACAGTGG CCCCTTGATA ATCTGGGTCT 60
CACGGGNCCA GCTAGGGGTC CAGGTTTCAN TCAGTAAATA AGAGTGGTCC ACGTCCTAAA 120
GACACCTCTC CTNNACAAAG ACTGTGATG CTCTGGGGNT TCTNTGGCCA AGCCCCACCC 180
TTTCCTGGTC ATGGTACCCG TACAGCGTTG ATGGCCACAG CTCGAAGGGG GGCTTTCGTG 240
TCCCCCTGTG CGGTCAGTGT TTTCAGTACC ACCTCTCTCC CGTGCCCACT TGGCTATTTA 300
CTTATTTATT TATTGTGTGC CAGTNATGGT GGGTGGGGGC TGGGCCTTCC CCGCCACCTN 360
CANCCTGTG GTGACCTGTC CTCCGTACT TAATAAAGTG CGCGTGNGGA GTTGTTAAA 419

2153480

SEQ ID NO:1518

LENGTH:418

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01729

SEQUENCE DESCRIPTION:

GATCTNAGCC CTCGGTTCC TGGGCAGAGA GAAAGGCTAC AGGTTTCATTT NCCTGACGAC 60
AGCAGTCACA AACAGCGCTC GCNTTATGGA GGCCATNAGT GAGGTGAAAG CCTGATGTTT 120
TTCCCGGCCA NTNTTGACAT CTTCCCTGAA CACATTCTC AGTGAGATGC AGGCATCTGG 180
CACCCAGCTG CTATAACCAA GTGTCCACCA ACTACCTGCT AAGAGCCGGG AGCATGGAAC 240
GTGTTGGGAT TTAGAGAACA TTATCTGAGA AAAGAGTTCA CTTCTGCTC CCAGGATATT 300
TCTCTTTTCT GTTTATGAAG TACAACCCAT GCTGCTAAGA TGCGAGCAGG AAGAGGCATC 360
CTTTGCTAAA TCCTGTTTGA ATGTCATTGT AAATAAAGCC TCTGCTCTCA GATGTAAA 418

SEQ ID NO:1519

LENGTH:404

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01730

SEQUENCE DESCRIPTION:

GATCCAATTT ACAGAAATCA GAGTTAGCTA CAGCTAGGAC TCGTTTGGTT GGGGTTTTTT 60
AGTTTGTCTT TCTAAAGTCA TGTGGACCTT AATTAAATTA CAAAAGTCTA CCCTGGTGGT 120
CATAAAATAG GCAGGCCTAT GAAGAAAGGC CTTTACTCT TCCATCTCGT CCCAGCCCCG 180
AGTTGACCCA CGTTGCTGCT CCTCACACCA TGGTGATGCA GGTCTCGTAG TGTGGGCACA 240
GGCCTGGCTA CCTCATCTTT TTAGTGCCTC TCTCCTCTC CACAGGATGG GGTCCCACAG 300
CTGCAGCAGC TGGCCCGGTA GTTGAGCATG TGTGGTTATC CTGTAGAGCT TTTCCAAGA 360
AGGGTGTGTTG AACTTAGAGT CTTAATAAAA TCTTACCAA TAAA 404

SEQ ID NO:1520

LENGTH:402

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01731

SEQUENCE DESCRIPTION:

GATCTACAGA TACGTGATAT TNTGGTATAA CTAGAATCTT GATTTCCTTC ATAAAGTTCT 60
GCCATGTTCT ATTTCTTTCC TTAATGTTTT TTTCTTCCCT ACTGTTTTAT CCTCCCTTG 120
CTTTGGAAGG ATATTNCTGC ATATCGAGCT AAAGGAAAGC CTGATGCAGC AAAAAAGGGA 180
GTTGTCAAGG CTGAAAAAAG CAAGAAAAAG AAGGAAGAGG AGGAAGATGA GGAAGATGAA 240
GAGGATGAGG AGGAGGAGGA AGATGAAGAA GATGAAGATG AAGAAGAAGA TGATGATGAT 300
GAATAAGTTG GTTCTAGCGC AGTTCTTTTT NNCTTGCTA TAAAGCATTT AACCCCCCTG 360
TACACAATC ACTCCTTTTA NNGAAAAAAA TTGAAATNTA AA 402

SEQ ID NO:1521

LENGTH:407

00678

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01732

SEQUENCE DESCRIPTION:

```
GATCTCAGCT GAACAAATTA GATGTTTCAG TTGCTCTTGG GTCAACTGGC TTACAGATTT 60
ACATGTGCAC ACACACACAA ATTTCTTATC ACATTTTCGC CTTCTTCACT TGACCTAACT 120
GATTATGCGA AATACCCAAG ATTCATGCTA CTGTACCACA GATTGTGTTT CACAGCAATA 180
AATCTTCAGT TCTTTGTTTA TGATTCCACT TAACAAAAGG CCTGCAGAAG TGATTTATTA 240
TTTGGGTATT TGGAGATAAT ACATTGTATG GTTTTTTGGG AAACCTTTTT CACTCCATAC 300
TCAGATATGC TTCATTGTCA AATGCATATT TAGGNTAGGT TAATNGAATT GTAATGTTTA 360
ACCTGCTGCT TTTTTTTTAA ATAAAAATTT GACTGAAAAAT GGTAAA 407
```

SEQ ID NO:1522

LENGTH:397

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01733

SEQUENCE DESCRIPTION:

```
GATCTAGTAG CCACGCTAAA AAACAAGTAA AATTAATTTT AATATATTTA ACTCAATACA 60
TTGGAGATAT TATTTAGAAA CGATATTTTT CATTCTTATG AAACCTAAGT TGTCTGGTTT 120
GCATATCTCA GTTGAGACAC TAAAGTTTTA CTGATAATAC TTAATCCATN NATTAGATTT 180
CATAAAATCT AAATTGCAA AGTAAATTTA CATACCCATG TNGGTCTAAA TGTGCTTAAA 240
AGTTTTCCAA TAACTGAAAT GAGTATCAGT TTTAAATTTA AAAATTTGTT ACTTGGTTAC 300
TCCATATTTT AGGTATTAGT GGCTACCATA TTGGTCAGAG CAGATTCATA GGGATGATTT 360
CCCAGGTTTG AAGTGTGTGT ATATTGCTGG TATTATN 397
```

SEQ ID NO:1523

LENGTH:395

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01734

SEQUENCE DESCRIPTION:

```
GATCTGTACG AAATGTGAAA TTTTAGGGA CATCTCCATG CTGTCACTTG TNATTTGCCC 60
TCTNATGTAT TTNGGTCATA TTGCCAACTG GAAAGTCAAA ATTCCTAAC AACTTTAAGT 120
AAGTCCTTTN AAGACTNAGT GCTGTTTNA ATCCAGTTA GAAAGTAACT TAATTTTAAT 180
ACCGCTACTA AAAATNCGAA AATTTCTCCT TTAATCACAT TCAATATGGT TAAANGAACA 240
ACACTAATTG ACATTGCGTG GGCTTTTCCT CCCTTTGTTT AAANANGTCA TTTGTGAG 300
CAAGNGGTTG TATAGTATTA TCTACTNNCT TGAGGCTGTT AAATTTNCNA TTCCAGNGGT 360
TTTGTAATG TATCCCGGGG CCNTGNTGCA TTGGN 395
```

SEQ ID NO:1524

LENGTH:391

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01735

SEQUENCE DESCRIPTION:

GATCTCAATG ACCTGGCGAA GACTGGAAAA TACAACTCCC ATCACCAGCA GAGTTGCTAG 60
 GCTGCTGCTG TATGGGTACA GAGAAGGGTT TGACAAAATT GACCTGACTG TGGAAGAACT 120
 TCCAGCAGTT TACACAGGAC TGTTTTATAA ACTCTATCAT AAGGAACTGC CAGAGAATTA 180
 TAAACTATG AAAGGAATTG ATTAAATTCA CATTATATG TTTAGAAACA TGTAGACTAA 240
 CGAATGACAT AAGAAATAGT GGACATTTTG GATTGATTAA ACATCTGACT GTGATTTTCT 300
 AATGTATATG ATTTCCATGA AGAAATTTTG TTTCTAAACA TGCACATTTT AAAAGCCTCT 360
 TTTCGAATAA AGCAAATGCG TGAANGAA A 391

SEQ ID NO:1525

LENGTH:388

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01736

SEQUENCE DESCRIPTION:

GATCCGGCGC CACAAGACCA CCATCTTCAC GGACGCCAAG GAGTCCAGCA CGGTGTTTCA 60
 ACTGAAGCGC ATCGTCGAGG GCATCCTCAA GCGGCCTCCT GACGAGCAGC GGCTGTACAA 120
 GGATGACCAA CTCTTGGATG ATGGCAAGAC ACTGGGCGAG TNTGGCTTCA CCAGTCAAAC 180
 AGCAGGCCCA CAGGCCAGC CACAGTGGGG CTGGCCTTCC GGGCAGATGA CACCTTTGAG 240
 GCCCTGTGCA TCGAGCCGTT TTCCAGCCCG CCAGAGCTGC CCGATGTGAT GAAGCNCCAG 300
 GACTCGGAAA GCAGTGCCAA TGAACAAGCC GTGCAGTGAG ACCCCCAAGA GGCCCATTTT 360
 CCCCAATAAA AGAGATTGAG GAGTCAAA 388

SEQ ID NO:1526

LENGTH:388

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01737

SEQUENCE DESCRIPTION:

GATCTTATTT CTCTACTCA ATTGTATATT TATACCCATT AATCAACTTC TGTCTTGCT 60
 CTCTCCGTGC TACCCTCTG GCCTTTGGTA ATCGCCAATC AATCTACTCT CTATCTTCAT 120
 GAGACCAGCG TATTTTAGCT CCCACATATG AATGAAAACA TATAATATTT GTCTTTCTGT 180
 GCTTGACTTA TTTTACTTAA CATAATGACC TCCAATTCCA TCCATCTTGT GGCCTGACA 240
 GTATTTTCATT CATTTTGTG TGAATTATAT TTCGTTGTGA ATATACATTA CATTTTCTTT 300
 ATCCATTCAT CACTGATGTG CACTTAGGTT GATTCCATAT TTGGGCTATT GTGAATAGTG 360
 TGTTAATAAA CATGAGAGTG CAGTAAA 388

SEQ ID NO:1527

LENGTH:385

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01738

SEQUENCE DESCRIPTION:

GATCTTCCTG GTCAGCGCTC TCTCTAGCAT ACTCTTCCTC TATTTGGCTC ACAAACAGGC 60
 ACCAGAGAAG CAAATGGCAC CTTGAACTTA AGCCTACTAC AGACTGTTAG AGGTGATACT 120

ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAAGTCAAG ACAATACTCA 180
 GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG CCAAGAAACT 240
 AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGAGATGT CTATGGTAGC TGAGCCAAAC 300
 ACGTAGGATT TCCGTTTTAA GGTTCACATG GAAAAGGTTA TAGCTTTGCC TTGAGATTGG 360
 CCTCATTAAT ATCAGNGACT GTAAA 385

SEQ ID NO:1528

LENGTH:377

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01739

SEQUENCE DESCRIPTION:

GATCCGTACT CAGAACGTCC AGGAGAGACG CATGGCCCGA AGTCAAAGTG CTGGAATTTT 60
 CCAAAACAGC CTGTTCTCTC CTCTCTCCTC CCCAGAGCAC CCCCTGCCAT CAGGGGGGGT 120
 GAAATCCCTC TCCCCCAGGA GCCCTGCTGC TTTGCTTGGT GGTAGGGCAG GAGAGCAAAC 180
 AAACAGTCAT GGTCTAAAAC CCACATAGCA CTTTGCTCTT AGTTACATGT AAAATTTTAG 240
 ATTTCTAAAA CAGGTGGGCA ATCATTTTGA ATACTGTTCT GTGACCCTGA CTGCTAGTTC 300
 TGAGGACACT GGTGGCTGTG CTATNGTGTG GCCATGCTCC NTTGTCCCCG TNCCTGTTGG 360
 CTGCTTCTGT TTAGGTN 377

SEQ ID NO:1529

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01740

SEQUENCE DESCRIPTION:

GATCCAAGGC CTGTGGTAAA CGGGAGANCT TGTNTTTTTC AAGTGGAAAA AAACCCAAGA 60
 GTTTGTNCAG ACATCCTGTC TTCCAGAGA AGGTGGACAC TCTTGGNCTC ATTGTAAAGT 120
 GCCTGCTGNA TCAATAAAGC TCTTGGCTTA TTAGTCTATA AAACAAA 167

SEQ ID NO:1530

LENGTH:372

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01741

SEQUENCE DESCRIPTION:

GATCCACACG TTCCGGGACT ACCTGCACTA CCACATCAAG TGCTCTAAGG CCTATATTCA 60
 CACACGTATG CGGGCGAAAA CGTCTGANTT CCTCAAGGTG CTGAACCGCG CACGACCAGA 120
 TGCCGAGAAA AAAGAAATGA AAACAATCAC GGGGAAGACG TTTTCATCCC GCTAATCTTG 180
 GGAATAAGAG GAGGAAGCGG CTGGCAACTG AAGGCTGGAA CACTTGCTAC TGGATAATCG 240
 TAGCTTTTAA TGTTCGCGCT CTTGAGGTTT TTAAGGGATT CTCCGTTTGG GTTCCATTTT 300
 GTACACGTTT GAAAATAAT CTGCAGAAAC GAGCTGTGCT TGCAAAGACT TTCATAGTTC 360
 CCAAGANTTA AA 372

SEQ ID NO:1531

LENGTH:372

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01742

SEQUENCE DESCRIPTION:

GATCCACTGT TGGGGCCTCG ACAGATTCTT GTCCTGGGAA AGGAGTACAC CGAGAAGACC 60
CCCATTCTCG AGCATGCTGT TTTCAATGTG GACCTCATGA GCAAGAAAAT TCATCTGACT 120
GAGAATGGGA TAAGGGTGGA TATTGGCGAT ACAATAATCT ATCTGGTTCA TTAAACTCAT 180
GCACATTGGA GATTATCCT GGTTCCTTAG GAATACTACT ACTCTGATTG TGTCTACTGA 240
TTGGCTATCA GAACCTTAGG CTGGACCTAA ATAGATTGAT TTCATTTCTA ACCATCCAAT 300
TCTGCATGTA TTCATAATTC TATCAAGTCA TCTTTGATTG CTGGACCTAA TAAATTTTTT 360
TTCCCTTTCA AA 372

SEQ ID NO:1532

LENGTH:368

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01745

SEQUENCE DESCRIPTION:

GATCCCAGTC ACAATTATCA CCGGGTATTT AGGTGCTGGG AAGACAACAC TTCTGAACTA 60
TATTTTGACA GAGCAACATA GTAAAAGAGT AGCGGTCATT TTAAATGAAT CTGGGGAAGG 120
AAGTCCGCTG GAGAAATCCT TAGCTGTCAG CCAAGGTGGA GAGCTCTATG AAGAGTGGCT 180
GGAACCTAGA AACGGTTGCC TCTNCTGTTT AGTGAAGTGA GGAATGTGTT TACTGTGTAC 240
ATGGTTTACT AGAAATGTTT ATTGATTATA TTTCCAGCTT TAATTTTCTT GAGTAATTTA 300
ACTGAATTTA CACAGTTTGC TTCATTGTAT TTTCAAACAA ATAGAAAATA AACTTATTAG 360
GAAGCAAA 368

SEQ ID NO:1533

LENGTH:364

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01746

SEQUENCE DESCRIPTION:

GATCGTCCCC GTATGATGAT TGTNAGAAGA CAGGACTAAG TAGCAGAGAA TAGCTAAGAG 60
ATAAATTGGG CTGGGGAAAC TTGTCAGAAA GCACTGAACA ATTAAGAAAT TTTCCAAGAA 120
AATGTGCAGT ATTCTCTGCT ACTTCTGAAT CTGTTTTGTC TTCCTAATCT ATCACAATTG 180
CCACCCATCG GGTTTTGGGT GTGTGTTTTT ATAGCGTGGT TACTTTCTAT AATGCTGTAC 240
CCAGATTCTA AGAACCTGGA GAAGGATTAG CAGTTCTTAG TAAGTTTACT GTGTATAGGA 300
ACGGTTTGTA TTTCATTACA GCTATTCATC TTTCTACAT TAAAAATATT TTTCTCTAAA 360
GAAA 364

SEQ ID NO:1534

LENGTH:362

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01747

SEQUENCE DESCRIPTION:

GATCTGTGCC ATAAAATTC AGTGAATAA GACTTCTTCA ATACATCTTC CAATAAGGGG 60
 TGCTTCTTTG TGACAGTATT TTTATTTCTG ACATTCATT TATTTGGGTA CATAGTGTGG 120
 TTGTTGATAC CTTGCAATAG TATTGCTTCT GAAAGTAATA AAAAATTTTA GGAGAATTG 180
 AGAAGTTTAC AGAATTACTT ATTCATTGTT TTCTTAGTAA GTCAGTTTAA TGTTTATTTT 240
 TCTCATTATT TCATCACTGC AATAAAGAAT AAGGGTGTTT GAGCTCACCT CCATGCAAAG 300
 ACTTCAGTTT TAAACATTA TTTGCCTAAA ATTAGCATTG TGATGCTTC TGAAAGAAAT 360
 AN 362

SEQ ID NO:1535

LENGTH:361

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01748

SEQUENCE DESCRIPTION:

GATCCACCTC TCCTGTGCTA AGATTAAGAN GACCAACGTC CCCGANTTCT TTNATTGCCA 60
 GAAATGCAAG GAACTGAGGC CAGAGGCCNN GCGGTTAGGG GGGCCTCCCA AATCTGGAGA 120
 GCCCTGATGG CACCAACTTT AGCCTGGAAC TTCCAAATNA CAACATGATT TGGGAACGA 180
 GCCTCAGGGT CCTCAGCCTA TCCCCTGGAG CTTGGATACT GTCTGCACTT CAAGGCAGGA 240
 ATTCTCAAGG GAGACTTGTT TGAATAATNAG TGTCTCACTT TCCCACCCTA TCCTTCCTCC 300
 CCACTCTGTG GACTTGAAAT TGAATCCATT ACGGTTGGGG ATGGGAGGCT GTCTGTGTCC 360
 N 361

SEQ ID NO:1536

LENGTH:360

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01749

SEQUENCE DESCRIPTION:

GATCGATTCT CTCTATGAAG GAATCGACTT CTATACNTCC ATTACCNGTG CCCGATTNNA 60
 AGAACTGAAT GCTGACCTGT TCCGTGGCAC CCTGGACCCA GTAGAGAAAG CCCTTCGAGA 120
 TGCCAAACTA GACAAGTCAC AGATTAATGA TATTNTCCTG GTTGGTGGTT CTA CTCTAT 180
 CCCCAGATT CAGANGCTTC TCCANGACTT CTTCAATGGA AAAGAACTGA ATANGAGCAT 240
 CAACCCTGAT GAAGCTGTTG CTTATGGTGC AGCTGTCCAG GCAGCCATCT TNNNTGGAGA 300
 CAAGTNTNNG AATGTTCAAG ATTNNGCTGGC TCTTAGGNTG TCACTACTCT TTTCCCTTAN 360

SEQ ID NO:1537

LENGTH:358

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01750

SEQUENCE DESCRIPTION:

GATCCCAGTG AATCCTGGGT CCAGGAGTAC GTGTATGACC TGGAAGTGAN CTGAGCTGCT 60
 CAGAGACAGG AAGTCTTCAG GGGAGGTCAC CTGAGCCCGG ATGCTTCTCC ATGAGACACA 120

TCTCCTCCAT ACTCAGGACT CCTCTCCGCA GTTCCTGTCC CTCTCTTAA TTTAATCTTT 180
 TTTATGTGCC GTGTTATTGT ATTAGGTGTC ATTTCCATTA TTTATATTAG TTTAGCCAAA 240
 GGATAAGTGT CCCCTATGGG GATGGTCCAC TGTCACGTGT TCTCTGCTGT TGCAAATACA 300
 TGGATAACAC ATTTGATTCT GTGTGTTTTC ATAATAAAAC TTAAAAATAA AATGCAAA 358

SEQ ID NO:1538

LENGTH:354

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01751

SEQUENCE DESCRIPTION:

GATCCCTCCT CTAGGGGCCT GGGGACTTTN ACTGATGCTC TTCCTGATTG TAGAGCAAAG 60
 GTGTGGGAAG GGGAAATGGA GGAATGCCCT CCTGTCTGTN TCGTTCTCTG TGCCACAGCT 120
 ACAGATGCAG AAGGTTTCTC TGGATAGCAC ACCTCTGANT GTAAATCATG ATAAATGGA 180
 TATTGGAAA CTACTCCTA AGCTGTGATT TAGGGTGTAT TTCTACTTCT GGAAGCCTC 240
 AATATCAAGG GCTGAGACTT TTGAATTTG AATATTCGTT GGGTTTCATG TTAAGANGCC 300
 TGTGGTCTAG GAGTGCTATT CAGTGTTCCT TTCCTGATA AACACTTTGA ATAN 354

SEQ ID NO:1539

LENGTH:352

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01752

SEQUENCE DESCRIPTION:

GATCTCAGTA TGGACAGTGT AACAACAAAA CCAAAATGGC TGGACAGACT TCTTGTGTTT 60
 TGTAATATA AACTAGGACA GTTCTGTAGG TTTGTTCACT GTGCTAGTGG AGTATTTTCT 120
 TAATGTAAAA CTTCACTTAA CAGAGAGATT CTTTGTTTAG CAAGCTTGGN GTGATGATAN 180
 AGNGGTAAGA AATAATATA ATGTTGAAGA AAGCATCACA ACAGAACTAT AGGAGTCTAA 240
 ATTTAATAAA TCTTTAAAAA AAACCAGTGT CTAGAATATA TACCATGTTT TATTATTTAA 300
 AATCATTGTC TTAATTTTTT GTTCAAAAAA TAAAAATTG AATACAATCA AA 352

SEQ ID NO:1540

LENGTH:351

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01753

SEQUENCE DESCRIPTION:

GATCAGACAA GCCCAAACCTG AGAGACACTC TACAAAATAA CTGGCCAGTA CGTTTTNCAA 60
 GTNCCAAGGC CGTGAACAAT AAGGAAAGAC TGAGGAACAG TCATGGACTG GAAGAGAGTA 120
 AAGAAATATG ATAATAACT GCATTGTGAG ATACCGATTT AGATGTTGGA TTAGAAAAAG 180
 GACCAGAAAT AAGATTTCAT CAATGTCAAT TATTGGTTT TGATAATTGT ACTGTGGTTA 240
 TGTAAGATGT TAACATTAGT AAGAGCTGGG TGAAGGGTAC ATGGAACTA TTATTTTTCG 300
 CACCCTTTGA AAGTCTAACT TTTTCAAAA TAAAAAGTTT TAAAAATAA A 351

SEQ ID NO:1541

LENGTH:357

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01754

SEQUENCE DESCRIPTION:

```
GATCCCAGAT GCAGTGA CTG GTTACTACCT GAACCGTGCT GGCTTTGAGG CCTCAGACCC 60
ACGCATAATT GGGCTCATCT CCTTAGCTGC CCAGAAATTC ATCTCAGATA TTGCCAATGA 120
TGCCCTACAG CACTGCAAAA TGAAGGGCAC GGCCTCCGGC AGCTCCCGGA GCAAGAGCAA 180
GGACCGCAAG TACACTCTAA CCATGGAGGA CTTGACCCCT GCCCTCAGCG AGTATGGCAT 240
CAATGTGAAG AAGCCGCACT ACTTNACCTG AGCCACCCAA CCTAAATGGT ACTTATCTGT 300
NCCCAGTNC NTACACCAGC CTGTTTNNAT AATAAACTTT ATTGGTGGTA GGGNAAA 357
```

SEQ ID NO:1542

LENGTH:412

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01755

SEQUENCE DESCRIPTION:

```
GATCAGGGCA GTAGGCATAA TTCAGCAACA AACAATCTTC CTTTGGGAGA AACCTNTTCA 60
TTCCAATCTT CTAATTACAG TGGTTCCTAT CTCAGGGATA CTGGACTTNN TGACGCAGAT 120
GAACAATTA GGGGAAAAGC TTCCCTTTTC CCTCTGTGGC AGTTACGATT TTNACTTCAG 180
TCCTGAGAAA AACTTCAGGT TTTGAAAATC AGATGATGTC TTCTCCTTTT CCAANCACCA 240
CACGTTGAAA GCNTTTATAA ATCCAAGTCT GAAACTCTGC GCTCTAGTAC TGCTGTTAAG 300
NTACACAAC TGTTCCTNN GTTCATATAA TCTNGGGGTA CNCACNCACA CACNCNTGTA 360
TGGGGGGGG GGNNTGGCGN TTNCACCGC GCGTTCNTT TTTGNNGGGT CN 412
```

SEQ ID NO:1543

LENGTH:343

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01756

SEQUENCE DESCRIPTION:

```
GATCCCAAAA TGCTGCGGGG CAATGACAGC TCAGTTCCCA GAAATAAAAA TCCATTCCAA 60
GAGGCCATTG TTTTGTGGT GGGAGGAGGC AACTACATTG AATATCAGAA TCTTGTGAC 120
TACATAAAGG GGAACAAGG CAAACACATT TTATATGGCT GCAGTGAGCT TTTAATGCT 180
ACACAGTTCA TAAACAGTT GTCACAACCT GGACAAAAGT AACACAGAAG AACCTTACTA 240
TGATAATCTA CTTGGAATGT GGATAAATGT AAAANGNAGA AAAGTTAGAA NGNGCANTAT 300
GTTTCCTTCT CTGTAACAGT GTCCTAACAG TGAAAATTCA GGN 343
```

SEQ ID NO:1544

LENGTH:340

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01758

SEQUENCE DESCRIPTION:

GATCGANCTT NCTATGGACT CAAGCAGGTG NNGAAGGCCA ATNAAGCCAT GGCAATTGAC 60
 ACATTGCTCA TCAGCGATGA GCTCTTCAGG CATCAGGATG TAGCCACACG GAGCCGGTAT 120
 GTNAGGCTGG TGGACAGTGT GAAAGAGAAT NCAGGCACCG TTAGGATATN CTCTAGTCTT 180
 CACGTTTCTG GGGAAACAGNT CAGCCAGTTG ACTGGGGTAG CTGCCATTCT CCGCTTCCCT 240
 GTTCCCGAAC TTTCTGACCA AGAGGGTGAT TCCAGTTCTG AAGAGGATTA NTGATTGAAA 300
 CTAAAAATTT GNGACAATCT TTGTGTTTTC CTAAACTGTN 340

SEQ ID NO:1545

LENGTH:339

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01759

SEQUENCE DESCRIPTION:

GATCTGCTTT CATTAAGTGG AATTCTGTAG GAGATACTGG TGACCTAAGC TAAGTTGCAC 60
 TCAGCATACT CAGTGTCAAG CTAATGAGGT TCTATTATAA AGGTTCTACT TTTAATCTGA 120
 GGGAAAAACAT GTTCAGGGCT TCTAGAACAC TAAAAAATTN GGNTTAAACC AGTGTNCAGT 180
 CTGGTGCCAA ACTTCGAATG GAATACAAAT NNCATAATC TGANCTTTGT NCACAGGTTA 240
 TCCTAATAGA GTAATTCTCC ACTTTGCTCT ATTGAACTGT CTTAAGGGAT TTGTTTAAAC 300
 AGCTAAGTTA CTTGATTAAA ATAATGATAA AATTGTAAA 339

SEQ ID NO:1546

LENGTH:362

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01760

SEQUENCE DESCRIPTION:

GATCTGGTAG AAGGTACCAG CTTCTTTTCC AGCTGGAGAG GCCCAACAC TGGATGGTTC 60
 TGTAGGGAGC CTAGGGAGCC TGGTCATCAA CTTGCAATAC CTCACAGAGC CAGTTCACAT 120
 CCCACTCTGA GCTCCACGA GAAACACTGC TTCTCCAGGC CCGGGGTTGT TGGGGAGAGA 180
 GGCAGAGGCA GCTGGAGCGC CGTTCTCTCC TGCTGGGACA CCGCTTGGGC TTTGGTATTG 240
 ACTGAGTGGC TGACAGTTAT CTTCCAACCC CAACTGGCTT GGGGGCAGGA CAAGGGCTTA 300
 GGCTTGATGG TGGNCAGGCT TGNCTGCTCC CCACCTGNGA TGCCCTGCT CTGGGACCTC 360
 TN 362

SEQ ID NO:1547

LENGTH:335

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01761

SEQUENCE DESCRIPTION:

GATCCTTTCA GAAAAGAAAC ACTGGGTCCC ATAGCTAAAT TCTCAACCGC CANGCACCTT 60
 CAGAAGAATC CAGCCTAATA CTGGAATTG TGCTATTATC TTCCTCTCCA GCCCCCCAAC 120
 TCCATCCCTC ACCACAGTTG TCTAGGAAAT GACATGAATT CAATATCTAA TGTCAACCAA 180
 TGGGGAGAGC CACAACCTCA GGAGAGGTTC CTGAGCTGAG TCCCTTAATT TCTGGATGAA 240
 GAAGACCAAC AAGTTTTGTC CAATGTATTT GTTCTCAGA CCTTGCCTAG GCACTAAAAA 300

TAAAATACTA GGTCATTGGA GGCTAATGTG GGAAA

335

SEQ ID NO:1548

LENGTH:330

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01763

SEQUENCE DESCRIPTION:

GATCATTAAAG GAAGGCGATG TAGATGTTTC AGATTCTGAT GATGAAGATG ATAATCTTCC 60
 TGCAAATNTT GACACATATC ACAGAGCCTT GCAAATAATA GCAAGATATG TACCATCATG 120
 AGTATACTGN TCCTTATTTT GAATGTTTAA TTCTCAAGAA AATTGTAATC AATTAGTAAA 180
 AATTATAAAA TGTTAATAGT ATTAAGCTT GAGTCTTACA TTGCATTTTT TTTTNGNA 240
 NCCACTGGG GAACCATTC ATNCTCCAA ANGCGGCATT CCCATTCCT NTTNATCCCC 300
 TNNAATGGTT TTNCAAAGTN NGTNTGCNGN 330

SEQ ID NO:1549

LENGTH:330

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01764

SEQUENCE DESCRIPTION:

GATCATGGTG GATGAGGAAG CCTCAACGTA GATTCCTGAA CTCAAGGTAC CAGCAAGANT 60
 GCNTTCTCCC AGTGTGCTCT CCCCACATC CTAGGCACAG CTTTCATAAC CCAGTTTCTT 120
 AGGTGTAAGA AACTGTTTTN ATCTCATTTA TTAAGTCTCA GAACTTAACA GAAAAGGAAG 180
 CCTTTTAAAT ATTCTTTTAA ATNTATTTT AGATTAACAG TTTTGNACTT TACATTTTTT 240
 TATACAACCA NCCAGTTTCT TTNCTAGCCA ATCATCTCTG ANGAGTTGCT GTTCTTACT 300
 GACAATAAAA NNTGTNCTCT TGGTTCGAAA 330

SEQ ID NO:1550

LENGTH:329

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01765

SEQUENCE DESCRIPTION:

GATCAACATC TTTCCTTGCC TCTGTCCCCT TCTCTCATCT CTTAGCTCCC CTCCAACCTG 60
 GGGGGCAGTG GTGTGGAGAA GCCACAGGCC TGAGATTCA TCTGCTCTCC TTCCTGGAGC 120
 CCAGAGGAGG GCAGCAGAAG GGGGTGGTGT CTCCAACCCC CCAGCACTGA GGAAGAACGG 180
 GGCTCTTCTC ATTTACCCCC TCCCTTTCTC CCCTGCCCCC AGGACTGGGC CACTTNTGGG 240
 TGGGGCAGTG GGTCCCAGAT TGGCTCACAC TGAGAATGTA AGAACTACAA AAAAAATTC 300
 TATTAAATTA AAATTNTGT GTCTCCAA 329

SEQ ID NO:1551

LENGTH:334

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01766

SEQUENCE DESCRIPTION:

GATCCCAACT GCTCCCTNCC CTCGCCGGTG ACTCCTGCAC CTGCGCCGGC TCCTGCAAAT 60
 GCAAAGAGTG CAAATNCACC TCCTGCAAGA AAAGCTGCTG CTCCTGCTGC CCTGTGGGGCT 120
 GTGCCAAGTG TGCCCAGGGC TGCATCTGCA AAGGGGCGTC GGACAAGTGC AGCTGCTGCG 180
 CCTGATGCTG GGACAGCCCC GCTCCCAGAT GTAAAGAACG CGACTTCCAC AAACCTGGAT 240
 TTTTATGTA CAACNTGAC CGTGACCGTT TGCTATATTC CTTTTCTAT GAAATAATGT 300
 GAATGNTAAT AAAACAGCTT TNACTTGAAA CAAA 334

SEQ ID NO:1552

LENGTH:328

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01767

SEQUENCE DESCRIPTION:

GATCTGTTTG GACTATGTTT TCTTTTCTTC TCCCACTTGC TCAGCAGCTT GGGCTTCCAT 60
 TCTAGTTCTT TTACCAAGAT TTTTGTGTGA CCATGTTGAC TTCATTTGGA TTGCCCTCTT 120
 TCAATTTCTT TGTGAAAACA CCCTTAACCT TCTCTTTACC CTTAGCTGAA ATGTTTACAT 180
 AGCTTCTGGT GATATCTTTN CATGATTTTA TATCTCTTAA AATGGTGATG GATGTGACAC 240
 CTCATAAAG TGAGCTTTGA ACTGTAGATA ACTCTTAAAG AAAATGTCAT TTTAGACAAT 300
 TAAAATATTT GTGCTCAACT GCTTGAAA 328

SEQ ID NO:1553

LENGTH:327

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01768

SEQUENCE DESCRIPTION:

GATCGAAATG TTAACACCGG GAGCTCTNCA GGACACTCAC CCAGCGACGC TCGTGGGGGA 60
 AACATACTAA ACGGACAGAC TCCAAGANCT GCCACCGCTG GGCCTGCACT GCGGCCCCC 120
 ACGTGAATC GGTGTAACG GGCCNCGGAA GAAAAGCAGA GAGAGAATTG CAGAGAATCA 180
 GACTCCTTTT CCAGGGCCTC AGCTCCCTCC AGTGGTGGCC GCCCTGTACT CCCTGACGAT 240
 TCCACTGTAA CTACCAATCT TCTACTTGGT TAAGACAGTT TTGTATCATT TTGCTAAAAA 300
 TTATTGGCTT AAATCTGTGT AAAGAAA 327

SEQ ID NO:1554

LENGTH:326

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01769

SEQUENCE DESCRIPTION:

GATCAGCAGA CCACGTATTT AAAATTCTGA ATCTTCTGGG ACAGGGTTGT AACTCAGCCT 60
 TCCAAAGGGA AGAGTGCAGG GGGACGGGGC CATGATATGG GGAAATGGTG TAACTAATG 120
 TATTTNTTTA TTGGCTGTTA TTCTGTATAA CACTCATATC TTTGCCAAAG TTCAATTTTA 180
 TATTTAGGCA ACTGATGGTC CTTTTGCATT TAGGATTTTN GTTGTGTGTA CTTATACCT 240

CATGATATAA GGAATGGGCT CATGTGTCTT CCGTCTTTTG GAAGGAGGTT GACATATTTT 300
AAATAAATGC TTTTAAATAC AGTAAA 326

SEQ ID NO:1555

LENGTH:387

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01770

SEQUENCE DESCRIPTION:

GATCAAAAAG AACAGAACCC TCTCCAGCCT GCTGACCCGA ACCCAACCAC ACAATGGTTT 60
GTCTCAATCT GACCCAGCGG CTGGACCCTC CGTAAATTGT TGACGCTCTT CCCCCTTCCC 120
GAGGTCCCGC AGGAGCCTAG CGCCTGGCTG TGTGTGCGGC CGCTCCTCCA GGCCTGGCCG 180
TGCCCGCTCA GGACCTGCTC CACTGTTTAA CACTAAACCA AGGTCATGAG CATTCTGTCT 240
AAGATAACAG ACTCCAGCTC CTGGTCCACC CGGCATGTCA GTCAGCACTC TGGCCTTCAT 300
CACGAGAGCT CCGCAGCCGT GGCTAGGATT CCACTTCCTG TGTCATGACC TCAGGAAATA 360
AACGTCCTTG ACTTTATAAA AGCCAAA 387

SEQ ID NO:1556

LENGTH:325

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01771

SEQUENCE DESCRIPTION:

GATCACAGAT GGAATNTGTT ATAAGCATCA ATGTGACACT TGCAGGNCAC TACAACGTGG 60
NACATTGTTT GTTCTTCCA TATTGGAAG ATAAATTAT GTGTAGACTT TTTTGAAGA 120
TACGGTTAAT AACTAAAATT TATTGAAATG GTCTTGCAAT GACTCGTATT CAGATGCTTA 180
AAGAAAGCAT TGCTGCTACA AATATTTCTA TTTTAAGAAA GGGTTTTTAT GGACCAATGC 240
CCCAGTTGTC AGTCAGAGCC GTTGGTGTTT TTCATTGTTT AAAATGTCAC CTGTAAATG 300
GGCATTATTT ATGTTTTTTT TTTTN 325

SEQ ID NO:1557

LENGTH:322

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01772

SEQUENCE DESCRIPTION:

GATCTGTAAT TCATAGTCAC ATCAAGGTCA TCAAGACCAG GAAAAACAAG AAAGACATAC 60
TCAATCCTGA TTCAAGTATG GAAACTTCAC CAGACTTTC CTTCTAAAAT CTGGATGTCA 120
TTGACGATAA TGTTTATGNN GATAAGGTCT AAGTGCTTAA NAAAATGTAC ATATACCTGG 180
TTGAAATACA AACTATACA TACACACCAC CATATATNCT AGCTGTTAAT CCTATGGAAT 240
GGGGTATTGG GAGTNCITTT TTAATTTNCC ATAGTTTTTT TTAATAAAAT GGCATATTTN 300
GCATCTACAA CTTCTATAAT TN 322

SEQ ID NO:1558

LENGTH:319

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01773

SEQUENCE DESCRIPTION:

GATCTTTCTT TAATAGTGAA CCCCTGGGCC ACTGAAGAGT AACATGGCTC CACTGGACAC 60
 AAAAGAGGGA TGGAATCAAC AGGCAGGGGG CCTTTTATAA GCCTTAGGAA AAGAAAATGA 120
 AACTATTTCA TCTTTGGACT TTTCAATACT ATTGGAGTGA TTTTTTTTTT TCTAAACAGG 180
 GAAAATAATG TTACAAAAGC ATCTTTTTTG TNATTTGTTT GCATCCCTCC CCCACACCCT 240
 GGTGTTTAA ANTGANGAAA AAAANCCATC ACCTTTTGTA CAAAANCTCT TAATGNTTAA 300
 CAAACAAACA AANCAGAAA 319

SEQ ID NO:1559

LENGTH:316

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01774

SEQUENCE DESCRIPTION:

GATCTGGCTG CGCTATGACT CCGGGAGCGN CACCCACAAC ATGTACCGGG AATACCGGGA 60
 CCTGACCACC GCAGCGCTGT CACCCAGTGC TACCGAGACA TGGGTGCCCG GCACGCGCCC 120
 GAGCCCACTC CATTANATC TNACAGCAGT GTTCTTGCAA TATGAGGAGA CAGTTACAGC 180
 CACATTATGG CTCTCATTGA ACAGTACGCA GCACCCCTGC CCCAGCCGT NTTTTGGGG 240
 CTTGCGCGAA AATCTACAAG CGGGAANGTG ACCTNGGATT CAAGGGCGGG GAGAGANGCT 300
 TNAATAAATA ATCGTN 316

SEQ ID NO:1560

LENGTH:390

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01775

SEQUENCE DESCRIPTION:

GATCTAGAGG GTCGGACCCA CATATTTAAG ATTACGNTC GTTCAATGAG TGTGAAAGA 60
 GATATCAGAT TTGAAGTGT AGCACGACTG TGNCCAAATA GCACTGGTGC TGAGATTAGA 120
 AGCGTCTGCA CAGAGGCTGG TATGTTTGCC ATCAGAGCAC GCGGAAAAAT TGCTACCGAG 180
 AAGGATTTCT TGAAGCTGT AAATAAGGTC ATTAAGTCTT ATGCCAAATT CAGTGCTACT 240
 CCTCGTTACA TGACATACAA CTGAACCCTG ANGGCTTTCA AGTGAAAACT TTAAATTGGA 300
 ATCCTAACCN TATATAGACT TGTTAATAAC CAATTCATAA ACAAATAAAT GGCTTCAAAA 360
 TTGAAAAAAA NNNGANNNN NNNNAGNNNN 390

SEQ ID NO:1561

LENGTH:311

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01776

SEQUENCE DESCRIPTION:

GATCTGCTTA GAGTGGATTT TCACTCAAGT CCTTAGTAAG TGGATTTTGG GGAAAAAGC 60

ACCTGGGCTT CTGGTTCTTT TTGATAATAT ATAAAATTAT TCATTATGAG GTTGCAAGTTG 120
 TTTGCAAAGG AGAGGCACTC AAATTTGAAA GGTTATTTTA ATGTGATAAT TTGGAAGACT 180
 TACTCAGATG TTGGTCATTG ACCACTCTGT GCATATATTT CTGCAGAGCT CTGTGAAGGC 240
 AATGAGTGTC ACTTCCCTCT GCTCTAATAA AGCAATAAAT AATAGCTAAA GGGCTGACTT 300
 TCACTTCGAA A 311

SEQ ID NO:1562

LENGTH:310

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01777

SEQUENCE DESCRIPTION:

GATCTTTCTA CAACATTTAT CCTGGTTGTT AAGCCCTCCT TACAACATTC TTCTCTCTTT 60
 GTTTTTATAG CTCCATCTCT CCTGCTTCTT TAACITGATA ATGCATACTT GATTTTCCTA 120
 TTTGTNATTT CATAAACCAA TTAATACACA GATAAAATGA CTGTATATCA AACCATGTTT 180
 GTATAGAAAA ANTGGATTN GGATGCCTCT CATATGTAAT TAGTTCTATT AAACATATTA 240
 ATNGTATTGT TTAATTNGTC AGGTTTTTGA CAGANTTTTG TTTACAGGTA ATAAANNNTNT 300
 TATCTCCAAA 310

SEQ ID NO:1563

LENGTH:307

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01778

SEQUENCE DESCRIPTION:

GATCGAAAAA AAAATCCAGA ACCTTGGGAA ACTGTGGACC CTACTGTACC TCAAAAGCTT 60
 ATAACAATCA ACCAACCAATG GAAACCCATT GAAGAGTTGC AAAATGTCCA AAGGGTGACC 120
 AAATGACGAG CCCTCGCCTC TTTCTTCTGA AGAGTACTCT ATAAATCTAG TGGAAACATT 180
 TCTGCACAAA CTAGATTCTG GACACCAGTG TCGGGAATG CTTCTGCTAC ATTTTtaggg 240
 TTTGTCTACA TTTTNGGGC TCTGGATAAG GAATTAAAGG AGTGCAGCAA TAACTGCACT 300
 GTCTAAA 307

SEQ ID NO:1564

LENGTH:305

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01779

SEQUENCE DESCRIPTION:

GATCCTGTGG TTGGCCACTG GCCATAGCTG CTGCCCAGCT CTACCCCTCC CAGGGACCTA 60
 CCCCTCCCAG GGACCGACCC CTGGCCCAAG CTCCCCTTGC TGGCGGGCGC TGGGTGGGCC 120
 CTGCACTTGC TGAGGTTCCC CATCATGGGC AAGGAAGGGA ATTCCACAG CCCTCCAGTG 180
 NACTGAGGGT ACTGGCCTAG CCATGTGGAA TTCCCTACNC TGACTCCTTC CCCAAACCCA 240
 GGGAAAAAG CTCTCAATTT TTNATTTTTA ATTTTGTGT GAAATAAAGT CCTTAGTTAG 300
 CNAAG 305

SEQ ID NO:1565

LENGTH:304

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01780

SEQUENCE DESCRIPTION:

GATCACAGCT AGAGAATTGA GAATTAAC TA TACTACTAGC CATTTTAGGG CACCAAAACT 60
TGGGATTAAA CACTTCCTAC TTCCCACTCC CAACTCCTGA AATGAAGTCT TGCTATCTGT 120
GACTAGTTTT ATTTTGTGC TTTTAATAGT CCGAGCAGTC TTACCTTGTT TACACATGTA 180
TTGACACCAT TTGCTTCAGG CCATGGAGCA CTGTTTCTCC CNTTTTACTA TTTATAGGAT 240
TCCGTTTTTT CACAAGACTT TTAATAAAAA GAAATTGTAG AAATAAACAC ATTAAAATTT 300
GAAA 304

SEQ ID NO:1566

LENGTH:304

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01781

SEQUENCE DESCRIPTION:

GATCTGCTTT CTCGTAATTA TAGATTGGTT TGCATTTTCT AGAAATTTT AAATAAATGG 60
AAACATATAG TGAGTACTCT TCTTGGGGTG GAAGGAAGTG TGTGTGGCTT TTTCACTCA 120
AGCATAATTA ATTTGATACT CATCCAGATT ATGCATGTAT CAATAGTTTA TTCCTTTTTT 180
ATTGCAGAGT AGTAGTTANN NNCCTGGGTA TNCACAATTT GTTACCTGTT CATCTATTGA 240
TGGNCAATTG GGGTATTTCC AGTTTGTAGCT ATTACAAATA AACCTGCTGT GACATCATGN 300
CAAA 304

SEQ ID NO:1567

LENGTH:304

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01782

SEQUENCE DESCRIPTION:

GATCTGCTAT AGCTGTCCAT CAGAGAGAAT ACACGTGGCT ATAACATCTA TAACAAAACG 60
ACGATTCCCTC TACAAGAGGC TGTTTCTNAC TGCTAACGTT GGTGTTTCTG GCGTGGGAAG 120
AAATGCACAG GCGTGCATGG CATGCACGTN CAGACAGCTG CATTGTAAGA NTNCTGTCAT 180
GCAGTCTGAA AAGGGAAGAA ACAGGATGGC TTTCTGTAGC CACACCTGTG AGGCGTGATG 240
ATTGTNGTAT TATTAGATTA CTGATTTTCC TTTTCTGAAA ATACATTTGN NTTTTAATCA 300
CAAA 304

SEQ ID NO:1568

LENGTH:304

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01783

SEQUENCE DESCRIPTION:

GATCTGCTGT TGCTGAGAGT NTGAGCGTGG ACTTGATGCA GTNATGACAA ATCATTGCTT 60
 AGAATTAATG TTTTCAAATG TGCAACTCTA GTTTTTAAAA CAAAATTGG TTCTTTACAT 120
 TCATTATTTC GTTTTGTGTT CCCTTTAGTA TTTAATGGTC TTTGGAGAAA AAATAATAAA 180
 ACAGAGTGTT ATATATATAT TTTTGGTGC AAGATAAGAT TTTCTGTTT TTGAAATAAG 240
 TCTGTAGCAT AAAAGGTTAA ACTATTTTAA GGACANANTA AAAATAGGAG TGTATTTAAA 300
 CAAA 304

SEQ ID NO:1569

LENGTH:303

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01784

SEQUENCE DESCRIPTION:

GATCCAGGGA TGAGGATAGA GTGGCCTGAG AGCAGTGCTT GGATTCAGCC TCCTGCTGGG 60
 TCCTTCTGCT GGATACAGGC ACCAAGAGGC GGGGGTGGAG CAGGGAGCTG CGCCTTCCTG 120
 GGGTGCCNGG TGGTGTGTAG AGAAAAGCTG CTTGTTTACT CCTTAAGTCA ATGTATTGGT 180
 GACTGTTGAT TTGTTGAACA ATTCAGGAAT CAAGGGCTGT GGAGAAACTC CCTCATGTTG 240
 TTGGCAACAG GTGAATGAAC CTAGAGCGGT GACATGAAAA TAAAGCTCAC TGTTACTCGC 300
 AAA 303

SEQ ID NO:1570

LENGTH:302

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01785

SEQUENCE DESCRIPTION:

GATCCCCGA CGACGTGCTC GAGTTCCTGA AGGTGTATGA GANGCACTCT GCCCAGTGAG 60
 CACCTGCCCT GCCTGCATCC GGAGAATTGC CTCTACCTGG ACCTTTGTG TCACACAGCA 120
 GTACCCGTGAC CTGCTGTGCA CCTTACATTC CTAGAGAGCA GAAATAAAAA GCATGACTAT 180
 TTCCACCATC AAATGCTGTA GAATGCTTGG CACTCCCTAA CCAATGCTG TCTCCATAAT 240
 GCCACTGGTG TTAAGATATA TTTTGAGTGG ATGGAGGAGA AATAAACTTA TTCCTCCTTA 300
 AA 302

SEQ ID NO:1571

LENGTH:307

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01786

SEQUENCE DESCRIPTION:

GATCCATTTT GCTTACACTG TTGCATCACA AGGGACTCAC CCAGGGACCA TGACCTGCTG 60
 GTGTGTGTGT ATATTACAA AAACAAAACA AACAAACCAC CCATTGGGAT ATAAGGTAGC 120
 AATCACAAC TAAAGACTGC GGCTTGTTGA GGTGCAATAC CCTGACTCCC AAAGTTAGTT 180
 ACAGTGGGTT TTATTGTTTT TGTGACTGAA GGATTTATTC AGACTGCTGT ACTCTTCATT 240
 TGATGTAACA AAATGCTATT AATCTAAATA TTTGTAAATA AAGTACCTGT ATCTAGATTA 300
 AATTAAA 307

SEQ ID NO:1572

LENGTH:301

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01787

SEQUENCE DESCRIPTION:

GATCCATTAC CTAGGGTAAA ATTCTCCTGA ATGTCAAACA AAGAGATAAA CTACATTTGG 60
GTTTTGGGAA GTCCCTGTA ATGATGAATC AAGAATCCTC AAGTCTGTCT TGCCACCCAT 120
TTAATACGTA TTTTGTAA GGCTGAAGTT TAGAGTTAGA ATCAGGACAT TTTGGCCTAT 180
TGAGAGGTTT TGAATCCAA CAGAAGATGC CATGTAAATC AGTGAATTTN ATTCTTTTAA 240
AAGCAACTTA CAAAATTTAC AAGATGTATT CAATAAAGCA GTTAGCTTT GGTATATCAA 300
A 301

SEQ ID NO:1573

LENGTH:303

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01788

SEQUENCE DESCRIPTION:

GATCCTCAGT GTGCTACGG GGCTGCTGTT CGGCAGCNAT GGCTACTACG TGGCGCTGGC 60
CTGGACCTCA TCGGCGCTCA TGTACTTNAT TGTGCGCTCT TTGCGGACAG CAGCCCTGGG 120
CCCCGACAGC ATGGGGGGCC CCGTCCCCCG GNAGCGTCTC CAGCTCTACC TGA CTGTTGGG 180
AGCTGCAGCC TTTNCAGCCC CTCATNATAT ACTGGCTGAC TTTCCACCTG GTCCGGTGAC 240
GTCTNGCCCC AGATGGNAAT NAGTTTTTTA ATTCATTGN AAGGATTTTG AANTTCCTTG 300
AAA 303

SEQ ID NO:1574

LENGTH:297

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01789

SEQUENCE DESCRIPTION:

GATCTGTGTT CGAATCCTCC CCACCCCTTT CTTTGTGGAG TTTCTAACC TGCTGCTGAA 60
GCACAATGTT TTGGTGCTTT CTTTCTCNN TTGTTAAAGG CAGTGTCAA AAGCCATTCC 120
AGATGCCAAG ACCAGGGGCT TATTCTAGG GAAGGTAGGT CGGTTCCAT GTTCCCTCC 180
CGTTATTTT ATTTTNACT TTTTGCTGA GACAAGCCGA GTATGAGGTG GTTGATTTA 240
AGAAAAATCA ATGAAATTGT TTACTACTGT TTTAAATAA AACCGTAAAC TCTGAAA 297

SEQ ID NO:1575

LENGTH:299

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01790

SEQUENCE DESCRIPTION:

GATCAGGCCG TTNCTGAGCT CAACGGGACC CAGGTGGAGT CTGTACAGCT CAAAGTCAAC 60
ATAGCCCGAA AACAGCCCAT GCTGGATGCC GCTACTGGCA AGTTTGTNTG GGGCTCCCTC 120
GCTGTCCAGA ACAGCCCTAA GGNTTGCCAC CGGGACAAGA GGACCCAGAT TGTTTACAGT 180
GATGACGTCT ACAAGGAAAA CTTTGTGGAT GGCTTCTAGG GAACAGNGCT GGATTCCTTG 240
TGCTCATAT GCCCCAAATG CTGGTTTCA GTAAANCACT TGAGGGTGGA AGCTTNAAA 299

SEQ ID NO:1576

LENGTH:300

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01791

SEQUENCE DESCRIPTION:

GATCCAAGAT AAAGAAGGCA TCCCCCGGA CCAGCAGAGG CTCATCTTTG CAGGCAAGCA 60
GCTGGAAGAT GGCCGCACTC TTTCTGACTA CAACATCCAG AAAGAGTCGA CCCTGCACCT 120
GGTCTGCGC CTGAGGNGGT GGCTGTTAAT TCTNCAGTCA TGGCATTGCG AGTGCCCACT 180
GATGGCATT CTCTGCACTA TAGCCATTTG NCCCAACTTA AGTTTAGAAA TTACAGGTTT 240
CAGTAATAGC TNGAACCTGT TCAAAATGTT AATANAGGTT TCGTTGNATG GGAGCATAAA 300

SEQ ID NO:1577

LENGTH:295

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01792

SEQUENCE DESCRIPTION:

GATCTGGCTT CTTTCCCAAG GNGGGGGTGG GGTGTNCCTN GCGTCCCTGT CCTTGANGGA 60
CCTCCTTCCC CCAGCCTCAT CACCGTGCTC TTCTCAGCGC CACCCTCAGC AGCCAGATTG 120
CAACACCAGG GAGAGGCGGA TGCAGAGCCC CACCGGTGGG AAAGTTGCCT GTGGAAGGGA 180
GCCTTTTGCT ACAATTTGTA ACTTATTNC TAAAGTCTAT TTTGTAACAA TTTATTTAAG 240
TTTAAAAAAA GAAAACTGC TGCCCNCCAA AAAAAGAAAT TTTCAAAACA AGAAA 295

SEQ ID NO:1578

LENGTH:297

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01793

SEQUENCE DESCRIPTION:

GATCTAAAGT TCTGGCTGTC CATTAACCTC CAACTATGGT CTTTATTCT TGTGGTAATA 60
TGATGTGCCT TTCCTGCTT AAATCCCTTC CTGGTGTGTA TCAACATTAT TTAATGTCTT 120
CTAATTCAGT CATTTTTTA TAAGTATGTC TATAAACATT GAACTTTAAA AAATTATTTT 180
ATTTATTCCA CTAATGTAGC AATTGACAGA TAAAAAAAT GTAACCTCAT AATTTCTTAC 240
CATAACCTCA ATGCTNNNTT TAAAAANATA AAAATTAAAA ATGAAAAGNG NTANAAA 297

SEQ ID NO:1579

LENGTH:289

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01794

SEQUENCE DESCRIPTION:

GATCTCTCTT GTCCNCTNCT GCTCTTNNCT TGGTGCTCTT TTTNCTCGGT GGGGTGTGGG 60
 TAATAGAACA GCCGTGGGCT TTTGGGGACC TTAACTTTT TTTNCTCTCT TTTGTTTATA 120
 AAAAACAATA AACATTCAAT TCCAGAGAAC CAAAAATCCC ACCTTCCCAC CGAACACTAC 180
 TAAGGGGCTT GTGTTCTGCN CCATACCTTT NCTCTTNNCT TTCTGTCTTG TTAATGCTTT 240
 TAAAAACAAA TGAGTTTTTT ATATAAATAA AGTTTTTAAA GTGTGTAAG 289

SEQ ID NO:1580

LENGTH:287

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01795

SEQUENCE DESCRIPTION:

GATCCCATCC GCATGGAGTT TGAAAAATAAG GAAGACTTGT CGGGAACACA GGCAGGGGCTC 60
 AACGTCATTA AAGAGGCAGA GGCACACNCC NGGTGGGCAG CCAAGGAGCT GAGAAGANCG 120
 AAGAAGCTTT CAGACTACGT GGGGAAGANT GAAAAANCCA AAATTATCGC CAAGNTTCAG 180
 CAAAGGGGAC AGGGAGCTCC AGCCCGAGAG CCTATTATTA GCAGTNAGGA GCAGAAGCAG 240
 CTGATGCTGT ACTATCACAG AAGNCANGAG GNGCTCANGA GATTGGN 287

SEQ ID NO:1581

LENGTH:285

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01796

SEQUENCE DESCRIPTION:

GATCTATTGG CATATTCGGG AGCTTCTTAG AGGGATGAGG TTCTTTGAAC ACAGTGAAAA 60
 TTAAATTAG TAACTTTTTT GCAAGCAGTT TATTGACTGT TATTGCTAAG AAGAAGTAAG 120
 AAAGAAAAAG CCTGTGGCA ATCTTGGTTA TTTCTTTAAG ATTTCTGGCA GTGTGGGATG 180
 GATGAATGAA GTGGAATGTG AACTTTGGGC AAGTTAAATG GGACAGCCTT CCATGTTTAT 240
 TTGTCTACCT CTAACTGAA TAAAAAGCC TACAGTTTTT AGAAA 285

SEQ ID NO:1582

LENGTH:280

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01797

SEQUENCE DESCRIPTION:

GATCCTCCCC TTTTGAAATG GCCCTGCTGT GTCAGTTTCC CTGTGGCCTT TTGAACTGTA 60
 CATCTCACAT GTTGGGAAAC GCTGGCCACT GGGAAATCAT TAGAAAGGAG GCTGTAGAAT 120
 ATTTGCCGAG CCTCTACTGT ATACCAGGGG CTAACACACC AAGCACATTC TAGGAATTGG 180
 GCCCTGCTCA TGAGGAGCCT TAGTGGAGAT TCCAGGTGAA TATTTATGAA AAAGTCAACA 240
 TTAGAAGTGA AAATGGAAAT AAAGTCTTG AAAAGACAAA 280

SEQ ID NO:1583

LENGTH:273

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01798

SEQUENCE DESCRIPTION:

GATCAGAATG GACTTCTNCC ACTGAGCATG ACANGCACTC GAAAGGCTAA ATCAACCAGA 60
 AACATCGAAA CAAAAGCTCA GGTGTGCCCC CCGGCACGCT CCACANCTGG TGACCCGACA 120
 GTTCCTGGCT CTTGTTCAG ACAGCTTGTC AGTNAAGAAG ACANCACGTC TGCACCTNCA 180
 TTATTCAAAC TTGGCTGGCT CTCTAGTATG ACTACGNACA TGGAACACAT CTGTCTCTCC 240
 CTAATAANT ACTACCACAT TATTNCTTCT AAA 273

SEQ ID NO:1584

LENGTH:270

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01799

SEQUENCE DESCRIPTION:

GATCCATATT TGTTTTGTGT TCTGCTTAAA TCAGCAAGAA TGATAAATTT GATGGTGTGA 60
 AATTGGAAGT ATCAAGGGCT TTCTTTGGTG ATTGAGGGAA ATAATGTCTC TACTTGTAAT 120
 TTATTGTGAC CCTTTTTCAC TGTATATGCT TTGTATGTCT AATATTTATT TCAATGCAAA 180
 TTCAATTNCC CCTTCATCTG TATTGTTATA TCTAAGATTT TATTGATGTT AAAATCTAAT 240
 TGTGGAATAA AAATCTCTCT GGAATTTAAA 270

SEQ ID NO:1585

LENGTH:270

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01800

SEQUENCE DESCRIPTION:

GATCTGCTTG ACAGTGATTA AATCCTTAGC TCACATCCAT TCCCATCTTT NGGGCTCCTT 60
 AGGCCCAAGG ATGGCATGTG ACTGGTCCCT GCAAGGTCCT TTCTTTGTCA CCAGCCAAGG 120
 CATTGATAAC CAAGTAGCCA TTTTCCTCTT AAGGTTTCCT CTACAACCCC AAGGACTTTC 180
 ATGATTATCC TCAGGGACAG GATTGGAGGC ATTGAGCGTG TTTATTAACA AATTGTTTTT 240
 GGTAATAAAA TAAATGCTTG GACTCTTAAA 270

SEQ ID NO:1586

LENGTH:269

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01801

SEQUENCE DESCRIPTION:

GATCTNGTAA ACTCTCTGTA TATCTTCCTA CCTTTCAAAA TCGTTCCTAG GGTTAGTCAA 60
 GTCTGGAATA TAATTGCTGA CTATAAAGTT AGCAATTATG CTTTAAAGGT GTTGTCACAT 120
 CAACCTAAAG AGAACCATCT ATGGAAGGTA TGGTTGAAAC ATCTGTAGGA ACACAGAACT 180

GGGATTTCAC TGAGTTTACC ANNTCAACTG TGTGAACTGT TTCTGCACTG CTTGCTAATG 240
GCTTCATCTA ATAAATGTTT ACTTATAAA 269

SEQ ID NO:1587

LENGTH:267

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01802

SEQUENCE DESCRIPTION:

GATCTAGGGA AGTCAACACA TAGTGTA AAA TAATTACATG CCTAATGAAA AGAAGATGTC 60
ATTCCTAAT TTNATATCT CATTTTCGGC ATTTTTTAAA ATGTAAAAGG AAAACCTCTT 120
GTGTTACAC AGATTGCTGA ATTGATTCT CCATATTGT TAATAATTTA CTATTATTTA 180
CAAAGATTCA AATGCTTTTA TGAATAATGT AAAATGAAA GAGGCTTACA TTTTAAATGT 240
TATTAAAATT ATGTACTTAA ATCTAAA 267

SEQ ID NO:1588

LENGTH:288

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01803

SEQUENCE DESCRIPTION:

GATCGCTTTG AGGTCAATAT TAGTGAGCTG CCTGATGAGA TAGACATCTC CTCCTACATT 60
GAACAGACAC GGTAAGAC TCGCCCATTT TGAATGTGA CCGTCTNTCC TTCAGGNGAG 120
GACACCAGGN TGGGGGTGAA GGAGACACTA CTGCCCCAC CCCTGACAGC CCCCACCCA 180
TGGCTTNCAT CTTTGCATN ACCANCACTC CTGAACCCN ATTTCTNATT TGTCAGAAAT 240
TTTTNNNTA ACAAACACTAG AAATGNANCA CATGGGGTCT GTGGTAAA 288

SEQ ID NO:1589

LENGTH:266

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01804

SEQUENCE DESCRIPTION:

GATCTTGCCT GTTTCACAAT GTAACAAGAC TCTACCTGGG TCCCCTGGTG ATGAGTTTCA 60
GCATAGAATA ATGTTCAAGG AAAAGAAAAC GAAAACAGTT TAAATCTCTA CCACAGCCTC 120
ACAAGCAAAT GCTAAGGGA ACATACATGT AAAANGCCAG CAAACTATCT TCAAACCTCT 180
CCGTCCTTAA TGTCTTCCAT GGCTATTGCC CCCACAATGG TCTCTTNNT CCCTGCTCCC 240
TTATTAANGA ACTCTTCTG AAGAAA 266

SEQ ID NO:1590

LENGTH:266

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01805

SEQUENCE DESCRIPTION:

GATCTATGAC TCCAACCGTA TGATTTTNTT GCCTCCCCAG TTTTCATCCC AGTGGTAACG 60
 CCTGATTTT GGTAGCTATG CCATCTTCTG CTGAGGATTA CCATTACTGG GTGTATCACC 120
 CCAGTACTTC CAAATNCCTC TCCTCTATTG ATTCAGTTGT TATTGCAGTG TCTGCTTCAT 180
 CCGTGGAAC TGAAGGCTCAG ATGCCCCCTG CTCTGTAACC CTGGGGAATG TCAGAGGCAG 240
 GTAATAAAGG TTGTTTAAAC AATAAA 266

SEQ ID NO:1591

LENGTH:265

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01806

SEQUENCE DESCRIPTION:

GATCAGGAGA CTTTGAATTN ATATATTTTA ATCCTNATTA AGCTTAAATA GGAAAGTTTC 60
 TTCAACAGGA TTACAGTGTA GCTACCTACA TGCTGAAAAA TATAGCCTTT AAATCATTTT 120
 NATATTATAA CTCTGTATAA TAGAGATAAG TCCATTTTTT AAAAATGTTT TCCCCAAACC 180
 ATAAACCCT ATACAAGTTG TTCTAGTAAC AATACATGAG ANAGATGTCT ATGTAGCTGA 240
 AAATAAAATG ACGTCACAGG GCAAA 265

SEQ ID NO:1592

LENGTH:254

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01807

SEQUENCE DESCRIPTION:

GATCTGAGAG AAGCCCTGTC CTCCACTCAC CTCACCCGCC GCTGCCACCA TCTCCTCTGT 60
 GCCAACTCCT TGTGGACCGC AAGAAAGCAT GACTTTGAAA AAGGGAAGCC ATTCGAGAT 120
 TTAAAAATGT TCATGGACTA TTCCATATTA AAAGCTGTTT TTGTTGTACA AAATCACTG 180
 ATGTTCAAGT CTATTTTATT TTGCCTTCAG AAAAGAAGAA AGTCAAAAAT AAAACTTTTG 240
 TGTATTACAG CAAA 254

SEQ ID NO:1593

LENGTH:255

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01808

SEQUENCE DESCRIPTION:

GATCCTGGAG GATTTCTAC CCCCCTCCTC TTCGAGNCCC CAGTCGTGAT GTGGAGGAAG 60
 AGCCACCTGC AAGATGGACA CGAGCCACAA GCTGCACTGT GAACCTGGGC ACTCCGCGCC 120
 GATGCCACCG GCCTGTGGGT CTCTGAAGGG ACCCCCCCCC AATCGGACTG CCAAATTCTC 180
 CGGTTTGCCC CGGGATATAA TAGAAAATTA TTTNTATGAA TAATGNAAAT AAAACACACC 240
 TNGTGCCATG GCAAA 255

SEQ ID NO:1594

LENGTH:282

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01809

SEQUENCE DESCRIPTION:

```
GATCCATGAA GGAGGCTGT GTGGAGAAGA TTGGGGACTG GCTGAGGAAA AATGTGCTGG 60
TGGTAGCTGC AGCAGCCCTN GNGAATTNCT TTTGTCGAGG TTTTGGGAAT TGTCTTTNCC 120
TGCTGCCTCG TGAAGAGTAT CAGAAGTGGC TACGAGGTGA TGTAGGGGTC TNGGCTCCTC 180
AGCCTNCTCA TCTGGGGGAG TGAATAGTA TCCTCCAGGT TTTCAATTA AACGGATTAT 240
TTTTTCAGNC CGAAAAGNGA TGGTCTGAGT TTNTCTTAGA AA 282
```

SEQ ID NO:1595

LENGTH:256

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01810

SEQUENCE DESCRIPTION:

```
GATCAAATAA ACCAGTGTAG GATATTAAGA CTATCAATTG GTGGGATTAG GCTTGACATT 60
TTATTTTAT AAATATATAT TTNTCCTGAA TGTGTCTGAG TCCAAGAGTG GGCAAAAAAT 120
AATTTNCTAC TTTGGACTAA TCTATAGAGG TTTTGAAG TCTGCATTAC TAAC TTGTG 180
AATTCATGAT ATTCTGCCTA TGGCACAAT TGTAACCTT TGT TTTNCTA AAATAANGTA 240
ATTGAAAACC TGNAAA 256
```

SEQ ID NO:1596

LENGTH:204

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01811

SEQUENCE DESCRIPTION:

```
GATCTGCGCT TCCAGAGCGC ACTAATNCGG TGCTTTGCAG GAGGCAAGTG AGGCCTATCT 60
GGTTGGCCTT TTTGAAGACA CCAACCTGTG TGCTATCCAT GCCAAACGTG TAACAATTAT 120
GCCAAAAGAC ATCCAGCTAG CACGCCGCAT ACGTGGAGAA CGTGCTTAAG AATCCACTAT 180
GATGGGAAAC ATTCATTCT CAAA 204
```

SEQ ID NO:1597

LENGTH:246

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01812

SEQUENCE DESCRIPTION:

```
GATCATTATT ATATATAGGT ATTGATTGCT ACCCTGACCA CAGTGCTTTG GACTATGAGA 60
AACTTCTTAG ATTTTATAT GTAAATNCTG TGGACCACTG GGAGCACAAT GCCACATCA 120
TCTTAAGNNG AGTTTATGTG CAGCATTTAA ATCACTGTGT TTTCTTGT TAACTAAAACA 180
GACATGGGCT TTGATTTTTT TCATACTATT AGACCATATC TCATAAAACC TTTTGAATTA 240
ATGAAA 246
```

SEQ ID NO:1598

LENGTH:285

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01813

SEQUENCE DESCRIPTION:

GATCAGGCAC ACACAATAAG TCTTCTCTC CGAAACCGGA AGTAAATCTA TATCTGTTAG 60
 AAATAATGTA GCCAAAAGAA TGTAATTG AGGATTTTT TGCCAATAGT TTATAGAAAA 120
 TATATGANCC AAAGTGATT GAGTTTGTA AAATGTAAAA TAGTATGANC AAAATTTGCA 180
 CTCTACCAGA TTTGAACATC TAGTGAGGT CACATTCATA CTAAGTTTC AACATTGTGT 240
 TCTTTTGCA TTCATTTTT ACTTTTATTA ANGGNTCAA CCGN 285

SEQ ID NO:1599

LENGTH:241

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01814

SEQUENCE DESCRIPTION:

GATCTAACTA TGTTCCTCCC CTTTCAAGAA TAGAACTATT GGGGTGAGGA TAAGGGGTGG 60
 GGGAGAAAA ATCACTGTT GTTTTAAAA AGCAAATCTT TCTGTAAACA GAATAAAAGT 120
 NCCTCTCCCT TCCCTTCCCT CACCCCTGAC ATGTACCCCT TTNCCCTTC TGGCTGTTCC 180
 CCTGCTCTGT TGCTCTCTA AGGTAACATT TATAGAAGAN NTGGAATGAA TCTCCANGAA 240
 A 241

SEQ ID NO:1600

LENGTH:239

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01815

SEQUENCE DESCRIPTION:

GATCCAGAAT ACCCTGACCT CGCCCCAGTT CCAGCAGATG TGGAAGCGTT TGCCAAAGCC 60
 ATGCAGAACA ACGCCAAGCC CGAGCAGAAA GAGGGCGACA CGAAGGACAA GAAGGACGAA 120
 GAGGAGGACA TGAGCCTGGA CTGAGCCACG CGCCGTCCTC CGAGGAACGT GCGCTTGCA 180
 GTGCGTTGCA CACCCTCACC TCCCACCCAC TGATTATTAA TAAAGTCTT TCTTTTAA 239

SEQ ID NO:1601

LENGTH:236

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01816

SEQUENCE DESCRIPTION:

GATCCAAAGT AATATGTAGG TTCAATATTT TGTAGGTTTT ATAATCAAAT GTCTCCCTAA 60
 AGAGATGACA TAGGGAAGAA AAGCCTAATG TATCATCTTA ATGGATTCAG TTTTATTAT 120
 GCACAAATA CTGGGCTTGT AACCTAGGAA TATGATTAGA GCGTGATGCT GGCTTAAAA 180
 ATAGGACTNG TGAATCACAG TTTGTNNNTA ATAACTACT GGTGGAAAT ATTTAA 236

SEQ ID NO:1602

LENGTH:235

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01817

SEQUENCE DESCRIPTION:

```
GATCTCCCCG CCGCAGCCTC CTCAGAAGAC ATCGAGCGGT CCTGAGAGCC TCCTGGGCAC 60
GTTTGTCTGT GTGCTGTAAC CTGAAGTCAA ACCTTAAGAT AATGGATAAT CTCGGGCCAA 120
TTTATGCAGA GTCAGCCATT CCTGTTCTCT TTGCCTTGAT GTTGTGTTGT TATCATTTAA 180
GATTTTTTTT TTTTGGNAAT NATTTTGAGT GGCAAANTAA NGATTAGCAN TTAAA 235
```

SEQ ID NO:1603

LENGTH:324

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01818

SEQUENCE DESCRIPTION:

```
GATCTGCCCC GGTGCGCCAG ACTTCCTAGC ACACGTGCGC GGGAGCAGCT GCTTTGAGTG 60
CACACACTAC CAATCGTTCC TGGAATACAG GGAGGTGGTG GACGGCCTGG AGAAGGCCAT 120
CTACAAGGGC CCAGGCAGCG AAGAGGGCCC TGACTGCCCC CCCCGGCCCC CCTCTCGGGC 180
TCTCTACCC AGCCTGGTAC TGAAGGTGCC AGACGTGNTC CTGCTGACCT TCTGCGGCTC 240
CGGGCTGTGT CCTAAATGCA AAGCACACCT CGGCCGAGGN CTGCGNCCTG ACANGGNNAC 300
CTCTCTGAAC TGCAACACTT GGAN 324
```

SEQ ID NO:1604

LENGTH:235

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01819

SEQUENCE DESCRIPTION:

```
GATCAAAAAG CAAGCAGAAA TGAATCCACA TTCTAGTCCT TTATGCAGTA TACAAGGAGA 60
ACTGTCTGT AGGATATTCT CTTCTGATG GTGCAGAACC CAGAATTAGA AGTTTGTGGT 120
TACAGCATAC TCTGTCCTTC AGAAAGGCGT GATTCTAGCT GTTGACCCCT TGCAGCTGTT 180
GGAATCTCTG CAAGAACCTC TGTATTCTTC TAATAAATC CCTCTTTTAT TTAAA 235
```

SEQ ID NO:1605

LENGTH:235

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01820

SEQUENCE DESCRIPTION:

```
GATCCCAACA ATGAAGCCAT TCGAAATGCT ATGGGCTCCC TGGCCTCCNA GGCCACCAAG 60
GACGGCAAGA AGGACAAGAA GGAGGAAGAC AAGAAGTGAG ACTGGAGGGA AAGGGTAGCT 120
GAGTCTGCTT AGGGGACTGC ATGGNAAGCA CGGAATATAG GGTTAGATGT GTGTNATCTG 180
TAACCATTAC AGCCTAAATA AAGCTTGGCA ACTTTTTTCC CTTTTTTGCT TCAAA 235
```

SEQ ID NO:1606

LENGTH:234

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01821

SEQUENCE DESCRIPTION:

GATCAAAAAG AGAGTGGTTG TGGAACCTGT TGGCCAGTT GGTTCAGC CAGAGACATT 60
CAGAAAGTTT TTAGCTCTAT ATTTGCATGG TGCTGCGTGA NGGAGGACCC CTCTGAATCC 120
TGAAACCCCT CTTGCCTCTC TTCCACGGAA GAGGGCCTGG GCCCCGTGGA GCCTCAGTGC 180
CCGTTTGGCC TGCTGCTCTC GCTGACAATA AAGAGCCCTT GCGTTGCACT GAAA 234

SEQ ID NO:1607

LENGTH:234

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01822

SEQUENCE DESCRIPTION:

GATCTGGAAC CTCAGCCTGG CCAGACACAG GCCCTCCCTG TTCCCAGAG AAAGGGGAGC 60
CCACTGTCCT GGGCCTGCAG AATTGGGTT CTGCCTGCCA GCTGCACTGA TGCTGCCCT 120
CATCTCTCTG CCCAACCTT CCCTCACCTT GGCACCAGAC ACCCAGGACT TATTAACT 180
CTGTTGCAAG TGCAATAAAT CTGACCCAGT GCCCCACTG ACCAGAACTA GAAA 234

SEQ ID NO:1608

LENGTH:356

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01823

SEQUENCE DESCRIPTION:

GATCACATAA AACAGATTTG CATAAAATTA CCATGATTGC TTTATGTTA TATTAACTT 60
GTATTTTGT ACAACAAGA TTGTGTAAGA TATATTTGAA GTTTCAGTGA TTTAACAGTC 120
TTTCCAACTT TTCATGATTT TNATGAGCAC AGACTTTCAA GAAAATACTT GAAAATAAAT 180
TACATTGCCT TTTGTCCATT AATCAGCAAA TAAACATGG CCTTAACAAA GTTGTGTTGTG 240
TTATTGTACA ATTTGAAAAT TATGTCGGGA CATAACCTAT AGAATTACTA ACCTTACTGC 300
CCCTTGTAGA ATATGTATTA ATCATTCTAC ATTAAAGAAA ATAATGGGTT CTAAA 356

SEQ ID NO:1609

LENGTH:230

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01824

SEQUENCE DESCRIPTION:

GATCACCTAT GCCAAGAAAT AACATTGGG ATAGTCGTCT TAAAAGACT TGGTGTATT 60
TACAGTGTGTT GTTTGATAA CATTTGGCTG GGTCATTTA ATAGTTAGAG ATGAGGAGGA 120
GTAAAAGTGA AATTTTGTG AAGGACTTAA ATTATCCAGT GTTCTTTAG CCTTGGTGAA 180

CTATGAAATA CGAAGNCCTT AATTTGTAC AATAAACTTT TATTTGTAAA

230

SEQ ID NO:1610

LENGTH:227

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01825

SEQUENCE DESCRIPTION:

GATCTGTTGA ATATTTGCTA AAGACCAGTT CTTTAAGCTA AGACATGTAA AAAATCCCAA 60
 ATGGCAGTAC CTCATTGTTT ACTTAGCTTT TGTACTTATA TTTTCAGAG GAAAAACAC 120
 TACTGTAAAT TGTGAATAGC CAATACATAA CTGTATTGTA TGCAAATCTG TGATTGTTGG 180
 CAGTGTATC TCTGAGAAAC AGATAAATAA AGTTTATTTA CTATAAA 227

SEQ ID NO:1611

LENGTH:234

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01826

SEQUENCE DESCRIPTION:

GATCTAGCCA AGGCTGGTCT GCAGTATCAG ATGTCCAAAC TCATCTACTA TTAGCCATAT 60
 TTTGTGAGTC GTTTGTCTAA ACTTTGTCAA AAATGCCTTT GCCATGATTT TGTGCTATC 120
 TGGATTTCAA ACATGGACAG TTAGGAAGAT GTGCATTGAA GTAGGAAAAT TTTGTTTCAA 180
 TTTGCTGTTA TTTATTTTTT AAATTAATAA TGGAAATGTA TTTTAAAGTT TAAA 234

SEQ ID NO:1612

LENGTH:226

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01827

SEQUENCE DESCRIPTION:

GATCTGTTGG GTTCTCTATT AATTTATTTT ATACATTATA GATTCTGGGT TGATAAATTC 60
 TGCTCAATTT GAAAAATTTT ATATTTTGTC TCAAATCTGT TACAATTTAT ATTGGTGGGN 120
 GCAAAAGTAA TTGCGGTTTT TGCCGTAGAC AGTAATGGCA AAACTGACA ATTGCTTTTG 180
 CACCACCCTA ATAATATTAA NTATAATCAT GACTTTAAAC ATCAAA 226

SEQ ID NO:1613

LENGTH:224

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01828

SEQUENCE DESCRIPTION:

GATCGGGAAC TGGCTCCGTT GTGCTGAGGT CATCTTTGGT CATCAGCCTC CAGCATNTGG 60
 AAACACCTCC AACGCAATGT GGCTTTTACA TTTCTTTCTT TCTTTCTTTT TTTTCCTGG 120
 TACTGGGAAT ACACAACACC AGCTGTTTTA TTATTATTTG GGGAGGGGGT TGTGATTTTA 180
 TTATTNGTTT TTTTAAAATG AAAAATAAAA NGTTATATAT TAAA 224

SEQ ID NO:1614

LENGTH:222

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01829

SEQUENCE DESCRIPTION:

GATCAGCAGA TACATGTCAG TGCAGAGGTT CTCTGCCCTC CAGAAGCCCT CGTCTGGGAA 60
 TTCGAGAGAG GAGGAGGACC CAGGGCCAAA GGAATCCTCA AACTTCCCTC CAAGGGAGAT 120
 ATTGTAAGGG GAAAACAAAG TGTTTATTTT CCCAAAACAA CCCAGCTTCA CCCCATGTCC 180
 CTTCTACAG CTTACTCACT GAGGGTGAGT GGGAACGNTA AA 222

SEQ ID NO:1615

LENGTH:222

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01830

SEQUENCE DESCRIPTION:

GATCAGAATA TGTATGCAGT TCTTTCTTTA ACCCTTTTTT CTCCTATGTA CTGTGAACAT 60
 TTAAAAAGTA CTTTAAATA TTCTTTGGAA ACTTAGCTTT TAGTAACTAC TTGGTTGTAT 120
 CATAATTNAT TAACTANTGN NTTATTGGTA AACATTGGCT TGCCTCCCAT GACTTGCCAT 180
 TATAATTAAA ACTGTGACTA CTATCTGTCT CCATTNCATA AA 222

SEQ ID NO:1616

LENGTH:219

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01831

SEQUENCE DESCRIPTION:

GATCCCNNTT CCACCTCTC TGTTGGCCTC AGAGTCACTC CTGCCCCCTC TCCCTGACTT 60
 GGTGCTCACA TGCACCTCAC TAGGGTTTGT GACCAGGCTC TGGATGAGCT TGAATTTGAA 120
 TGAATTGAGT TTGTATTNT AGAACCTGG GTTTTTACAT GTTTGGTCTT TTTTNGTTTT 180
 GGTGTGTCAC CNTCGATAAA GGAAGTATAT TCATCCAAA 219

SEQ ID NO:1617

LENGTH:220

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01832

SEQUENCE DESCRIPTION:

GATCGCGGCG GANTNGGCCG CGCCGCCTGG TACTCAAGCC CGCGGGGACA TTGGGAAGGG 60
 GACCCCGGCC CCCTGCCCTC CCCTCTCTGC ACCGTACTGT GGAAGAGAAA CACGCACTTA 120
 GTCTCTAAAG AGTTTATTTT AAGACGTGTT TGTGTTTGTN TGTGTTTGTN CTTTNNATTG 180
 AATCTATTTA AGTAAAAAAA AAAATTGGTT CTTTATTAAA 220

SEQ ID NO:1618

LENGTH:216

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01833

SEQUENCE DESCRIPTION:

GATCANGGCA CTTCAACTCA TTTGGAAAAT NTGAACACTG ATGACATGGT ATAGGAGTGG 60
 GNGGGGTGTT GAGCCACCCA TCANACCCTC TTTAGCTGTG CAAGATAAAA GCAGCCTGGG 120
 TCACCCAGGG CCACAAGGCC ATGGTTAATT NTTANCGGCA AGGCAATCC ATNGTTGNGA 180
 AGTGCANTGG GCATAGTAAA NGTGCATGAT TTAAAN 216

SEQ ID NO:1619

LENGTH:214

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01834

SEQUENCE DESCRIPTION:

GATCATAGAA AATAAATAGA AGAGACAGTG AAGCAAGTAA AAAGAAAAGC ATTGTTTAA 60
 TTTGTTTGCA TTAATTTTT TCATTGTGCA AAATGCTTCT TTTGTTGCCA CAGTAAAGAA 120
 CAGTTTTTAT TGTTTTGTAA GTAAAATTAC GTAGCTGATT TTGTATGTAA AGATTAATTT 180
 CCATAATAAA AATTATTGTA TGTTTACTGT GAAA 214

SEQ ID NO:1620

LENGTH:214

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01835

SEQUENCE DESCRIPTION:

GATCAGAGTG GCCACAGAC ATTGCTTCT TATCACCTAT CATGTGAATT CTACCTGTAT 60
 TCCTGGGCTG GACCACTTGA TAACTCCAG TGTCTGGCA GCTTTTGAA TNACAGCAGT 120
 GGTATGGGGT TTATNATGCT ATAAACAAT GTCTGAAAAG TTGCCTAGAA TATATTTGT 180
 TACAACTTG AAATAAACCA AATTTGATGT TAAA 214

SEQ ID NO:1621

LENGTH:211

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01836

SEQUENCE DESCRIPTION:

GATCTGTGTC ATAAGTGACT CCGGATGCAT CAGTGTCAC CAGTTGGAAG CAATGACAAG 60
 GATGGCTGGC TGGTGTGTTT CAGCCTCCG GTTTATAGAC TGTATTTATC TAGTGGATTG 120
 CTGCAGGCC CATACTGAGC CTGGACTGAA AGTATCCACT CGGACCATCT GTTATCTCTC 180
 TACTACTGAAA ATAAACCTC TTCCACCCAA A 211

SEQ ID NO:1622

2153480

LENGTH:211

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01837

SEQUENCE DESCRIPTION:

GATCTGAGAT GGAAGAGTTT CATCCCCAAA CCATCTCCCC CTGACCCCCA GTCCATGGAA 60
AAATTGTCTT CCACAAAACC GGTCCCTGGT GCCAAAAGG TTGGGGAAGT GCTGGTCGGT 120
ACAAAAGTAA TTGTGGTTTT TGCACNGTTG GAATTTGTCA TNTGATATTG GAATACATT 180
TTAAATAAAT GTGGTTATGT TATACATCAA A 211

SEQ ID NO:1623

LENGTH:212

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01838

SEQUENCE DESCRIPTION:

GATCAGCGAG GTTCTCCAGG ACCTTAGGTT TGATGCGGAA TCTGCCGAGT GATGGCGGCT 60
CCCCAGGGAT GCCGCCGAGG GAGATGGGAA ACGGGGCGGA TGGCGCCCAG CCCAGCCCTA 120
ACTGCCAGCT GGCTGGGGTC GCGCCCCACT GCGCTGCTGA CCTTCCTGCA GTTCCAGACA 180
CCTCCCACAA TAAAGAGCTC CTCCTCTGTA AA 212

SEQ ID NO:1624

LENGTH:208

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01839

SEQUENCE DESCRIPTION:

GATCTATGAC AATGTATAGT CAATAAATGA TAGCAATTAT TTTTAATTAT CAAAATAAAT 60
TGTTAGAGAT TCAAGTTAGC ATACAAAATG GAAATACATT GACAATCTAA AACTATACT 120
AAACATAAA CTCAAGACTT TATTCCTCTT CCTGTTCTAT CAAAATTGTG CCAAGTAAAA 180
AANTAAAANT TGTTCTTTTT ATTTCAAA 208

SEQ ID NO:1625

LENGTH:210

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01840

SEQUENCE DESCRIPTION:

GATCTAGATG GCAGATAGGA ACTTNTTGT CACAAAAATA CTGGAGGAAA ATNTTGTA 60
AATAGACTTT TGGACACACA GCTGTTGGGG CTGCACTGAG CTGCAATTTT TAACATGGAT 120
TTATAACTTA ATGTTTCTGT TTATAAATA CTAATGATT GCAATGTATT TTAATGGCCA 180
ATTAAACAG ATGTTTATT CTTTCTGAAA 210

SEQ ID NO:1626

LENGTH:208

00707

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01841

SEQUENCE DESCRIPTION:

GATCCAGGAT TCTGGGAGGC TTCAGTTACC GCTGGCCGAG CTGAAGAACT GGGTATGAGG 60
CTGGGNCGGG GCTGGAGGTG GCGCCCCCTG GTGGGACAAC AAAGAGGACA CCATTTTCC 120
AGAGCTGCAG AGAGCACCTG GTGGGGAGGA AGAAGTGTA CTCACCAGCC TCTGCTCTTA 180
TCTTTGTAAT AAATGTAAA GCCAGAAA 208

SEQ ID NO:1627

LENGTH:203

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01842

SEQUENCE DESCRIPTION:

GATCTCACAG CCACGAATTT AGAACTTCCT CCTATAGCAT TTTCTATCTT TTTTATGGCA 60
TTTATTTTAT TCTATCTTGT TATGATTACA TAATCTGTTT AATCCCCAAT TATATATTGT 120
AAATACCTTG AAGGAAAGGA GTCTTTATTA TCTTTGGTGC CTGGTGTTTA GTTTAATAT 180
TTTATTAAAT ACATCCAAGG AAA 203

SEQ ID NO:1628

LENGTH:203

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01843

SEQUENCE DESCRIPTION:

GATCCACTGT TCAATCTGCA CAAGATTNGG GNNCCAGACA TGGGAGACTT CAGCTGCCTC 60
AGAGGACCGT GGACAGGGAA GGCAGCCTCG CATCCCTCTG TCCATGCCTG GNNTGACTTT 120
AATAACCAAG AGTTTTATTT TTGAATTTGT AGCTGTCGTT CACTTTTTAC CCACCCATTC 180
AATAAACCTT ACAGAATTGC AAA 203

SEQ ID NO:1629

LENGTH:201

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01844

SEQUENCE DESCRIPTION:

GATCCAAGTA ACAGTGACTG CAGTTAGGGT CGAGAGCTTC TCCGAAGCAG CGGTCATGCA 60
GGCTTTTGTG TGGCTGACGC TTCCCTTTT CACAACAGTA AAAAGCTATC AATGGGAAAT 120
TGTGGACTTT TCCACCAGG GACTCAATGG GGA CTCAATG TGCAATATTC AGTCAACATA 180
AAACTCTTTA AGAACTCCAA A 201

SEQ ID NO:1630

LENGTH:201

TYPE:nucleic acid

2153480

TOPOLOGY:linear

CLONE:HUMGS01845

SEQUENCE DESCRIPTION:

GATCACAGAC CACGAGTGCC TTTCCCGGAC CTGGACGTG CCTCCAGAGC AGGCACCANC 60
TCTTTCCCTC TCTAGACAGA AATATTTTGT TAAGGTTCTG GGCAGGGAG GGAGCATGAA 120
GTACGAGGAA AACTTGAATT CCAGATTTN AATGCAAAGT ATTTATCATT TCTACCAGAA 180
ATAAACGTTT TAAGTTTAA A 201

SEQ ID NO:1631

LENGTH:217

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01846

SEQUENCE DESCRIPTION:

GATCTTGAGG TCACTTCGTT TAGGTCATTN TCTCAACCCA ACCTCCCCAA ACTCTGGTTT 60
GAGCCAATAT GTGTTCTATT GTTCTCAGAG CACCAGCCGA CTGTACAACA ATTGTTATAA 120
AAATGTTTAT TGTTTACCAA AACCAGTGGA CCTCTTATCA AATGCTGCTT GGTAACAAAA 180
TCTATCACAG TTTTAATAAA AAGAAAAAAA AAGGAAA 217

SEQ ID NO:1632

LENGTH:200

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01847

SEQUENCE DESCRIPTION:

GATCTGTTTT NNTAAACAC TAACAGAATA ATTCTTTATA AATAGGTAAG CCTTACACTT 60
GTAAAGAAA TTTACCTCTA ATTTAGTCT CACTAATGTA AAATACTGGG ACTTAAGTAT 120
ACAATTCAGT CACTAAGTGT ACAGTTTAT GTGGGGAACA ATTCATGCAG GCTACTGGAA 180
AATTAAATCT TATTACCAA 200

SEQ ID NO:1633

LENGTH:200

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01848

SEQUENCE DESCRIPTION:

GATCCNGGGC ATTNCTCTG GGGAGACAGG CCTGAGGCCA GCTCGGNAGC CAAGCAGATT 60
CCAAACCACT ACAACCCTTG CCAAACACAG CCCACTCCAT TTANACCGC CTCCTGAGG 120
AGAAAATGCA GACTCAGGGT TCCAGTAACC AGTGATGGAT TCACCCCATC TCCCAAATAA 180
TGTTTACTT GTTTTACAAA 200

SEQ ID NO:1634

LENGTH:333

TYPE:nucleic acid

TOPOLOGY:linear

00709

CLONE:HUMGS01849

SEQUENCE DESCRIPTION:

GATCTTCTAA GAATTTTGCA AAATTCTAAA CAAATATAGA GATGGTATAT AGAATTCATA 60
 TCTAGAAAAC TTTGATTTTA ATGTGAGCTT ATCAAATTTG TNCTGGCTTT TTTGGCACTA 120
 AGGCAAAAAC ATGTTAACCA GAAATAATTT ATTCTTCATG TATGTAAAT ATTTGAGAAT 180
 GTTAGCCTT TTATTAGAAT TTTATTTGGA AAATATTTAT CTTTCTACAC ATTTTACACT 240
 TATGTNCCTT TGCTTATAAC CCAATTTCTT AACTTTTTTG TTACTTAAGC AAATATCAAT 300
 NATGTTTTAT TATCTAATAA AGTGAAGAT TCN 333

SEQ ID NO:1635

LENGTH:199

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01850

SEQUENCE DESCRIPTION:

GATCGAATGG CTTTTGCGAG CTAACACTA TGTGTAGACA GGTTTTATAT TATAAAGTAT 60
 GCATTCTTAT CACCTAGTAT ATAGTTAGTT TGTAGAGTGA TTTCCCCCA GTTCTTGAA 120
 CATGGTATCT TCACATCTTG GACCTTGGTC AGTTGTGCTA TTCATTATTA AACACTAAAA 180
 CTTTGCGCGT TCTTGCAA 199

SEQ ID NO:1636

LENGTH:196

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01851

SEQUENCE DESCRIPTION:

GATCTGGATG TTGAAAAGAG TCTGGCACCT CCTCCNTCTC TCTTGCTCAC ACTCTCACCA 60
 CGTGATATGC TGCCTCCTCC TGTGCCTTCC ACCATGAGTA NAAGCTTCCT TANNCTCTTN 120
 TNAGAAGCAG ATGCTGGCAG CATGATTCTT GTACAGTCTG CAGAACAGTG AGCCAAATAA 180
 ACCTCTTTTC TCTAAA 196

SEQ ID NO:1637

LENGTH:196

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01852

SEQUENCE DESCRIPTION:

GATCCAAGTA TTTCTNCATC AAGCAGTTTT TAAAAGGAAA ACGATAATAA TCAGTAGGCT 60
 CCATGGAAGC CTTTNCCTTA ATAGCTATGT GCCAAATACT TTNATCTNGT GTGACAGTCA 120
 TGTCAGAGTG AAATCTCTCA GGAAAAGTGT AACTAGTAGT TACAAAGTAA ATAAAGGATT 180
 TCATTTTAAG GTGAAA 196

SEQ ID NO:1638

LENGTH:195

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01853

SEQUENCE DESCRIPTION:

GATCCTCCTG CAGGGCTAGG CGGATTGTC TGGATTTCCT TTTGTTTTTC CTTTtagTTT 60
TCCATCTTTT CCCTCCCTGG TGCTCATTGG AATCTGAGTA GAGTCTGGGG GAGGGTCCCC 120
ACCTTCCTGT ACCTCCTCCC CACAGCTTGC TTTGTTGTA CCGTCTTTCA ATAAAAAGAA 180
GCTGTTTGGT CTAAG 195

SEQ ID NO:1639

LENGTH:194

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01854

SEQUENCE DESCRIPTION:

GATCTTAGCT TTGATAATG ACTGANGCTG GAGAAGCCGT GGTGAAGTC AGCCTACACT 60
ACAGTGCACA GTTGAGGAGC CAGAGACTTC TTAAATCATC CTTAGAACCG TGACCATAGC 120
AGTATATATT TCCCTCTTGG AACAAAAAAC TATTTTCCT GTATTTTAC CATATAAAGT 180
ATTTAAAAAA CAAA 194

SEQ ID NO:1640

LENGTH:268

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01855

SEQUENCE DESCRIPTION:

GATCTGAGTA ATTAGCAGGT ATGATGCTGG GACTGGAAAA TAGAAAGTAA TAACTAAAGG 60
GTAAATGTGC AACGTTATTT TTTGGCCTTG TTCATAATTT TATGTTTTCA GTGGCNTGTG 120
TACATATAGA ATTGTTAAAG TTGTCATTTC CAATATTTAT ATTAGAAAAA TTATTTAGAT 180
ACTTTATAAT TTTAACCGGC ATTTTAAATA ATGACACTTG CATTTATTGT ATTGTAATAA 240
ATTTCACTTT TAACTTTAAA AGTTTAAA 268

SEQ ID NO:1641

LENGTH:193

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01856

SEQUENCE DESCRIPTION:

GATCTCTGCT CAGAGAAAGTG CAGGGGGAGC CTTCCAGCTC ACTCTCCCTG AGGACTGGCT 60
TGACAGGGGC TATGGGTTTG CTTTGGTGTT GTTTTAAAA AAAGAAAATA TATTTTTTTG 120
AAAAAACGAC TGCCCATCCC GGGTCCTTC CCTGATGGGT TGGGGCAGTT ACCTGGTTGC 180
TGTTTTAATT AAA 193

SEQ ID NO:1642

LENGTH:193

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01857

SEQUENCE DESCRIPTION:

GATCACATCA CTCCACCCCT GCCAGGCCCC AGGTTAGGAA TAGTGGTGGG AGGAAGGGGA 60
AAGGGCTGGG CCTCACCGCT CCCAGCAACT GAAAGGACAA CACTATCTGG AGCCACCCAC 120
TGAAAGGGCT GCAGGCATGG GCTGTACCCA AGCTGATTTC TCATCTGGTC AATAAAGCTG 180
TTTAGACCAG AAA 193

SEQ ID NO:1643

LENGTH:193

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01858

SEQUENCE DESCRIPTION:

GATCCTTAGT ACAACATGTG AAAGAAGATA TGTTGTCTTT ACTCACAGTG GAGGCATTTT 60
TCTAGCTGTG TTGATTTGG CTTCCCTATA GATTCAGGAC CCATAACTCT TGTCTCACT 120
CATCTGCTAT GCTGCTGATA AGGACTTTCA GGTCAACAGC TGTAAGTCT AAATGAAGTT 180
AATACTCTGG AAA 193

SEQ ID NO:1644

LENGTH:192

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01859

SEQUENCE DESCRIPTION:

GATCTAGGCA AACCTTTATA AAGTTGCAGT ACCTAATCTG TTATTCACAC TTCTCTGTTA 60
TTTTTGTGTG TCTTTTAA TATATAATAT ATATCAAGAT TTTCAAATTA TTTAGAAGCA 120
GATTTNCCTG TAGAAAACT AATTTNCTG CCTTTTACCA AAAATAAACT CTTGGGGGAA 180
GAAAAGTGGA AA 192

SEQ ID NO:1645

LENGTH:188

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01860

SEQUENCE DESCRIPTION:

GATCTGTCTG TTGCTTGTTT AATATATTTT TTTTATGACA TTAAGTAAAG TTTAAAAGGG 60
TTTTNTATCC ACTGTCAATT TCAATTGGAT AACATTTTGT CAAGNTTTTT TTTCTCTGAT 120
TATTTGATGC TAGCTGGAAT TCAAGAAATG GCATTGACCT TATTCAAATA AAGAAATATT 180
TTAGTAAA 188

SEQ ID NO:1646

LENGTH:190

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01861

SEQUENCE DESCRIPTION:

GATCAAAAAC TAATTGGGA TATGTATGGG TAGGGTAAAT CAGTAAGAGG TGTATTGG 60
 AACCTTGTTT TGGACAGTTT ACCAGTTGCC TTTTATCCCA AAGTTGTTGT AACCTGCTGT 120
 GATACGATGC TTCAAGAGAA AATGCGGTTA TAAAAAATGG TTCAGAATTA AACTTTTAAT 180
 TCATTGCGAAA 190

SEQ ID NO:1647

LENGTH:183

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01862

SEQUENCE DESCRIPTION:

GATCAGTTGG GTGCTATGTG CTCAGCTTTC CTACTGCAGC TTCATTTAAT GCAGAGTGGT 60
 GTTTGAATTT GGCTTAGATG GGCTGGCAGG CATGATTTTA AAAATGTAA TCATCAGTAA 120
 GAAGTACTTC CATGTAAAG ATGCAAAAAA AAAAGTCTTC ATTAATAATN CTATTTAANG 180
 AAA 183

SEQ ID NO:1648

LENGTH:361

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01863

SEQUENCE DESCRIPTION:

GATCCAAACA AATACACATT CTGTNTTTTA GCTCAGTGTT TTCTAAAAAA AGAAACTGCC 60
 ACACAGCAAA AAATTGTTTA CTTTGTTGGA CAAACCAAT CAGTTCTCAA AAAATNACCG 120
 GTGCTTATAA AAAGTTATAA ATATCGAGTA GCTCTAAAAC AAACCACCTG ACCAAGAGGG 180
 AAGTGAGCTT GTGCTTAGTA TTTACATTGG ATGCCAGTTT TGTAATCACT GACTTATGTG 240
 CAAACTGGTG CAGAAATTCT ATAAACTCTT TGCTGTTTTT GATACCTGCT TTTNGTTTCA 300
 TTTTGTTTTG TTTTGTAATA ATGGTAAANC TTCAGAAAAT AAAATGTCAG TGTGNNTAA 360
 A 361

SEQ ID NO:1649

LENGTH:183

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01864

SEQUENCE DESCRIPTION:

GATCAGGACC TGGGGGCCTA CAGTTCTGCC AGGAAGTGCC TGGCCAAACA GAGGCAGAGG 60
 ATGCTGCAAG AGAGAAAAGC TGCAAAANAG GCCGCCGCTG CCACCTCCTG AGGCAGNTGT 120
 GGGTGCCCCCT GCTGTGTGGC TCTGTATGAC TGTGCTGAA ATATAAGCC CTGCAACCTG 180
 AAA 183

SEQ ID NO:1650

LENGTH:178

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01865

SEQUENCE DESCRIPTION:

GATCTCAGCA CAAGCAGGGG AGCAGCTGGG GGAACACAGC TTTATGTAAT TACCTCTGTT 60
CAATATTTAG CAAGTTGCAT TGTAACATTG TAACTGTTTG TTTCTCCTTG GATGATGAGC 120
TACCCCAAG AAGGGGTCAT ATCAGATTGG GTCTCATTAA AATGTCTGAT GAATGAAA 178

SEQ ID NO:1651

LENGTH:178

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01866

SEQUENCE DESCRIPTION:

GATCTATGGC TTAAAAAATT TGTTTCTGTG ACAATNTTTG TAAATCTAGC CAATAGAGTC 60
ATTTACAGAA GAAAAATNAG CATGTAATAA TACAAGAACT GTTCCCCCT CAAAACCTGA 120
ACCTGAATTA TTTGTAAAAA CTGAAATTTA ATGATTAAAG AGAAGCCAGA ATTGTAAA 178

SEQ ID NO:1652

LENGTH:189

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01867

SEQUENCE DESCRIPTION:

GATCTGGAGC TAATAATGAC TGAGATGGAG ATATCTCGAG CAGCAGCAGA ACGCAGTTTG 60
CGGGAACACA TGGGCAACGT GGTAGAGGCG CTTATTGCCC TAACCAACTG ATGCGTGCTT 120
TCTCAAATAT ACCTACTGGA TTAATTTATG GCAATAAAAT TTTTTTTTGT CTTTTTCAGT 180
TTTATCAAA 189

SEQ ID NO:1653

LENGTH:174

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01868

SEQUENCE DESCRIPTION:

GATCTCTGCT CTGCCCTCTC CCAGATTGGT GGGGAGGGAG GCGGGGAGGT AGATATAGGC 60
CTGTCCTTTT TAGCAATGTG ATTCTTGTG TTGATTCTCT CTCTGGAGTT CATGTGCTGC 120
CTCANNNGAC TCTGATTTTA TATTTNAGAA AAATAAAGGC GTTCAATCTG CAAA 174

SEQ ID NO:1654

LENGTH:173

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01869

SEQUENCE DESCRIPTION:

GATCAGGCTC ATCTCATCTG CACCAACTGC TCTACCTGTT AGATGGAGAC CTTGCNTCAT 60
 GAATTTCTCG AAATGCTCCT GGAACCTATT TATATGCCTC AAAATCCTCT AAATCATT 120
 ATAGTAACCC ATAGTTTAA TTTTATAAAT AAACGTATTT ATTAAATCTT AAA 173

SEQ ID NO:1655

LENGTH:172

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01870

SEQUENCE DESCRIPTION:

GATCTCTAAT TTAAAGAAAC AGTTTTTATA TACCTAGAAT GAAGATTCTG TTAAAGCGG 60
 TTTTGGTTAA CTTGGTTCTT GACATTTGCC TAAATNTTN TTGGATTGGG ACTAAAATGT 120
 NCTATTAGCC AATGAATAAC GTCCAAGTAA ATTTNTGTTT TATTTGGGA AA 172

SEQ ID NO:1656

LENGTH:171

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01871

SEQUENCE DESCRIPTION:

GATCTCAAAG GAGTCTGAAA TATCATATTT CTGTGTGTGT CTCTCTCAGC CCCTGCCAG 60
 GCTAGAGGGA AACAGCTACT GATAATCGAA AACTGCTGTT TGTGGCAGGA ACCCCTGGCT 120
 GTGCAATAA ATGGGGCTGA GGCCCTGTG TGATATTGAA AGGTAAGAA A 171

SEQ ID NO:1657

LENGTH:171

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01872

SEQUENCE DESCRIPTION:

GATCGNCATT ATCCCCAGNA AAAAGCTCCG CAACAAGATA GCAGNTAATG TCACGCATCT 60
 GATGAAGCGA ATTCAGAGAG GCCCAGTAAG AGGTATCTCC ATCAAGCTGA NCGAGGAGGA 120
 GAGAGAAAGG AGAGACAATT ATGTTCTGA GGTCTCAGCC TTGGNNCCNN N 171

SEQ ID NO:1658

LENGTH:171

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01873

SEQUENCE DESCRIPTION:

GATCAAAGAC ATCTCATCC AGTATGACCG GACCNCTGG TAGCTGACCC TCGTCGNTGC 60
 GAGTCAAAA AGTTNGGAGT CCTGTGCCG AGTTCGTACC AGAATCCACC GTAAGCCATC 120
 GGNCTAAAAC TTAATTNATA ATAACAGTTT TGAGGGATT AAAAGTTCAA A 171

SEQ ID NO:1659

LENGTH:170

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01874

SEQUENCE DESCRIPTION:

GATCAAAAAT CCAAGGAGAA TGGTGCCAGT GTATGATAAA ATCCATGTAG TGATGAGGAA 60
TGGTGTTAAA TAATGTAATA TATAANANTC ATGATATANG ANTGTTTGAA GGTGATGCAT 120
GTTTGATTTT NGTAGTATAA NTGTATTNA GTTCAAATGA TGTATAANGN 170

SEQ ID NO:1660

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01875

SEQUENCE DESCRIPTION:

GATCCTCGCT CCGTTGCACG GGCGCCNTAA GTTATTGGAC TATCTAATAT CTATGTATTT 60
ATNTCGCTGG TTCTTTGTAG TCACATATTT AATAGTCTTA ATATCTTGTT TTTGCATCAC 120
TGTGCCCAT GCAAATAAAT CACTTGGCCA GTTGCTTTT CTACAAA 167

SEQ ID NO:1661

LENGTH:167

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01876

SEQUENCE DESCRIPTION:

GATCTGGGCG ATTCTGAAGC CATGCCATTT TTAACCTTAT GTCTGCTAGA AAGTGTGTA 60
GTTGATTGAC CAAACAGTT CATAAGGGGA ATTTTTTTTA AAAACAACA AAAAAAAAAAC 120
CATCCAAGGN NGGGTTTNG ATTAATTTT GTGGNGTTAC CAGTAAA 167

SEQ ID NO:1662

LENGTH:165

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01877

SEQUENCE DESCRIPTION:

GATCTTCCCC AAGAGGGACT GGGGTTTCTG GGGTCCATTC TCTGAGTCAG TGGTTATTTG 60
AAAATTTGAT TTTGATTTTA TTTTCTCT GTAACTTCC AAGCTGGCTT TTCCCATTTT 120
AATCCTGTG ATTTATGCCA ATAAAGTTT CCCATGATTT TCAAA 165

SEQ ID NO:1663

LENGTH:165

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01878

SEQUENCE DESCRIPTION:

GATCCCTNCC TTGGTGGGCA GTTCTGCCTT CCAAGGAAGA AGGGGAAGAA AAGGACCTGT 60
 GGGTGGCTCA GGNCAAGCA GACCCCGGGC TCCACCCAG CCCCNCAG GNTGCTGCA 120
 GTNCACACTT TTCAAATTT AATATAAAGC AAGTCCAGTN TAAA 165

SEQ ID NO:1664

LENGTH:161

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01880

SEQUENCE DESCRIPTION:

GATCAGGCTG CTGAGGGAAT AAATTTAATC AAGGTCTTTG CAAAAACAGA AGCACAGAAG 60
 GGAGCCTATA TAGAACTAAC ACTGCAGACT TATCAAGAAG CACTCAGTCG CCATTCTGCA 120
 GCTTCCTAAA AATATTTTAA AAATACATTT ATTTTACTAA A 161

SEQ ID NO:1665

LENGTH:158

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01881

SEQUENCE DESCRIPTION:

GATCAGTCCA TCCCAGAGGG ACCGGAGTTA TGACAAGCTT TCCAAATATT TTGCTTTATC 60
 AGCCGATATC AACACTTGTA TCTGGCCTCT GTGCCCCAGC AGTGCCTTGT GCAATGTGAA 120
 TGTGCGCGTC TCTGCTAAAC CACCATTTTA TTTGGAAA 158

SEQ ID NO:1666

LENGTH:158

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01882

SEQUENCE DESCRIPTION:

GATCGTGTAT TGAGATTCT TAAATAATGC TTCAGATATT ATTGCTTTAT TGCTTTTTTG 60
 TATTGGTTAA AACTGTACAT TAAAATTGC TATGTTACTA TTTNTACAA TTAATAGTTT 120
 GTCTATTTTA AAATAAATTA GTTGTTAAGA GTCTTAAA 158

SEQ ID NO:1667

LENGTH:155

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01883

SEQUENCE DESCRIPTION:

GATCTTTGTT AGTTGCATAT TATATTCAG TGTTTATCTT CTTGGTGAAT TGACCCTTTT 60
 ATCATATGT AATCCCCTA TATTATATC TTTATATTA ANATAGGTTT CCTTAACATT 120
 TGAGAAGTAA AANTAAAATA AAATGTAATA GCAA 155

SEQ ID NO:1668

LENGTH:155

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01884

SEQUENCE DESCRIPTION:

GATCACTCTG GGCTCACTTG CCTGCCTAAT GGTCATCTCC CCAGTAGACT GTAAGCTCCT 60
TGAGGGCAAG GATTGTGTTG GAATTTTGT ATTAACAGTG CCTGGCTTGG TGCCTGGCAC 120
CTAGAAAGCA CTCAATAAAT GTTTGTTTAA TGAAA 155

SEQ ID NO:1669

LENGTH:161

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01885

SEQUENCE DESCRIPTION:

GATCAGATGC TTGAAATTTA ACACTTTCA CTTGGTTCTT ATACTGAATG CCGACTCTGC 60
TCTGTGTTAG AGATATGAAA TGGTGTGTTGA TACTGTTGA GACATTATGG AGAGATTTAA 120
TTATTTGTAA TAAANGNTT GCTGCAGTCT GAAAACTGAA A 161

SEQ ID NO:1670

LENGTH:153

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01886

SEQUENCE DESCRIPTION:

GATCTATTGT AATGTGTTAT TTNGGCTGAN GTATGTNAAG AAAATACTAC CTTACAAAGN 60
TATGTATTNT CAAAAGGAAA TACATATCAG AAAGTTTAAC AGGGCCAGTG GGTGATACTG 120
AAGTTGTCGG GATGGATGGT GTCTATCTGG NNN 153

SEQ ID NO:1671

LENGTH:444

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01887

SEQUENCE DESCRIPTION:

GATCTAGAAG TTTTACTTTT ATAAAGATGG TGTCCGGAAG ATGTTGCTAA TGTATTTTAC 60
TTCAACATAG GGAACAACT TTTTAAGTAT ATTAATAAAC CTGTATGGTT AGTTTTTAAC 120
AGTTTTTTAA AATAAACTAT GGATATGACA AATATTCTGT GTTTTACTAA GTGCTTGGAT 180
AGGCTTTCTA ATTTNGTATA CGTGCTAGAG TTAATTATTG ANCATTTTAA TCCAAATTAA 240
GTTGTAACCTC TGTTTATACT ACTGATTGCT CATTCGTTTA AATGATATTN TNNNGTAAAA 300
GTCATAACCA ACATATGANC AGACAGATTT ATGTCTTTAA ACACAGATTG TNAGCTATAG 360
GTTTAATCTG ATACCAGTTG CTGGAAGGTT GCCATTTGGT TTTTCTNAAA ACCTATACCN 420
CTAAAACTTT CTTTNAAGGT TAAA 444

SEQ ID NO:1672

LENGTH:151

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01888

SEQUENCE DESCRIPTION:

GATCAGCAGC CCTCGCAATG TGCTCAGCGA GTACCAGCAG AGGCCGCAGC GGCTGGTGAG 60
CTACTTCATC AAGAAGAACT GAGCAAGGCC TGAGCGCTGC CTGAACTCCG AAGNCCTGTG 120
TGATGCTTTC CATTAAAAAN NATTGTCCAA A 151

SEQ ID NO:1673

LENGTH:150

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01889

SEQUENCE DESCRIPTION:

GATCCAGATG ATAAACCAGT GAACTATGTC AAAAGCACTC TCAATATTAC ATTTGACAAA 60
AAGTTTTGTA CTTTNCACAT AGCTTGTTGC CCCGTAAAAG GGTTAACAGC ACAATTTTTT 120
AAAAATAAAT TAAGANGTAT TTATNGGAAA 150

SEQ ID NO:1674

LENGTH:148

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01890

SEQUENCE DESCRIPTION:

GATCCGNCCG TCTCTGCCTT CCAAAGTGCT GGGATTACAG GCGTGAGCAC ATCTGCCCGG 60
CTTATTTTTT TTTATGTTTT TNCTTCGTAA GAGGTTCTGT TGAGCAGTGA TTTGCAACTC 120
TTGCTGACGT TGCTGGGGAA GCTTTAAA 148

SEQ ID NO:1675

LENGTH:568

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01891

SEQUENCE DESCRIPTION:

GATCTACCCC AGGGAGAATC TGAGACATCT TGCCTACTTT TCTTTATTAG CTTTCTCCTC 60
ATTCATTTCT TTTATACCTT TCCTTTTTGG GGAGTTGTTA TGCCATGATT TTTGGTATTT 120
ATGTAAAAGG ATTATTACTA ATTCTATTTT TCTATGTTTA TTCTAGTTAA GGAAATGTTG 180
AGGGCAAGCC ACCAAATTAC CTAGGCTGAG GTTAGAGAGA TTGGCCAGCA AAAACTGTGG 240
GAAGATGAAC TTTGTCATTA TGATTTTATT ATCACATGAT TATAGAAGGC TGTCTTAGTG 300
CAAAAAACAT ACTTACATTT CAGACATATC CAAAGGGAAT ACTCACATTT TGTTAAGAAG 360
TTGAAGTATG ACTGGAGTAA ACCATGTATT CCCTTATCTT TTTACTTTTT TCTGTGACAT 420
TTATGGTCTC ATGTAATTTG CATTACTCTG GTGGATTGTN CTAGTACTGT ATTGGGCTTC 480
TCGGTAATAG GTTATTTCCA TATACTATAA TTGGNAATAT TTTTGTACCA ATGGTTATAA 540
CNCTAGGGGT NTAAAAACCA GGTTCTGN 568

SEQ ID NO:1676

LENGTH:146

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01892

SEQUENCE DESCRIPTION:

GATCTCTAAG GTATTATGTT TGCCTTCTCT TAGTTATTTT TGGGTTGTCA CAAAGCTCAG 60
TATCATGGTT TGACAGAAGC AGTTATGTGA ACTTTTATGT TAGGACATTA CTAAATAAAG 120
AATTCCTAG CTGCTTATAA AGTAAA 146

SEQ ID NO:1677

LENGTH:144

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01893

SEQUENCE DESCRIPTION:

GATCCATTCT CCNTTTANTT CCCCCACCCT CCTCTCTNGG ATATGGTTGG NTTGGCTCA 60
TTTACAATC AGCCCAAGGC TGGGAAAGCT GGAATGGGAT GGGAACCCCT CCGCCGTGCA 120
TCTNAATTTN AGGGGTCATG CNCN 144

SEQ ID NO:1678

LENGTH:151

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01895

SEQUENCE DESCRIPTION:

GATCGAGATG AGCTTTAAAA ACTTGAAAAA CAGTTTGTA GCCTTTCAAC AGCAGCATCA 60
ACCTACGTGG TGGAATAGT AAACCTATAT TTCATAATT CTATGTGTAT TTTATTTTG 120
AATAAACAGA AAGAAATTTT GGGTTTTTAA A 151

SEQ ID NO:1679

LENGTH:140

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01896

SEQUENCE DESCRIPTION:

GATCTTGATG GTCGCTGCAG AGTAACTTCA GCGCTGAGTT CGTTTGAAAC CTCGGTTTG 60
TTAAGATTCA GAATAACCAA TTGCTTTGTC TGTTAAATCT CCCGATTCT GTTAGGAAAA 120
TAAAAGCCTC ATTTCTTAAA 140

SEQ ID NO:1680

LENGTH:139

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01897

SEQUENCE DESCRIPTION:

GATCACTATG TAGGCAATGC TGGATACTGG NCTGTTATTT ACACATTGT ATCACCTTTT 60
ATTCATAAG ATAGCATTGT CAGANTAATT TAGTATTTCACATAATCAA CAAGTAAAT 120
AAAATTAATG AGAATGAAA 139

SEQ ID NO:1681

LENGTH:139

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01898

SEQUENCE DESCRIPTION:

GATCTCCACA TTCAGGTTTC CTGATGCACT TTNCGACTCT TTGGGCAACC TCTGGACTCC 60
TTGTNCCCAG GGTCCACATT TAGTTTTATC TTTACTGCAT TGCTTTTATG AAAAAGAATA 120
AAATTGGATG AAACAGAAA 139

SEQ ID NO:1682

LENGTH:143

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01899

SEQUENCE DESCRIPTION:

GATCAGTTAA TTTGTATGTA GCAGTGTATG CTCTCATATA CAATNACTGA CCTATGCTCT 60
AAAACATGAA TGCTTTGTGA CAGACCCAAG CTGTCCATTT CTGTGATGGG TTTTGAATAA 120
AGTATTCCTT GTCTTAAATG AAA 143

SEQ ID NO:1683

LENGTH:136

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01900

SEQUENCE DESCRIPTION:

GATCGAATCA CCTGAATGTT CTATGTANTG TAAAATATTC TTTTCTTGCT TTCTTGTGTT 60
AAGGTATATA TTCTATTTGT ATGGAATTCT TATTCAAATA CAGTTCTATT AAAGAGTATA 120
CTCCTATTGG ATGAAA 136

SEQ ID NO:1684

LENGTH:136

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01901

SEQUENCE DESCRIPTION:

GATCTCAGCG GCATTAAGCT GTGCCTGAGC GAGTTTGTAG TGACTCACTG CACAGCACCN 60
CCAGACTAGC ATGTGGTTCT ATATTTGTAA AGTTATTGGG ATAAGAAACA ATTAAACAGT 120
TTGTAGTAAA CACAAA 136

SEQ ID NO:1685

LENGTH:136

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01902

SEQUENCE DESCRIPTION:

GATCTTCTAC TTCCCTNTGG GGAGGGGAGT GACAGGTCCA CACACCACAC TGGGTCACCC 60
TGTCTGGAT GCCTCTGAAG AGAGGGACAG ACCGTCAGAA ACTGGAGAGT TTCTATTAAA 120
GGTCATTAA ACCAAA 136

SEQ ID NO:1686

LENGTH:135

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01903

SEQUENCE DESCRIPTION:

GATCTTTAAA AAAATTTTCC ATATGTCAA GTGTAGAGAT GTTCTAGCA GCATTTATCT 60
TGTCTCTAT AGATTGAACA AAAAGTGGTA GCTGTNAAAT TGTGATTAT AATAAATACA 120
TATTTGGTCT TCAAA 135

SEQ ID NO:1687

LENGTH:135

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01904

SEQUENCE DESCRIPTION:

GATCAGCAGT TCCAGCCCCT ACGCTNGCTG GGGGCGCAAC CACCCCTTCC TTAGGTTGAT 60
GTGCTTGGNA AAGTCCCTC CCCCTCCTC CCCAAGAGAG GAAATAAAAG CCACCTTCGC 120
CCTAGGGCCA AGAAA 135

SEQ ID NO:1688

LENGTH:136

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01905

SEQUENCE DESCRIPTION:

GATCTTCATC TGTAAGCAAG AAGAGAGCAT TAAACCAAG ANCATTGTGG AGAAGATTGA 60
CTTTGACAGT GTGTCCAGCA TCATGGCCTC CTCCCAGTAA CTCAGGTGT TTAATAAAGA 120
TGTGTTGACT CAGAAA 136

SEQ ID NO:1689

LENGTH:134

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01906

SEQUENCE DESCRIPTION:

GATCTTAATG TTTCAAAGGA GTGCAGCCCT TCACAGCCAT CAGATATGAG GGCAGTGTTC 60
TGTCTGGTGT TGTAGCCATC TCAAGAACAA ATCAACAGCA ACAAAGAGA AAGAATAAAT 120
TTTAAAATT TAAA 134

SEQ ID NO:1690

LENGTH:134

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01907

SEQUENCE DESCRIPTION:

GATCTGTGAC CCTGGGCGCT GAAAATGGGA CCCAGGAATC CCCCCGTCA ATATCTTGGC 60
CTCAGATGGC TCCCCAAGGT CATTCAATC TCGGTTGAG CTCATATCTT ATAATAACAC 120
AAAGTAGCCA CAAA 134

SEQ ID NO:1691

LENGTH:134

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01908

SEQUENCE DESCRIPTION:

GATCTCTACT ACCACAAGGA AAATAGTTTA GGAGAAACCA GCTTTTACTG TTTTNAAAA 60
ATTACAGCTT CACCCTGTCA AGTTAACAAG GAATGCCTGT GCCAATAAAA GGTTTCTCCA 120
ACTTGAAGTC TAAA 134

SEQ ID NO:1692

LENGTH:140

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01909

SEQUENCE DESCRIPTION:

GATCAGTGTG GAGGACCCGC CCCAGCGCAC GGCCGGCGTC AAGGTGGAGA CCACTGAGGA 60
CCTGGTGGCC AAGCTGAAGG AGATTGGGCG GATTGAGCC CCTCCAGAG ATGGCAATAA 120
AACTGACTCT CAACATCAA 140

SEQ ID NO:1693

LENGTH:133

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01910

SEQUENCE DESCRIPTION:

GATCTAACCT TTGANGCTT AAAAAAGGAG AAAGAGGGTA GGGGTGGGAA ACTGGCATAC 60
TGTGTGTATA GCACTGCCGA TTGGCTAGGC CACTGTGTCT CTGCTACAAA TTAAAGAAAT 120
CCTAAAAGTT AAA 133

SEQ ID NO:1694

LENGTH:133

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01911

SEQUENCE DESCRIPTION:

GATCGCGAAT AAAAATCAAC AAATGTGAAA GCCCAGAAAA ATATATTCGT ATTTCTGGTT 60
TTGCTGGATT TTTACATTTT TATATAATAA AAATGNTATT TTGAAATAAA GATTATGCTG 120
ACTCAAATGC AAA 133

SEQ ID NO:1695

LENGTH:131

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01912

SEQUENCE DESCRIPTION:

GATCTATTGC AGATATTTGA TGTAGTTTTC TCTTTTAAAT TAATCAGAAA CCCCACTTCC 60
ATTGTATTGT CTGACACATG CTCTCAATAT ATAATAAATG GGAAATGTCG ATTTTCAATA 120
ATAGACTTAA A 131

SEQ ID NO:1696

LENGTH:130

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01913

SEQUENCE DESCRIPTION:

GATCCGCCCG GCTCAGCAGA ATTCAGGCTC CTGTATGCCT CAGCCCCTCG ATATAACTCC 60
ATCGGATTCT AGCAGCCTGG TATTCTAGCA ATAAAACCCA AGGCCTGAGA AACAGGGGCC 120
ATCCTGCAAA 130

SEQ ID NO:1697

LENGTH:130

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01914

SEQUENCE DESCRIPTION:

GATCAGACTG TCACTTTTATA GTTTTCTAT ATAAAGATTA TATAGTTGCA AACAAAGGTT 60
GTGAAATTC CCTTTTGTG TTTTNACTT TTAATTAATA AAAGTACATT GTTTTCATAG 120
CAAACCTAAA 130

SEQ ID NO:1698

LENGTH:130

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01915

SEQUENCE DESCRIPTION:

GATCGAAGCT ACCGTAATGT GTTCTTGAGG TCAACATGTT TTGTGGAAGT CACTGTATTT 60
GCCCCNTTAT GTCAATTACC TATTATAAAC CGAGAGAAAT GGGAAAATTA AAAACCTGTT 120
TTGAATTAAA 130

SEQ ID NO:1699

LENGTH:129

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01916

SEQUENCE DESCRIPTION:

GATCCCTTGT AAACATGAAA TCATTCCATG GATGGCTGCC TTATAATTTT GTCTCTTTCC 60
ACTTTAATTG TGAATGGTTA AAAAAATGCT GTTTCTGAT ATTAAATTTT TATTAGTGCA 120
TACCTTAAA 129

SEQ ID NO:1700

LENGTH:82

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01917

SEQUENCE DESCRIPTION:

GATCTGTACC TAGTACCCCT CCCATCTACT GATTGTTTG TTTTGTAAC CAAACACATT 60
TTCAGATAGA AGGAGCCTTA AA 82

SEQ ID NO:1701

LENGTH:128

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01918

SEQUENCE DESCRIPTION:

GATCCCCTAT TCCCTCCACA ATAACAGAAA CACTCCCAGG GACTCTGGGG AGAGGCTGAG 60
GACAAATACC TGCTGCTACT CCAGAGGACA TTTTITTTAG CAATAAAATT GAGTGTCAAC 120
TATTTAAA 128

SEQ ID NO:1702

LENGTH:137

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01919

SEQUENCE DESCRIPTION:

GATCTACAAT NAAGCCCTCA AGGGCTGAAA ATAAATAGGG AAGATGGAGA CACCCTCTGG 60
GGGTCCTCTC TGAGTCAAAT CCAGTGGTGG GTAATTGTAC AATAAATTTT TTTGGTCAA 120
ATTTAAAAAA AAATAAA 137

SEQ ID NO:1703

LENGTH:128

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01920

SEQUENCE DESCRIPTION:

GATCTGAGGA GGAAATGTGA CGCCGGACGC TTCNTGTNT TTGACCTTTT NAAAGGANGA 60
GGAAGTTCAC CGACANTACC CATCACCCAC AAAAGTCTCA CTTCTTGGA GATTGTGTT 120
AGGCTGNN 128

SEQ ID NO:1704

LENGTH:127

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01921

SEQUENCE DESCRIPTION:

GATCTGGCGT NCTACTATGA GGCTTCTTTT GACCTCATN NTGTGGTNGC CGGCGTAGCC 60
AGACCATCCT ATACTGTGAC TACTTCTACT NGTACATTAC AAAAGTACTC AAGGGAAAGA 120
AGCTCNN 127

SEQ ID NO:1705

LENGTH:146

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01922

SEQUENCE DESCRIPTION:

GATCATAGCT AACTGTATG TTTAGGTGGT GTGAAATNAT TTATAATCAC AGCTTGAAC 60
GTGTTTGCTT GGTACTGTCA TAGTGATTAC AAATTCATG GAATGCGAAG AGCAACAATA 120
AATAAAAAAT ACCACTCACC CTCAAA 146

SEQ ID NO:1706

LENGTH:240

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01923

SEQUENCE DESCRIPTION:

GATCAAAAAG GACTGAACCC CCACTATCAT AATCCATACA TTCATTTCCA TGTTGTTTGA 60
CTAGCAGTGC ATATATGAAT GAATATGGTA ATTAATCTTA CCTATAAGAA CCAAATACTT 120
TAATTATATT AAGATAGTGA ATAAAGATGT ATAATATTTT NATTAATACC TTGAATATAT 180
TCAGTGGATT GAATGTGACT TCATAACTGT ACTACGATTG TATTAATAAATA TTTCTGGAAA 240

SEQ ID NO:1707

LENGTH:124

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01924

SEQUENCE DESCRIPTION:

GATCTTATGA AGGAAGATTT GTGACCCTAC GTATATATAT ACACACACAT ACATATATAT 60
ATATATCCCG AACCAACANC GGGACTTTGT TTATATTGCA AATAAATATT ATTTTCCTT 120
TAAA 124

SEQ ID NO:1708

LENGTH:124

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01925

SEQUENCE DESCRIPTION:

GATCCCCCTT CTCTATGTCG GGACACTCAT TAGCAAGAAC TTTNCTGCTC TACTNGAGGN 60
ACATGACATT TTTGTTCCAG AGGATGATGA TGATGATGAC TAACAGGAAT TACAGAANGN 120
NGAN 124

SEQ ID NO:1709

LENGTH:146

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01926

SEQUENCE DESCRIPTION:

GATCCGAGCA GTCCTCTGCC CGCCTCCCGT GAAGAAGAGG AAGAGAAAAT GCCTGCTGTT 60
GTAAATGTCT CAGCCCCTCG TTCTTGGTCC TGTCCTTGG AACCTTTGTA CGCTTTGCTC 120
AAAAAAAAAC AAAAAAAAAA AAAAAA 146

SEQ ID NO:1710

LENGTH:120

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01927

SEQUENCE DESCRIPTION:

GATCCTGTGT AGAAGCTGTT CTCATTAAAC ACCAAACAGT TAAGTCCATT CTCTGGTACT 60
AGCTACAAAT TCGGTTTCAT ATTCTACTTA ACAATTTAAA TAACTGAAA TATTTCTAAA 120

SEQ ID NO:1711

LENGTH:121

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01928

SEQUENCE DESCRIPTION:

GATCTGCGCC TCTCAGTGCC TTTTGAGGGG TTCCCATCAT CCCTCCCTGA TATTGTATTG 60
AAAATATTAT GCACACTGTT CATGCTTCTA CTAATCAATA AACGCTTTAT TTAAAGCCAA 120
A 121

SEQ ID NO:1712

LENGTH:125

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01929

SEQUENCE DESCRIPTION:

GATCGGGGCA AGAGAAGGCT GAGTACGGAT GGGAACTAT TGTGCACAAG TCTTTCCAGA 60
GGAGTTTCTT AATNAGATAT TTGTATTAT TTCCAGACCA ATAAATTTGT AACTTTGCAG 120
CGAAA 125

SEQ ID NO:1713

LENGTH:338

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01930

SEQUENCE DESCRIPTION:

GATCAGCCCA TCTCAGCTTG CTGTTTCAAT CACAATGGAA ACATATTTGC ATACGCTTCC 60
AGCTACGACT GGTCAAAGGG ACATGAATTT NATAATCCCC AGAAAAAAN TTACATTNC 120
CTGCGTAATG CAGCCGAAGA GCTAAAGCCC AGGAATAAGA AGTAGTGGCT GGAGACTCTG 180
GCTCAGCCAG AGTTGTTTCT CTCCANTCTG CCTCATCTCT GTACGANTTT GGGTCCCAGC 240
CTTGTGGGT TGTCAGCCAT GGACATGGAT TTCAACCCCT GGAGAAAACG NTGTCATTGT 300
TCAGCAGCTG AGNGCCCCAG GCGTCCGNGG CGNCTTTN 338

SEQ ID NO:1714

LENGTH:85

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01931

SEQUENCE DESCRIPTION:

GATCCCATAT CTATTACCGT GTCCATAGGA ATAATAGGTA AGGGCTCTGT CTCTGTCAAG 60
CCATGTAAACA AAGGACACTG TTAAA 85

SEQ ID NO:1715

LENGTH:260

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01932

SEQUENCE DESCRIPTION:

GATCCAGCCC TGGTTCTGGC TGTGGTCAGC AGATGCCAGT NAAGGGTTTT GTGTGTTTAG 60
GCCTCATTTT TTTGTCTTTT TCCTACTCCG TTCCTGGCAT TTGCTGATTT CTAGTGATATA 120
CTCTGTAGTC TCAGTTCGTG TTTGATTCCA TTCCATGGAA ATAAAAAGTA TGTGTACAT 180
ACTGCCGAAG AATTGTCTTG CAAGTNAAGG CTTCCCCCTT TACTATAAGA CTATAAATAA 240
AANCTTATTT NATCCNAAA 260

SEQ ID NO:1716

LENGTH:430

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01933

SEQUENCE DESCRIPTION:

```
GATCTTGTC TGTGCTATCC GCAGAACCGC GAGATGGTCT AGAGTCAGCT TACATCCCTG 60
AGCAGGAAAG TTTACCCATG AAGATTGGTG GGATTTTTTG TTTGTTTGT TTNNTTTGTT 120
TGTTGTTTGT TGTTTGTTTT TTTGCCACTA ATTTTAGTAT TCATTCTGCA TTGCTAGATA 180
AAAGCTGAAG TTACTTTATG TTTGTCTTTT AATGCTTCAT TCAATATTGA CATTGTAGT 240
TGAGCGGGGG GTTTGGTTTG CTTTGGTTTA TATTTTNCA GTTGTGTTT TTTGCTTGTN 300
ATATTAAGCA GAAATCCTGC AATGAAAGGT ACTATATTG CTAGACTCTA GACAAGATAT 360
TGTACATAAA AGAATTTTTT TGNCTTTAAA TAGATACAAA TGTCTANCAC CTTTAATCAA 420
GTTGTACCTN 430
```

SEQ ID NO:1717

LENGTH:171

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01934

SEQUENCE DESCRIPTION:

```
GATCGAGCCA CTGCGCTCCG GCCTGGGTGA CAGGAGACTC CATCTCAAAA AATAAAATTA 60
AAAAAAAAAC TACTACAATA AATTATCACC TTGGACTGTA TAAACAAC TTNAACTAG 120
TCTTTTNAAG AAGTACACTT AAATAAAAT CTAANCATAA GNGANTGTAA A 171
```

SEQ ID NO:1718

LENGTH:115

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01935

SEQUENCE DESCRIPTION:

```
GATCGCTCAG AAAATGGGAA CCCAGGGCAA ATTGTATGTG CTCCTTACTG GGTTTATTAT 60
AAGTGTCACTA TGTTTTTTAT AATAAACAT AGGTGATTTC ACCTTAATGG ACAA 115
```

SEQ ID NO:1719

LENGTH:115

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01936

SEQUENCE DESCRIPTION:

```
GATCCTCCCA CCTCAGCCTC CTGAGTAGCT GGGACCATAG GCTCACAACA CCACACCTGG 60
CAAATTTGAT TTTTTTTTTT TTTCCAGAGA NGGGGTNTTG NANCATTGCC CAGNN 115
```

SEQ ID NO:1720

LENGTH:115

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01937

SEQUENCE DESCRIPTION:

GATCTAGCAC TTTACAAAGT AAGTTTTTCT GTNACTTAGA GCTGAAAATA AAAGCAATGT 60
AGAGTTACGC TTTTATAAGT ATTTNANGTT TCANAAATNA TGCATACAGC AATTN 115

SEQ ID NO:1721

LENGTH:114

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01938

SEQUENCE DESCRIPTION:

GATCATTTAG TTCTATCTAT TTAGAAATAT GTAAACTGG ATTTTTTTTT AAGTAATATG 60
TGACCAAAGT TAATTTTGTC CCAAAGGTCT AAATAAAGAG CAGTTCCCA TAAA 114

SEQ ID NO:1722

LENGTH:119

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01939

SEQUENCE DESCRIPTION:

GATCGCCACA GCCCTTCTTG GAAGAAAGGC GTCTGTGTTT CAGGTTCCAC GCGAGTCACC 60
TCTTTCGTCT TAATGTTTAC CGTCCACAGC TTTGGAATAA ACCATCCTGG GAAGTTAA 119

SEQ ID NO:1723

LENGTH:113

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01940

SEQUENCE DESCRIPTION:

GATCTTTGAC TGTATCATGC ATTGTACAAT TGATTTCATA TTTTATGAAA TGCCTTAATT 60
TTCCTACTAT AACATAAAGA CAATGATGAA TAAAGTTTAT GTGTATGATT AAA 113

SEQ ID NO:1724

LENGTH:113

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01941

SEQUENCE DESCRIPTION:

GATCAGAAAC ATACATACCC TNCCTAGGGA TTTAGAAAGT GGGTTGGCAG TCTTTCCTCA 60
CGTCCATCAC GCANTTGGNA CCTACTNCAG TGTATTGTAA ACTTTTTTCT CNN 113

SEQ ID NO:1725

LENGTH:111

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01943

SEQUENCE DESCRIPTION:

GATCCCAGAG GTCANGACCA AANCCAATCA GTGAAAATTC AACTNTAGCT GTGAAAACAT 60
TGCACTAACA GGAGCTATCC AACAATGGAC CAGAATGTTG ACAATAAAGT N 111

SEQ ID NO:1726

LENGTH:113

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01944

SEQUENCE DESCRIPTION:

GATCCCGCAG GTGGCACGTG ACAGCTAGGG TTCAAAACGT TCTCACCAAA TCCAATGCTC 60
CTCATATATT AATTTTATAA CCAGACAAAT AAATATTAGA GACAACCACC AAA 113

SEQ ID NO:1727

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01945

SEQUENCE DESCRIPTION:

GATCTCAAAA TTCCAGAATT CCCTGTACAT CTNTCCACGT GCTTGTGCTC CAGGTGTGAC 60
TTGTAAACTG TCTAGTGTTC GCNTTAAATA AAATGGCACC GAGCATAAA 109

SEQ ID NO:1728

LENGTH:329

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01946

SEQUENCE DESCRIPTION:

GATCCGTATC GGTTTAAGAA GCGGACGGAG CTGTTTATTG CCGCCGAGGG CATTACACAG 60
GGCCAGTTTG TGTATTGCGG CAAGAAGGCC CAGCTCAACA TTGGCAATTT GCTCCCTGTG 120
GGCACCATGC CTGAGGGTAC AATCGTGTGC TGCCTGGAGG AGAAGCCTGG AGACCGTGGN 180
AAGCTGGCCC GGGCATCAGG GAACTATGCC ACCGTTATCT CCNACAACCC TGAGACCANG 240
ANGACCCGTG TGNAGNTGCC CTCGGANTCC AAGANGGTTA TNTCCTNAGN CATCAGNGCT 300
GTGGTTGGTG TGGTGGCTGG NGNTNGNCN 329

SEQ ID NO:1729

LENGTH:109

TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS01947

SEQUENCE DESCRIPTION:

GATCTGTCAA TTCTTTTGTN CAGAATGATT TGAAGTATTG TATTCAGTTT ACATGCATTA 60
TTGGNTTATA ATNAATATCT AATGAAAATA CATGTTGTTA TATTGTAAA 109